

Schreiber, David

136374

From: Swope, Sheridan  
Sent: Friday, October 22, 2004 3:41 PM  
To: STIC-Biotech/ChemLib  
Cc: Schreiber, David  
Subject: 09/980,881

Please forward to David Schreiber

David,

For 09/980,881,

pls search and interference search:

SID 9 against the NT and AA data bases, wherein the maximum length of the polypeptide hit is 19 amino acids and the maximum length of the polynucleotide hit is 57 nucleotides.

pls interference search only:

SID 1, residues 18-1097, against the NT and AA data bases  
SID 2 full-length regular and oligo against the NT and AA data bases  
SID 3 full-length regular and oligo against the NT and AA data bases  
SID 4 full-length regular and oligo against the NT and AA data bases

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
E02B71 Remsen Bld (Office)  
E02C70 Remsen Bld (Mailbox)

PD 4/30/99

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 23:09:56 ; Search time 111 Seconds  
(without alignments)  
45.245 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVKKLLPLSLK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 662259

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 23Sep04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	14	3 AAB11461	Aab11461 Human bra
2	35	50.0	9	2 AAY55419	Aay55419 HLA bindi
3	35	50.0	17	2 AAW62069	Aaw62069 Human lun
4	32	45.7	15	5 ABB75868	Abb75868 Human pho
5	31	44.3	14	4 AAM97138	Aam97138 Human pep
6	31	44.3	18	5 ABG71595	Abg71595 S. cerevi
7	30	42.9	14	3 AAB26736	Aab26736 ATM kinas
8	30	42.9	14	3 AAB24149	Aab24149 Rat megli
9	30	42.9	14	4 AAG64287	Aag64287 Rat megli
10	30	42.9	15	6 ABR30640	Abr30640 Human can
11	30	42.9	15	6 ABR30899	Abr30899 Human can
12	30	42.9	15	6 ABR31213	Abr31213 Human can
13	30	42.9	15	6 ABR31621	Abr31621 Human can
14	29	41.4	10	7 ADD94616	Add94616 Human SIM
15	29	41.4	14	2 AAW48905	Aaw48905 Cyclic pe
16	29	41.4	15	4 AAB84887	Aab84887 Human gal
17	29	41.4	15	5 ABG99831	Abg99831 Conus sp
18	29	41.4	17	8 ADK12493	Adk12493 Antigenic
19	29	41.4	18	2 AAR49494	Aar49494 PAI-1 pos
20	29	41.4	19	2 AAW5054	Aaw5054 E. tenell
21	28	40.0	5	5 AAG69227	Abg69227 Protein S
22	28	40.0	5	7 ADE44908	Ade44908 Structura
23	28	40.0	8	4 AAM22269	Aam22269 HIV pepti
24	28	40.0	8	4 ABP13991	Abp13991 HIV A02 s
25	28	40.0	8	4 ABP16394	Abp16394 HIV A24 s

26	28	40.0	9	4 AAM23273	Aam23273 HIV pepti
27	28	40.0	9	4 AAM22955	Aam22955 HIV pepti
28	28	40.0	9	4 AAM22911	Aam22911 HIV pepti
29	28	40.0	9	4 AAM23272	Aam23272 HIV pepti
30	28	40.0	9	4 AAM23288	Aam23288 HIV pepti
31	28	40.0	9	4 AAM23288	Aam23288 HIV pepti
32	28	40.0	9	4 AAM23274	Aam23274 HIV pepti
33	28	40.0	9	4 AAM23271	Aam23271 HIV pepti
34	28	40.0	9	4 AAM22257	Aam22257 HIV pepti
35	28	40.0	9	4 ABP14004	Abp14004 HIV A02 s
36	28	40.0	9	6 ABR58752	Abt58752 Alzheimer
37	28	40.0	9	7 ADC71090	Adc71090 HLA motif
38	28	40.0	9	7 ADC70982	Adc70982 HLA motif
39	28	40.0	9	8 ADN32071	Adn32071 Human Alz
40	28	40.0	9	8 ADN63663	Adn63663 HLA bindi
41	28	40.0	10	2 AAY45249	Aay45249 HIV-1 (la
42	28	40.0	10	4 ABP21883	Abp21883 HIV A03 m
43	28	40.0	10	4 ABP23711	Abp23711 HIV A11 m
44	28	40.0	10	4 ABP16403	Abp16403 HIV A24 s
45	28	40.0	10	4 ABP14009	Abp14009 HIV A02 s

ALIGNMENTS

RESULT 1  
AAB11461  
ID AAB11461 standard; protein; 14 AA.  
XX  
AC AAB11461;  
XX  
DT 01-MAR-2001 (first entry)  
XX  
DE Human brain carboxypeptidase B protein SEQ ID NO 9.  
XX  
KW Carboxypeptidase B; human; brain; hippocampus; APP cleavage; peptidase;  
KW treatment; Alzheimer's disease; beta-amyloid precursor protein; vaccine;  
KW cerebroprotective; antialzheimers; nootropic; neuroprotective;  
KW hemostatic; gene therapy; senile dementia; inherited cerebral hemorrhage;  
KW Down's syndrome; head trauma.  
XX  
OS Homo sapiens.  
XX  
PN WO200066717-AL.  
XX  
PD 09-NOV-2000.  
XX  
PF 01-MAY-2000; 2000WO-JP002878.  
XX  
PR 30-APR-1999; 99JP-00125169.  
XX  
PA (MATS/) MATSUMOTO A.  
XX  
PI Matsumoto A;  
XX  
DR WPI; 2000-687534/67.  
XX  
PT Human brain carboxypeptidase B isolated from the hippocampus useful for  
PT screening agents for the treatment of Alzheimer's and other brain  
PT disorders.  
XX  
PS Example 4; Page 78; 84pp; Japanese.  
XX  
CC This invention describes a novel protein with peptidase activity against  
CC brain beta-amyloid precursor protein which has been isolated from human  
CC hippocampus and which has cerebroprotective, antialzheimers, nootropic,  
CC neuroprotective and hemostatic activity and which can be used as a  
CC vaccine or for gene therapy. The protein, and compounds identified by  
CC screening as promoters or inhibitors of its activity, are used to  
CC regulate beta-amyloid accumulation in the brain and treat or prevent  
CC diseases in which this occurs, such as Alzheimer's, senile dementia,  
CC inherited cerebral hemorrhage, Down's syndrome, and head trauma  
XX

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SQ      Sequence 14 AA;
Query Match      100.0%; Score 70; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNPPVEKLLPLSLK 14
        |||||
Db      1 SNPPVEKLLPLSLK 14

RESULT 2
AAVS5419
ID      AAVS5419 standard; peptide; 9 AA.
XX
AC      AAVS5419;
XX
DT      17-JAN-2000 (first entry)
XX
DE      HLA binding plu-1 peptide.
XX
KW      Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
KW      breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
KW      therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
PN      WO9949034-A1.
XX
PD      30-SEP-1999.
XX
PF      19-MAR-1999; 99WO-GB000866.
XX
PR      20-MAR-1998; 98CB-00005877.
XX
PA      (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI      Taylor-Papadimitriou J;
XX
DR      WPI; 1999-591090/50.
XX
PT      New nucleic acid encoding the cancer-associated polypeptide plu-1, for
PT      diagnosis, treatment and prevention of cancer, especially of breast and
PT      ovary.
XX
PS      Example 2; Fig 12; 173pp; English.
XX
CC      The invention relates to a human cancer-associated polypeptide plu-1. The
CC      plu-1 polypeptide can be recombinantly expressed by standard recombinant
CC      methodology. Detection of the plu-1 nucleic acid or the polypeptide is
CC      used for the following: (i) diagnosis (including imaging) and prognosis
CC      of, and determination of susceptibility to, cancer, specifically ovarian
CC      or breast cancer; and ii) treating cancer (by inducing an immune response
CC      against cancer cells, e.g. as a vaccine, or by antisense inhibition).
CC      Antigens derived from the polypeptide are used to generate activated
CC      cytotoxic T lymphocytes, or dendritic cells, for subsequent return to the
CC      patient for treatment of cancer. The polypeptide may also be used to
CC      identify inhibitors of plu-1 activity. Fragments of the polypeptide, and
CC      antibodies raised against plu-1, are useful as assay and imaging agents,
CC      also therapeutically (to induce an anti-idiotypic response or where
CC      conjugated to cytotoxic agents). The plu-1 antigen is expressed more
CC      commonly in breast tumors than some known tumor antigens. Sequences
CC      AAV55320-629 represent predicted peptides from the plu-1 polypeptide which
CC      may bind to the human class I alleles B27, A2, A3 and A11
XX
SQ      Sequence 9 AA;
Query Match      50.0%; Score 35; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PVEKLLPL 11
        |||
Db      1 PVEKLLPL 11

us-09-980-881a-9.rag
Db      1 PLEXILPL 8
        |:|:|
RESULT 3
AAW62069
ID      AAW62069 standard; peptide; 17 AA.
XX
AC      AAW62069;
XX
DT      14-SEP-1998 (first entry)
XX
DE      Human lung tissue gene LU103 protein fragment 1.
XX
KW      Human; lung tissue gene; LU103; detection; lung cancer; diagnosis.
XX
OS      Homo sapiens.
XX
PN      WO9820143-A1.
XX
PD      14-MAY-1998.
XX
PF      05-NOV-1997; 97WO-US020680.
XX
PR      05-NOV-1996; 96US-00744211.
XX
PA      (ABBO ) ABBOTT LAB.
XX
PI      Cohen M, Friedman PN, Gordon J, Hodges SC, Klass MR;
PI      Kratochvill JD, Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR      WPI; 1998-286957/25.
XX
PT      Lung tissue derived polynucleotide LU103 - useful to detect, diagnose,
PT      stage, monitor, prognose, prevent, treat or determine pre-disposition to
PT      lung disease, e.g. lung cancer.
XX
PS      Disclosure; Page 70; 86pp; English.
XX
CC      The present sequence represents a protein fragment from lung tissue gene
CC      LU103. A method has been developed for detecting the presence of a target
CC      LU103 polynucleotide in a test sample, comprising: (a) contacting the
CC      sample with at least 1 LU103-specific polynucleotide, and (b) detecting
CC      the target LU103 polynucleotide in the test sample, where the LU103
CC      polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519
CC      bp nucleic acid sequence given in AAV38066 to AAV38070. The methods and
CC      products of the present invention may be used to detect, diagnose, stage,
CC      monitor, prognose, prevent, treat or determine the predisposition
CC      diseases and conditions of the lung, e.g. lung cancer
XX
SQ      Sequence 17 AA;
Query Match      50.0%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 74;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      4 PVEKLLPLSL 13
        ||:|
Db      6 PVDKLAFLPL 15

RESULT 4
ABB75868
ID      ABB75868 standard; peptide; 15 AA.
XX
AC      ABB75868;
XX
DT      01-JUL-2002 (first entry)
XX
DE      Human phospholipase 9 peptide fragment.
XX
KW      Phospholipase; human; enzyme; tumour; haemopathy; HIV infection;
KW      immunological disease; inflammation; antitumour; haemostatic; anti-HIV;

```



virucide; immunomodulatory; antiinflammatory; gene therapy.

Homo sapiens.

WO200183537-A1.

08-NOV-2001.

28-APR-2001; 2001WO-CN000629.

29-APR-2000; 2000CN-00115568.

(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

Mao Y, Xie Y;

WPI; 2002-055456/07.

Human phospholipase 9 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammations.

Example 5; Page 19; 39pp; Chinese.

The present invention relates to human phospholipase 9 (see ABB75867).

The enzyme and its coding sequence are useful in the diagnosis and treatment of malignant tumor, haemopathy, HIV infection, immunological diseases and various inflammations (all claimed). The present sequence is an N-terminal peptide fragment of the phospholipase, which was used in a method from the invention

Sequence 15 AA;

Query Match 45.7%; Score 32; DB 5; Length 15;  
Best Local Similarity 85.7%; Pred. NO. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVEKLP 10  
DB 7 PVEKLP 13

RESULT 5

AA97138

ID AA97138 standard; peptide; 14 AA.

AC AA97138;

XX 24-JAN-2002 (first entry)

DE Human peptide #413 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiotensin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease.

OS Homo sapiens.

XX WO200147944-A2.

PN 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

PF 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;  
XX WPI; 2001-465210/50.  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.  
XX Disclosure; Page 3758; 4143pp; English.  
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases.  
XX The present sequence is a peptide encoded by one such oligonucleotide.  
XX The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms

Sequence 14 AA;

Query Match 44.3%; Score 31; DB 4; Length 14;  
Best Local Similarity 46.2%; Pred. NO. 2.8e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPPVEKLLPLSL 13  
DB 2 SNPKGSGMQPISL 14

RESULT 6

ABG71595

ID ABG71595 standard; peptide; 18 AA.

XX AC ABG71595;

XX 08-JAN-2003 (first entry)

DE S. cerevisiae peptide useful for replacing G. multiflorum rGel Y4.

XX Modified protein; reduced antigenicity; modified toxin; gelonin; designer toxin; immunotoxin; proteinaceous compound; cancer; microbial pathogenesis; acquired immunodeficiency syndrome; AIDS; autoimmune disease; hyperproliferative disorder; leukaemia; arthritis; inflammatory disease; cardiovascular disease; diabetes; pathogenic disease; cytostatic; antiarthritic; antiinflammatory; cardiant; antidiabetic; virucide; protozoacide; fungicide; recombinant gelonin; rGel; antigenic; Y4.

XX Saccharomyces cerevisiae.

XX WO200269886-A2.

PN 12-SEP-2002.

XX 12-FEB-2002; 2002WO-US004195.

PF 12-FEB-2001; 2001US-0268402P.

PR (RERE-) RES DEV FOUND.

XX Rosenblum MG, Cheung L;

XX WPI; 2002-750431/81.

XX Generating a modified protein with reduced antigenicity for treating  
 PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region  
 PT antigenic in the first subject using antiserum from either the first or a  
 PT second subject.

XX Example 3; Page 114; 176pp; English.

CC The present invention relates to a method of generating a modified  
 CC protein with reduced antigenicity while maintaining its biological  
 CC activity. The method comprises identifying a region of the protein that  
 CC is antigenic in a first subject using antiserum from either the first  
 CC subject or a second subject of the same species as the first subject. In  
 CC particular the invention discloses modified toxin compounds, for example  
 CC gelonin toxin derived from Gelonium multiflorum, that are truncated  
 CC and/or possess reduced antigenicity. Such designer toxins have  
 CC immunotoxins. The method, and preventative benefits, particularly as  
 CC proteinaceous compounds with less antigenicity. The immunotoxin and  
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,  
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,  
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall  
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The  
 CC compositions of the invention are also useful for treating microbial  
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune  
 CC diseases, hyperproliferative disorders including cancer, leukaemias,  
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic  
 CC diseases, and diabetes. The method provides less antigenic proteins,  
 CC peptides and polypeptides, which are more effective than prior art. The  
 CC present sequence represents a potential replacement peptide for G.  
 CC multiflorum recombinant gelonin (rGel) antigenic sequence Y4

XX Sequence 18 AA;

Query Match 44.3%; Score 31; DB 5; Length 18;  
 Best Local Similarity 58.3%; Pred. No. 3.7e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLSLK 14  
 ||| : |||  
 Db 6 PLVESVIVLSLK 17

RESULT 7  
 AAB26736  
 ID AAB26736 standard; peptide; 14 AA.

XX AAB26736;

XX 12-JAN-2001 (first entry)

DE ATM kinase substrate recognition peptide SEQ ID 31.

XX Ataxia telangiectasia-mutated; ATM; kinase; ataxia telangiectasia;  
 KW tumour; cardiovascular disease; restenosis; revascularisation; obesity;  
 KW retroviral infection; HIV; human T cell leukaemia virus; HTLV.

XX Unidentified.

XX WO200047760-A2.

XX 17-AUG-2000.

XX 09-FEB-2000; 2000WO-US003386.

XX 10-FEB-1999; 99US-00248061.

XX 21-SEP-1999; 99US-00400653.

XX (SUJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
 PA (UYJO ) UNIV JOHNS HOPKINS.

XX Kastan M, Canman C, Kim S, Lim D;

DR WPI; 2000-559218/51.

XX Identifying proteins with ataxia telangiectasia-mutated kinase substrate  
 PT recognition sequences, useful for investigating ATM kinase specificity  
 PT and treating human T cell leukemia virus.

XX Example 3; Page 77; 106pp; English.

CC This invention relates to a method for identifying an ataxia  
 CC telangiectasia-mutated (ATM) kinase substrate recognition sequence in a  
 CC protein. The method comprises contacting an ATM kinase with a fusion  
 CC peptide containing a structural portion and a candidate ATM kinase  
 CC substrate recognition sequence, where the fusion protein does not contain  
 CC a sequence of 14 amino acids represented in AAB26709 which is a p53  
 CC derived ATM kinase substrate peptide. Ataxia telangiectasia (AT) is a  
 CC rare autosomal recessive multi-system disorder, one of the clinical  
 CC manifestations is an increased risk of cancer. The gene mutated in AT,  
 CC ATM is related to the phosphatidylinositol 3-kinase (PI-3-K) family of  
 CC proteins. The method of the invention can be used to investigate ATM  
 CC kinase specificity and to identify ATM target proteins other than p53.  
 CC The modulation of ATM activity may be used to treat cancer (e.g. to  
 CC radiosensitise tumours), cardiovascular disease (e.g. restenosis),  
 CC revascularisation, obesity and retroviral infections (e.g. HIV and  
 CC especially human T cell leukaemia virus (HTLV). The present sequence  
 CC represents an ATM kinase substrate recognition peptide sequence  
 CC identified in the invention

XX Sequence 14 AA;

Query Match 42.9%; Score 30; DB 3; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 4.1e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12  
 ||| : |||  
 Db 4 PPVSQELPCS 13

RESULT 8  
 AAB24149  
 ID AAB24149 standard; peptide; 14 AA.

XX AAB24149;

XX 30-JAN-2001 (first entry)

DE Rat megin domain peptide SEQ ID NO:17.

XX Megsin; mesangium-predominant gene; serpin regulated; nephropathy; IGA;  
 KW immunoglobulin A; detection; renal function; renal disorder; diagnosis;  
 KW biological sample; blood; urine.

OS Rattus norvegicus.

XX WO200057189-A1.

XX 28-SEP-2000.

XX 17-MAR-2000; 2000WO-JP001646.

XX 19-MAR-1999; 99JP-00075305.

XX 28-OCT-1999; 99JP-00306623.

XX (KURO/) KUROKAWA K.

XX (FUSO ) FUSO PHARM IND LTD.

XX (MIYA/) MIYATA T.

XX Miyata T;

XX WPI; 2000-611642/58.

XX Evaluating renal function comprises assaying megin protein in biological  
 PT sample.

XX PS Example 2; Page 29; 93pp; Japanese.

XX CC The present invention describes a method for evaluating renal function.

CC The method comprises assaying megin protein in biological sample. Also

CC described are: (1) use of an anti-megsin protein antibody for diagnosing

CC renal function; and (2) a kit for detecting megin protein comprising:

CC (a) anti-megsin protein antibody attached to solid magnetic particles; (b)

CC direct or indirect fixing for the antibody to the particles; and (c) a

CC magnet. The process is useful for evaluating renal function and

CC diagnosing renal disorders by assaying megin protein in biological

CC samples (preferably urine or blood). The process is reproducible and

CC gives accurate results. The present sequence represents a rat megin

CC domain peptide, which is used in an example from the present invention

XX SQ Sequence 14 AA;

Query Match 42.9%; Score 30; DB 3; Length 14;

Best Local Similarity 87.5%; Pred. No. 4.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 VEKLLPLS 12

DB 5 VEKLLPES 12

RESULT 9

AAG64287

ID AAG64287 standard; peptide; 14 AA.

XX AC AAG64287;

XX DT 21-SEP-2001 (first entry)

XX DE Rat megin peptide fragment.

XX KW Rat; megin; renal mesangial cell; mesangium proliferative nephritis.

XX OS Rattus norvegicus.

XX PN WO200148019-A1.

XX PD 05-JUL-2001.

XX PF 26-DEC-2000; 2000WO-JP009251.

XX PR 28-DEC-1999; 99JP-00373677.

XX PA (KURO/) KUROKAWA K.

XX PA (MIYA/) MIYATA T.

XX PI Miyata T;

XX DR WPI; 2001-425651/45.

XX PT New antibody recognizing a partial sequence of rat megin protein for

PT diagnosis of mesangium proliferative nephritis.

XX PS Claim 1; Page 29; 63pp; Japanese.

XX CC The present invention relates to a novel antibody which recognises a

CC peptide (the present sequence) consisting of residues 341-354 of rat

CC megin protein. Megsin is highly expressed in renal mesangial cells and

CC its level is elevated in mesangium proliferative nephritis. Assay of the

CC serum or urine level using the antibody is therefore indicative of this

CC type of disorder. For the full-length rat megin protein see AAG64286

XX SQ Sequence 14 AA;

Query Match 42.9%; Score 30; DB 4; Length 14;

Best Local Similarity 87.5%; Pred. No. 4.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 VEKLLPLS 12

DB 5 VEKLLPES 12

RESULT 10

ABR30640

ID ABR30640 standard; peptide; 15 AA.

XX AC ABR30640;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 83P4B8 HLA peptide #1702.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and

PT diagnostic reagents for eliciting cellular or humoral immune response in

PT cancer patients.

XX PS Claim 13; Page 478; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention

XX SQ Sequence 15 AA;

Query Match 42.9%; Score 30; DB 6; Length 15;

Best Local Similarity 50.0%; Pred. No. 4.5e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 NPPVEKLLPLSL 13

DB 1 NQPVKAIIMQL 12

RESULT 11

ABR30899

ID ABR30899 standard; peptide; 15 AA.

XX AC ABR30899;

```

XX 19-MAY-2003 (first entry)
XX Human cancer-related protein 83P4B8 HLA peptide #1961.
DE Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
OS
XX WO200283921-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011654.
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX Claim 13; Page 483; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX SQ Sequence 15 AA;
XX Query Match 42.9%; Score 30; DB 6; Length 15;
XX Best Local Similarity 50.0%; Pred. No. 4.5e+02;
XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 2 NPPVEKLLPLSL 13
DB 1 NQPVKAIIMQL 12
RESULT 12
ABR31213
ID ABR31213 standard; peptide; 15 AA.
XX AC ABR31213;
XX 19-MAY-2003 (first entry)
XX Human cancer-related protein 83P4B8 HLA peptide #2275.
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
OS
XX WO200283921-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011654.
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX Claim 13; Page 483; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX SQ Sequence 15 AA;
XX Query Match 42.9%; Score 30; DB 6; Length 15;
XX Best Local Similarity 50.0%; Pred. No. 4.5e+02;
XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 2 NPPVEKLLPLSL 13
DB 1 NQPVKAIIMQL 12
RESULT 13
ABR31621
ID ABR31621 standard; peptide; 15 AA.
XX AC ABR31621;
XX 19-MAY-2003 (first entry)
XX Human cancer-related protein 83P4B8 HLA peptide #2683.
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
OS
XX WO200283921-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011654.
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX Claim 13; Page 488; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX SQ Sequence 15 AA;
XX Query Match 42.9%; Score 30; DB 6; Length 15;
XX Best Local Similarity 50.0%; Pred. No. 4.5e+02;
XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 2 NPPVEKLLPLSL 13
DB 1 NQPVKAIIMQL 12

```

PA (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX WPI; 2003-075555/07.  
DR  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
XX Claim 13; Page 495; 1021pp; English.  
XX  
XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 42.9%; Score 30; DB 6; Length 15;  
Best Local Similarity 50.0%; Pred. No. 4.5e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 NPPVEKLLPLSL 13  
DB 4 NQPEKAIIMQL 15  
RESULT 14  
ADD94616  
ID ADD94616 standard; peptide; 10 AA.  
XX  
XX ADD94616;  
AC  
XX 29-JAN-2004 (first entry)  
DT  
XX Human SIMP-derived peptide 136.  
DE  
XX source of immunodominant MHC-associated peptide; SIMP; MHC;  
KW major histocompatibility complex; human leukocyte antigen; HLA;  
KW cytostatic; immunosuppressive; antisense therapy; gene therapy; cancer;  
KW lung cancer; intestine cancer; sarcoma; prostate cancer;  
KW testicular cancer; breast cancer; melanomas; pancreatic cancer;  
KW haematological cancer; immune response; lymphoid cell proliferation;  
KW autoimmune disease; transplant rejection; SIMP-derived peptide; human.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W02003054008-A2.  
PN  
XX  
XX 03-JUL-2003.  
PD  
XX  
XX 18-DEC-2002; 2002WO-CA001967.  
PF  
XX  
XX 20-DEC-2001; 2001US-00028384.  
PR  
XX  
XX (COMP-) COMPATIGENE INC.  
PA  
XX  
XX Perreault C, McBride K;  
PI  
XX WPI; 2003-559122/52.  
DR  
XX  
XX New human source of immunodominant MHC-associated peptide (SIMP) nucleic  
PT acids and proteins, useful for diagnosing and treating cancers, e.g. lung  
or breast cancer, or for suppressing an immune response in an autoimmune  
disease.  
XX  
XX Claim 24; Page 19; 66pp; English.  
XX  
XX This invention relates to a novel isolated or purified human protein, termed source of immunodominant major histocompatibility complex (MHC)-associated peptide (SIMP), which is expressed ubiquitously in human cells, where the protein has the potential of generating several protein fragments binding with high affinity to a human leukocyte antigen (HLA) molecule. The invention may allow development of therapeutics with cytostatic or immunosuppressive activity or provide sequences useful for antisense therapy or gene therapy. The source of immunodominant MHC-associated peptide (SIMP) nucleic acids, proteins and fragments are useful for diagnosing and treating cancers, for example lung cancer, breast cancer, melanomas, pancreatic cancer or haematological cancer. The SIMP proteins are also useful for modulating an immune response. Decreasing lymphoid cell proliferation is useful for suppressing an immune response responsible for an autoimmune disease or a transplant rejection. The present sequence is that of a human SIMP-derived peptide (with a high affinity binding motif for HLA molecules) of the invention.  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 41.4%; Score 29; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NPPVE 6  
DB 4 NPPVE 8  
RESULT 15  
AAW48905  
ID AAW48905 standard; peptide; 14 AA.  
XX  
XX AAW48905;  
AC  
XX 23-SEP-1998 (first entry)  
DT  
XX Cyclic peptide gramicidin S14 analogue Y2/F2 V3/L3.  
DE  
XX Cyclic; gramicidin S; GS; beta-pleated structure; therapeutic index; hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi; mycoplasma; food additive; antimicrobial activity.  
KW  
KW Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..14 /note= "Residue 1 is in a peptide linkage with residue 14"  
FT Misc-difference 4 /note= "D-form residue"  
FT Misc-difference 6 /note= "D-form residue"  
FT Misc-difference 13 /note= "D-form residue"  
FT  
XX W09816549-A1.  
PN  
XX  
XX 23-APR-1998.  
PD  
XX  
XX 10-OCT-1997; 97WO-US018693.  
PF  
XX  
XX 11-OCT-1996; 96US-0028315P.  
PR  
XX  
XX (PENC-) PENCE INC.  
PA  
XX (DEHL/) DEHLINGER P J.  
PT

PI Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, McElhaney R;  
PI Premier EJ, Lewis RNAH;  
XX  
XX WPI; 1998-251231/22.  
XX  
XX Cyclic peptide analogues of gramicidin S with broad spectrum  
PT antimicrobial activity - and reduced haemolytic activity, have beta-  
PT plated sheet structure disrupted or eliminated by amino acid  
PT substitutions.  
XX  
XX  
PS Disclosure; Page 45; 88pp; English.  
XX  
XX The invention provides for cyclic peptide analogues of gramicidin S14  
CC (GS14; AAM48876), such as the present one. These cyclic peptide GS14  
CC analogues do not have the beta-pleated structure present in Gramicidin S  
CC (GS). These analogues are claimed to have an advantage over GS as they  
CC have broad spectrum antimicrobial activity and an increased therapeutic  
CC index because they lack the hemolytic effect of GS. The cyclic peptide  
CC GS14 analogues are also claimed to be useful therapeutically in human or  
CC veterinary medicine to kill or inhibit Gram-positive and -negative  
CC bacteria, fungi and mycoplasma. They may also be used to control  
CC mycoplasma contamination of cultured cells and as food additives  
XX  
XX  
SQ Sequence 14 AA;  
  
Query Match 41.4%; Score 29; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 6.1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 KLLPLSLK 14  
|||  
Db 4 KLFPLKX 11  
  
Search completed: October 27, 2004, 01:02:51  
Job time : 116 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 00:54:50 ; Search time 42 Seconds  
(without alignments)  
22.106 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLPLSLK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 179518

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/6CTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	50.0	17	2	US-08-964-725-15
2	33	47.1	12	4	US-09-007-288E-88
3	30	42.9	14	3	US-09-400-653A-31
4	30	42.9	14	3	US-09-248-061B-27
5	29	41.4	18	2	US-08-480-190-204
6	29	41.4	18	2	US-08-488-379-204
7	29	41.4	18	4	US-08-475-399A-204
8	29	41.4	18	4	US-08-077-255A-204
9	29	41.4	18	5	PCT-US93-07545-204
10	28	40.0	5	1	US-08-477-509B-13
11	28	40.0	5	3	US-08-482-085B-13
12	28	40.0	5	3	US-09-444-791A-13
13	28	40.0	15	1	US-08-230-047-31
14	28	40.0	15	3	US-09-141-882A-10
15	28	40.0	15	3	US-09-452-142-10
16	28	40.0	17	4	US-09-355-398C-2
17	28	40.0	18	4	US-09-355-398C-5
18	28	40.0	19	3	US-08-943-173-8
19	27	38.6	10	3	US-08-836-561-51
20	27	38.6	10	4	US-09-434-122-51
21	27	38.6	16	1	US-08-185-432-14
22	27	38.6	16	4	US-09-715-923-8
23	26.5	37.9	16	3	US-08-602-999A-204
24	26.5	37.9	16	4	US-09-500-124-204
25	26	37.1	9	1	US-08-615-181-100
26	26	37.1	10	4	US-08-983-157B-8
27	26	37.1	10	4	US-09-653-465B-11

Sequence 15, Appl  
Sequence 15, Appl  
Sequence 519, Appl  
Sequence 43, Appl  
Sequence 121, Appl  
Sequence 79, Appl  
Sequence 79, Appl  
Sequence 1, Appl  
Sequence 100, Appl  
Sequence 156, Appl  
Sequence 322, Appl  
Sequence 156, Appl  
Sequence 33, Appl  
Sequence 71, Appl  
Sequence 34, Appl

ALIGNMENTS

RESULT 1  
US-08-964-725-15  
; Sequence 15, Application US/08964725  
; Patent No. 5939265  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STROUPE, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,725  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5997.US.PI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: No. 5939265e
US-08-964-725-15

Query Match      50.0%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLSL 13
Db 6 PVDKLAFLPL 15

RESULT 2
US-09-007-288E-88
; Sequence 88, Application US/09007288E
; Patent No. 6495357
; GENERAL INFORMATION:
; APPLICANT: Fuglsang, Claus
; APPLICANT: Okkels, Jens
; APPLICANT: Petersen, Dorte
; APPLICANT: Patkar, Shamkant
; APPLICANT: Thellersen, Marianne
; APPLICANT: Svenden, Allan
; APPLICANT: Borch, Kim
; APPLICANT: Royer, John
; APPLICANT: Kretschmar, Titus
; APPLICANT: Halkier, Torben
; APPLICANT: Vind, Jesper
; APPLICANT: Jorgensen, Steen
; TITLE OF INVENTION: No. 6495357e1 Lipolytic Enzymes
; FILE REFERENCE: 4455-404-US
; CURRENT APPLICATION NUMBER: US/09/007,288E
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide addition
US-09-007-288E-88

Query Match      47.1%; Score 33; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 3 PPRRLPLFIS 12

RESULT 3
US-09-400-653A-31
; Sequence 31, Application US/09400653A
; Patent No. 6348311
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/1F142
; CURRENT APPLICATION NUMBER: US/09/400,653A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-400-653A-31

Query Match      42.9%; Score 30; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 4 PPVSQELPCS 13

RESULT 4
US-09-248-061B-27
; Sequence 27, Application US/09248061B
; Patent No. 6387640
; GENERAL INFORMATION:
; APPLICANT: Kastan, M.
; APPLICANT: Canman, C.
; APPLICANT: Kim, S-T.
; APPLICANT: Lim, D-S.
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/0F142
; CURRENT APPLICATION NUMBER: US/09/248,061B
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-248-061B-27

Query Match      42.9%; Score 30; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 4 PPVSQELPCS 13

RESULT 5
US-08-480-190-204
; Sequence 204, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

```



APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 204:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-204

Query Match 41.4%; Score 29; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLLPLS 12  
| | | | : | | |  
Db 3 PYKEVPLS 11

RESULT 6  
US-08-488-379-204  
Sequence 204, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 204:  
SEQUENCE CHARACTERISTICS:

LENGTH: 18  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-204

Query Match 41.4%; Score 29; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLLPLS 12  
| | | | : | | |  
Db 3 PYKEVPLS 11

RESULT 7  
US-08-475-399A-204  
Sequence 204, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: Fast-SEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 204:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-204

Query Match 41.4%; Score 29; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLLPLS 12  
| | | | : | | |  
Db 3 PYKEVPLS 11

RESULT 8

US-08-077-255A-204  
; Sequence 204, Application US/08077255A  
; Patent No. 6696061  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/077,255A  
; FILING DATE: June 15, 1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-077-255A-204

Query Match 41.4%; Score 29; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLS 12  
| | | : | | |  
Db 3 PYKEVPLS 11

RESULT 9  
PCT-US93-07545-204  
; Sequence 204, Application PC/TUS9307545  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 273  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts

COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07545  
; FILING DATE: 19930811  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
PCT-US93-07545-204

Query Match 41.4%; Score 29; DB 5; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLS 12  
| | | : | | |  
Db 3 PYKEVPLS 11

RESULT 10  
US-08-477-509B-13  
; Sequence 13, Application US/08477509B  
; Patent No. 5770697  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W  
; APPLICANT: Dorman, Mary A  
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,509B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-13

Query Match 40.0%; Score 28; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7  
Db 1 PPVEK 5

RESULT 11  
US-08-482-085B-13  
Sequence 13, Application US/08482085B  
Patent No. 6018030  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James  
APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,085B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-085B-13

Query Match 40.0%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7  
Db 1 PPVEK 5

RESULT 12  
US-09-444-791A-13  
Sequence 13, Application US/09444791A  
Patent No. 6355776  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James  
APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,791A  
FILING DATE: 22-NO. 6355776-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-444-791A-13

Query Match 40.0%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEK 7  
Db 1 PPVEK 5

RESULT 13

US-08-230-047-31  
Sequence 31, Application US/08230047  
Patent No. 5541109  
GENERAL INFORMATION:  
APPLICANT: Searfoss III, George H.  
APPLICANT: Iwashchenko, Yuri D.  
APPLICANT: Jaye, Michael C.  
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcoia Road, 3c43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/230,047  
FILING DATE: 19-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A1465-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3817  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

Query Match 40.0%; Score 28; DB 1; Length 15;  
Best Local Similarity 44.4%; Pred. No. 1.7e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLPL 11  
Db 6 PPLPQFLPW 14

RESULT 14

US-09-141-882A-10  
Sequence 10, Application US/09141882A  
Patent No. 6022540  
GENERAL INFORMATION:  
APPLICANT: Bruder, S. and Jaiswal, N.  
TITLE OF INVENTION: Ligands That Modulate  
TITLE OF INVENTION: Differentiation of Mesenchymal Stem Cells  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/141.882A  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/057,928  
FILING DATE: September 4, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: SEMIONOW, R.  
REGISTRATION NUMBER: 39,022  
REFERENCE/DOCKET NUMBER: 640100-249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: peptide

Query Match 40.0%; Score 28; DB 3; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NPPVEKLL 9  
Db 6 NPPPEEFL 13

RESULT 15

US-09-452-142-10  
Sequence 10, Application US/09452142  
Patent No. 6379553  
GENERAL INFORMATION:  
APPLICANT: Bruder, S. and Jaiswal, N.  
TITLE OF INVENTION: Ligands That Modulate  
TITLE OF INVENTION: Differentiation of Mesenchymal Stem Cells  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2

Thu Oct 28 07:16:18 2004

OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/452,142  
FILING DATE: 01-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/141,882  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SEMIONOW, R.  
REGISTRATION NUMBER: 39,022  
REFERENCE/DOCKET NUMBER: 640100-249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS: <Unknown>  
TOPOLOGY: LINEAR  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-452-142-10

Query Match 40.0%; Score 28; DB 3; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NPPVEXLL 9  
Db 6 NPPPEEFL 13

Search completed: October 27, 2004, 01:06:58  
Job time : 45 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:05:26 ; Search time 1033 Seconds  
(without alignments)  
4.388 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62

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Searched: 1364641 seqs, 323758627 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	33	47.1	12	14	US-10-232-544-88
3	30	42.9	14	14	US-10-024-123-31
4	29	41.4	15	14	US-10-072-602B-616
5	29	41.4	17	15	US-10-378-089-1
6	28	40.0	5	14	US-10-096-986-13
7	28	40.0	8	15	US-10-182-252A-154
8	28	40.0	9	15	US-10-264-309-397
9	28	40.0	9	15	US-10-182-252A-142
10	28	40.0	9	15	US-10-182-252A-273
11	28	40.0	9	15	US-10-182-252A-796
12	28	40.0	9	15	US-10-182-252A-840
13	28	40.0	9	15	US-10-182-252A-1156

14	28	40.0	9	15	US-10-182-252A-1157	Sequence 1157, Ap
15	28	40.0	9	15	US-10-182-252A-1158	Sequence 1158, Ap
16	28	40.0	9	15	US-10-182-252A-1159	Sequence 1159, Ap
17	28	40.0	9	15	US-10-182-252A-1173	Sequence 1173, Ap
18	28	40.0	9	16	US-10-415-014-516	Sequence 516, App
19	28	40.0	9	16	US-10-415-014-624	Sequence 624, App
20	28	40.0	10	9	US-09-055-744-5	Sequence 5, Appli
21	28	40.0	10	16	US-10-415-014-572	Sequence 572, App
22	28	40.0	12	9	US-09-055-744-7	Sequence 7, Appli
23	28	40.0	14	14	US-10-148-936-2	Sequence 2, Appli
24	28	40.0	16	16	US-10-481-180-682	Sequence 682, App
25	28	40.0	18	9	US-09-880-713A-9	Sequence 19, Appli
26	28	40.0	18	9	US-09-226-248B-9	Sequence 9, Appli
27	27	38.6	8	15	US-10-182-252A-1296	Sequence 1296, Ap
28	27	38.6	9	15	US-10-182-252A-140	Sequence 140, App
29	27	38.6	9	15	US-10-182-252A-272	Sequence 272, App
30	27	38.6	9	15	US-10-182-252A-884	Sequence 884, App
31	27	38.6	9	15	US-10-182-252A-885	Sequence 885, App
32	27	38.6	9	15	US-10-182-252A-899	Sequence 899, App
33	27	38.6	9	15	US-10-182-252A-900	Sequence 900, App
34	27	38.6	10	14	US-10-283-349-51	Sequence 51, Appli
35	27	38.6	12	9	US-09-997-579-10	Sequence 10, Appli
36	27	38.6	12	14	US-10-360-522-6	Sequence 6, Appli
37	27	38.6	14	9	US-09-826-290-224	Sequence 224, App
38	27	38.6	14	14	US-10-162-134A-3	Sequence 3, Appli
39	27	38.6	14	15	US-10-264-309-47	Sequence 47, Appli
40	27	38.6	16	14	US-10-357-479-8	Sequence 8, Appli
41	27	38.6	17	14	US-10-225-567A-753	Sequence 753, App
42	27	38.6	18	14	US-10-225-567A-752	Sequence 752, App
43	27	38.6	19	9	US-09-997-579-8	Sequence 8, Appli
44	26.5	37.9	16	14	US-10-161-791-204	Sequence 204, App
45	26	37.1	8	9	US-09-055-744-4	Sequence 4, Appli

## ALIGNMENTS

### RESULT 1

US-10-334-726-111  
; Sequence 111, Application US/10334726  
; Publication No. US20030211521A1  
; GENERAL INFORMATION:  
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE  
; TITLE OF INVENTION: BREAST CANCER ANTIGEN  
; FILE REFERENCE: 1090-36  
; CURRENT APPLICATION NUMBER: US/10/334,726  
; CURRENT FILING DATE: 2003-01-02  
; PRIOR APPLICATION NUMBER: US/09/645,446  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: PCT/GB99/00866  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: GB 9805877.9  
; PRIOR FILING DATE: 1998-09-20  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:predicted  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: peptide  
US-10-334-726-111

Query Match 50.0%; Score 35; DB 14; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 PVEKLLPL 11  
|:|:|:|:  
Db 1 PVEKLLPL 8

## RESULT 2

US-10-232-544-88  
; Sequence 88, Application US/10232544  
; Publication No. US20030199069A1  
; GENERAL INFORMATION:  
; APPLICANT: Fugisang, Claus  
; APPLICANT: Okkels, Jens  
; APPLICANT: Petersen, Dorte  
; APPLICANT: Pakkar, Shamkant  
; APPLICANT: Thellersen, Marianne  
; APPLICANT: Svenden, Allan  
; APPLICANT: Borch, Kim  
; APPLICANT: Royer, John  
; APPLICANT: Kretschmar, Titus  
; APPLICANT: Halkier, Torben  
; APPLICANT: Vind, Jesper  
; APPLICANT: Jorgensen, Steen  
; TITLE OF INVENTION: NO. US20030199069A1el Lipolytic Enzymes  
; FILE REFERENCE: 4455.404-US  
; CURRENT APPLICATION NUMBER: US/10/232,544  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US/09/007,288  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide addition  
US-10-232-544-88

Query Match 47.1%; Score 33; DB 14; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12  
Db 3 PPRPRLPLS 12

## RESULT 3

US-10-024-123-31  
; Sequence 31, Application US/10024123  
; Publication No. US20030022263A1  
; GENERAL INFORMATION:  
; APPLICANT: Kastan, Michael  
; APPLICANT: Canman, Christine  
; APPLICANT: Kim, Seong-Tae  
; APPLICANT: Lim, Dae-Sik  
; APPLICANT: St. Jude Children's Research Hospital  
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
; FILE REFERENCE: 2427/1F142  
; CURRENT APPLICATION NUMBER: US/10/024,123  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 09/400,653  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: 09/248,061  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-123-31

Query Match 42.9%; Score 30; DB 14; Length 14;  
Best Local Similarity 60.0%; Pred. No. 4.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy

3 PPVEKLLPLS 12  
Db 4 PPVSQELPCS 13

## RESULT 4

US-10-072-602B-616  
; Sequence 616, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Wren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 616  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Conus flavidus  
US-10-072-602B-616

Query Match 41.4%; Score 29; DB 14; Length 15;  
Best Local Similarity 60.0%; Pred. No. 6.6e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNPPVEKLLP 10  
Db 4 SNPPCSYLNLP 13

## RESULT 5

US-10-378-089-1  
; Sequence 1, Application US/10378089  
; Publication No. US20040052780A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KAZUHISA  
; APPLICANT: KAWAMOTO, SEIJI  
; APPLICANT: GOTO, TAKESHI  
; APPLICANT: SATO, SHUJI  
; APPLICANT: GOTO, SIGERU  
; TITLE OF INVENTION: IMMUNOSUPPRESSANT  
; FILE REFERENCE: 7388/80237  
; CURRENT APPLICATION NUMBER: US/10/378,089  
; CURRENT FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: JP P2002-260681  
; PRIOR FILING DATE: 2002-09-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-378-089-1

Query Match 41.4%; Score 29; DB 15; Length 17;  
Best Local Similarity 55.6%; Pred. No. 7.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



Qy 1 SNPPVEKLL 9  
| : : :  
Db 5 SGPPVSELI 13

RESULT 6

US-10-096-986-13  
; Sequence 13, Application US/10096986  
; Publication No. US20030083464A1  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; Richardson, Charles  
; Chambers, James  
; Causey, Stuart  
; Pollock, Thomas J.  
; Cappello, Joseph  
; Criseman, John W.  
; TITLE OF INVENTION: No US20030083464A1 Peptides Comprising Repetitive  
; Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Flehr Hobbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/096,986  
; FILING DATE: 12-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/444,791  
; FILING DATE: 22-No. US20030083464A1-1999  
; APPLICATION NUMBER: US 08/482,085  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard P.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-096-986-13

Query Match 40.0%; Score 28; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEK 7  
| : : : :  
Db 1 PPVEK 5

RESULT 7

US-10-182-252A-154  
; Sequence 154, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 154  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-154

Query Match 40.0%; Score 28; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5  
| : : : :  
Db 2 SNPPV 6

RESULT 8

US-10-264-309-397  
; Sequence 397, Application US/10264309  
; Publication No. US20040022794A1  
; GENERAL INFORMATION:  
; APPLICANT: DURHAM, L. KATHRYN  
; APPLICANT: FRIEDMAN, DAVID L.  
; APPLICANT: HERATH, HERATH  
; APPLICANT: KIMMEL, LIDA H.  
; APPLICANT: PAREKH, RAJESH B.  
; APPLICANT: POTTER, DAVID M.  
; APPLICANT: ROHLFF, CHRISTIAN  
; APPLICANT: SILBER, B. MICHAEL  
; APPLICANT: SNYDER, PETER J.  
; APPLICANT: SOARES, HOLLY D.  
; APPLICANT: STIGER, THOMAS R.  
; APPLICANT: SUNDERLAND, P. TREY  
; APPLICANT: TOWNSEND, ROBERT R.  
; APPLICANT: WHITE, W. FROST  
; APPLICANT: WILLIAMS, STEPHEN A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,  
; INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
; FILE REFERENCE: POA-002.01  
; CURRENT APPLICATION NUMBER: US/10/264,309  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: 60/326,708  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO 397

Query Match 40.0%; Score 28; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-397

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LPLSLK 14
Db 4 LPLSLK 9

RESULT 9
US-10-182-252A-142
; Sequence 142, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-142

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5
Db 3 SNPPV 7

RESULT 10
US-10-182-252A-273
; Sequence 273, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-273

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5
Db 3 SNPPV 7

RESULT 11
US-10-182-252A-796
; Sequence 796, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 796
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-796

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5
Db 3 SNPPV 7

RESULT 12
US-10-182-252A-840
; Sequence 840, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE

```

```

; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-273

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5
Db 3 SNPPV 7

RESULT 11
US-10-182-252A-796
; Sequence 796, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 796
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-796

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5
Db 3 SNPPV 7

RESULT 12
US-10-182-252A-840
; Sequence 840, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE

```

```

; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-273

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEKL 8
Db 4 PPIERL 9

RESULT 12
US-10-182-252A-840
; Sequence 840, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE

```

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; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 796
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-796

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEKL 8
Db 4 PPIERL 9

RESULT 12
US-10-182-252A-840
; Sequence 840, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE

```

```

; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-840

```

```

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 3 PPVEKL 8
DB 4 PPIERL 9

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```

RESULT 13
US-10-182-252A-1156
; Sequence 1156, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1156

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```

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SNPPV 5
DB 3 SNPPV 7

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RESULT 14
US-10-182-252A-1157
; Sequence 1157, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1157

```

```

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SNPPV 5
DB 3 SNPPV 7

```

```

RESULT 15
US-10-182-252A-1158
; Sequence 1158, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1158

```

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5  
|  
|  
|  
|  
|  
Db 3 SNPPV 7

Search completed: October 27, 2004, 01:30:40  
Job time : 1034 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 21:31:56 ; Search time 1888 Seconds

(without alignments)  
350.665 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1863394

Minimum DB seq length: 0

Maximum DB seq length: 57

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=57  
-USER=US09980881 @CNG\_1\_1\_5600 @runat\_26102004\_083352\_5573 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46	65.7	43	6	AX093019 Sequence
C 2	37	52.9	41	6	AX519039 Sequence
C 3	36	51.4	51	6	CQ001968 Sequence
4	35.5	50.7	39	6	A24246 Oligonucleo

C	5	35	50.0	45	6	CQ767550	Sequence
C	6	35	50.0	45	6	AX201424	Sequence
	7	34	48.6	34	6	AR364159	Sequence
	8	34	48.6	40	6	AR053703	Sequence
	9	34	48.6	40	6	AR258638	Sequence
C	10	34	48.6	40	6	AX107547	Sequence
C	11	34	48.6	41	6	AR036483	Sequence
C	12	34	48.6	41	6	AR069442	Sequence
C	13	34	48.6	41	6	I73464	Sequence 16
	14	34	48.6	48	6	BD243527	Nucleotid
	15	34	48.6	48	6	AX034950	Sequence
	16	34	48.6	51	6	AR077572	Sequence
	17	34	48.6	51	6	AR265635	Sequence
	18	33	47.1	36	6	AR088742	Sequence
	19	33	47.1	36	6	AR095469	Sequence
	20	33	47.1	36	6	AR112470	Sequence
	21	33	47.1	36	6	BD070735	Vectors h
	22	33	47.1	36	6	BD070761	Vectors h
C	23	33	47.1	41	6	AR036485	Sequence
C	24	33	47.1	41	6	AR069444	Sequence
C	25	33	47.1	41	6	I73466	Sequence 18
	26	33	47.1	44	6	BD091851	Novel cyt
	27	33	47.1	44	6	BD091885	Novel cyt
C	28	33	47.1	46	6	AI6157	Primer. 10/
C	29	33	47.1	48	9	HS3B3VB19	X84265 H.sapiens m
C	30	33	47.1	48	9	HSU14066	Human cell
C	31	33	47.1	48	9	HSU14068	Human cell
C	32	33	47.1	50	6	CQ002840	Sequence
C	33	33	47.1	51	6	CQ003669	Sequence
C	34	33	47.1	51	6	AX165250	Sequence
C	35	33	47.1	51	6	AX190175	Sequence
	36	32	45.7	20	6	AX379575	Sequence
C	37	32	45.7	23	6	AX587292	Sequence
	38	32	45.7	32	6	BD061431	Novel pol
	39	32	45.7	33	6	AR368900	Sequence
	40	32	45.7	33	6	AR422234	Sequence
C	41	32	45.7	39	10	S86280	TCR V beta
C	42	32	45.7	47	6	AR291010	Sequence
C	43	32	45.7	51	6	CQ001695	Sequence
	44	32	45.7	51	6	AX162153	Sequence
	45	32	45.7	51	6	AX162154	Sequence

ALIGNMENTS

RESULT 1	AX093019/c	AX093019	Sequence 24 from Patent WO0118192.	43 bp	DNA	linear	PAT 30-MAR-2001
LOCUS	AX093019	AX093019	AX093019.1	GI:13509494			
DEFINITION	AX093019	AX093019	AX093019.1	GI:13509494			
ACCESSION	AX093019	AX093019	AX093019.1	GI:13509494			
VERSION	AX093019	AX093019	AX093019.1	GI:13509494			
KEYWORDS	AX093019	AX093019	AX093019.1	GI:13509494			
SOURCE	AX093019	AX093019	AX093019.1	GI:13509494			
ORGANISM	AX093019	AX093019	AX093019.1	GI:13509494			
REFERENCE	AX093019	AX093019	AX093019.1	GI:13509494			
AUTHORS	AX093019	AX093019	AX093019.1	GI:13509494			
TITLE	AX093019	AX093019	AX093019.1	GI:13509494			
JOURNAL	AX093019	AX093019	AX093019.1	GI:13509494			
FEATURES	AX093019	AX093019	AX093019.1	GI:13509494			
source	AX093019	AX093019	AX093019.1	GI:13509494			
ORIGIN	AX093019	AX093019	AX093019.1	GI:13509494			
Alignment Scores:	AX093019	AX093019	AX093019.1	GI:13509494			
Pred. No.:	AX093019	AX093019	AX093019.1	GI:13509494			
Score:	AX093019	AX093019	AX093019.1	GI:13509494			

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Percent Similarity: 90.91%      Conservative: 1
Best Local Similarity: 81.82%    Mismatches: 1
Query Match: 65.71%             Indels: 0
DB: 6                           Gaps: 0

US-09-980-881A-9 (1-14) x AX093019 (1-43)

Qy 1 SerAsnProValGlulysLeuLeuProLeu 11
Db 38 TCGACCGCTCCGTTGAAAGGCGTTCTACCATTA 6

RESULT 2
LOCUS AX519039 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 5237 from Patent WO02052044.
ACCESSION AX519039
VERSION AX519039.1 GI:23569098
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
AUTHORS Detection of genetic polymorphisms
TITLE Detection of genetic polymorphisms
JOURNAL Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 381 Length: 41
Score: 27.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 52.86% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX519039 (1-41)

Qy 3 ProProValGlulysLeuLeuProLeu 11
Db 33 CCACCTGTGGAGMCTTCTCCTACCACTG 7

RESULT 3
LOCUS CQ001968 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 608 from Patent WO0147944.
ACCESSION CQ001968
VERSION CQ001968.1 GI:41008600
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0147944-A 608 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Accession number cg43927434"

ORIGIN
Percent Similarity: 90.91%      Conservative: 1
Best Local Similarity: 81.82%    Mismatches: 1
Query Match: 65.71%             Indels: 0
DB: 6                           Gaps: 0

US-09-980-881A-9 (1-14) x CQ001968 (1-51)

Qy 1 SerAsnProValGlulysLeuLeuProLeuSerLeu 13
Db 1 AGCAGGCTCTGCTAGCTCGCTAATTACCCGTGACTTTA 39

RESULT 4
LOCUS A24246 39 bp DNA linear PAT 04-DEC-1994
DEFINITION Oligonucleotide.
ACCESSION A24246
VERSION A24246.1 GI:833653
KEYWORDS Rattus rattus (black rat)
SOURCE Rattus rattus
ORGANISM Rattus rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 39)
AUTHORS HUMANIZED INTERLEUKIN-2 RECEPTORS ANTIBODIES
TITLE Patent: WO 9301289-A 30 21-JAN-1993;
JOURNAL Location/Qualifiers
FEATURES
source /organism="Rattus rattus"
/mol_type="unassigned DNA"
/db_xref="taxon:10117"

ORIGIN
Alignment Scores:
Pred. No.: 677 Length: 39
Score: 35.50 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 50.71% Indels: 1
DB: 6 Gaps: 1

US-09-980-881A-9 (1-14) x A24246 (1-39)

Qy 3 ProProValGlulysLeuLeuProLeuSerLeu 14
Db 5 CCCCCTGGTG---AAGCTGTACTCTTTCACAGAAA 37

RESULT 5
LOCUS CQ767550 45 bp DNA linear PAT 04-MAR-2004
DEFINITION Sequence 17 from Patent EP1386931.
ACCESSION CQ767550
VERSION CQ767550.1 GI:45095665
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, J.
AUTHORS Human neurotrophin homologue
TITLE Patent: EP 1386931-A 17 04-FEB-2004;
JOURNAL Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..45
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Sequence"

ORIGIN

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Alignment Scores:  
 Pred. No.: 953 Length: 45  
 Score: 35.00 Matches: 7  
 Percent Similarity: 80.00% Conservative: 1  
 Best Local Similarity: 70.00% Mismatches: 2  
 Query Match: 50.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x CQ767550 (1-45)

QY 1 SerAsnProValGluLysLeuLeuPro 10  
 ||||| |||||::: |||||  
 DB 32 AGCAATGCCCGGTTCAAGCGCTGCTCCCC 3

RESULT 6  
 AX201424/c  
 LOCUS AX201424 45 bp DNA linear PAT 30-AUG-2001  
 DEFINITION Sequence 103 from Patent WO0153486.  
 ACCESSION AX201424  
 VERSION AX201424.1 GI:15391230  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,  
 Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V.,  
 Stone, D.M., Watanabe, C.K. and Wood, W.I.  
 TITLE Compositions and methods for the treatment of tumour  
 JOURNAL Patent: WO 0153486-A 103 26-JUL-2001;  
 Genentech, Inc. (US)

FEATURES  
 source  
 1..45  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetic Oligonucleotide Probe."

ORIGIN

Alignment Scores:  
 Pred. No.: 953 Length: 45  
 Score: 35.00 Matches: 7  
 Percent Similarity: 80.00% Conservative: 1  
 Best Local Similarity: 70.00% Mismatches: 2  
 Query Match: 50.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX201424 (1-45)

QY 1 SerAsnProValGluLysLeuLeuPro 10  
 ||||| |||||::: |||||  
 DB 32 AGCAATGCCCGGTTCAAGCGCTGCTCCCC 3

RESULT 7  
 AR364159  
 LOCUS AR364159 34 bp DNA linear PAT 03-SEP-2003  
 DEFINITION Sequence 42 from patent US 5256545.  
 ACCESSION AR364159  
 VERSION AR364159.1 GI:34426485  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 34)  
 AUTHORS Brown, M.S., Goldstein, J.L., Russell, D.W. and Sudhof, T.C.  
 TITLE Sterol Regulatory Elements  
 JOURNAL Patent: US 5256545-A 42 26-OCT-1993;  
 FEATURES  
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 Location/Qualifiers  
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 /mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 1.11e+03 Length: 34  
 Score: 34.00 Matches: 7  
 Percent Similarity: 70.00% Conservative: 0  
 Best Local Similarity: 70.00% Mismatches: 3  
 Query Match: 48.57% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR364159 (1-34)

QY 2 AsnProValGluLysLeuLeuProLeu 11  
 ||||| |||||::: |||||  
 DB 4 AATCACCCTCACTGCAGAAACTCTCCCTG 33

RESULT 8  
 AR053703  
 LOCUS AR053703 40 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 127 from patent US 5834952.  
 ACCESSION AR053703  
 VERSION AR053703.1 GI:5978565  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 40)  
 AUTHORS Stemmer, W. Peter, Christiaan, and Lipshutz, R.J.  
 TITLE End-complementary polymerase reaction  
 JOURNAL Patent: US 5834252-A 127 10-NOV-1998;  
 FEATURES  
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 1..40  
 Location/Qualifiers  
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ORIGIN

Alignment Scores:  
 Pred. No.: 1.29e+03 Length: 40  
 Score: 34.00 Matches: 5  
 Percent Similarity: 90.00% Conservative: 4  
 Best Local Similarity: 50.00% Mismatches: 1  
 Query Match: 48.57% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR053703 (1-40)

QY 3 ProProValGluLysLeuLeuProLeuSer 12  
 |||||::: |||||::: |||||  
 DB 3 CCGCCTTTGAGTGAGTGATACCGCTCGCC 32

RESULT 9

AR258638  
 LOCUS AR258638 40 bp DNA linear PAT 20-DEC-2002  
 DEFINITION Sequence 127 from patent US 6489146.  
 ACCESSION AR258638  
 VERSION AR258638.1 GI:27309014  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 40)  
 AUTHORS Stemmer, W.P.C. and Lipshutz, R.J.  
 TITLE End-complementary polymerase reaction  
 JOURNAL Patent: US 6489146-A 127 03-DEC-2002;  
 FEATURES  
 source  
 1..40  
 Location/Qualifiers  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 1.29e+03 Length: 40  
 Score: 34.00 Matches: 5  
 Percent Similarity: 90.00% Conservative: 4

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Best Local Similarity: 50.00% Mismatches: 1
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR258638 (1-40)

Qy 3 ProProValGluLysLeuLeuProLeuSer 12
Db 3 CGCGCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 10
LOCUS AX107547 40 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 366 from Patent WO0123606.
ACCESSION AX107547
VERSION AX107547.1 GI:13923032
KEYWORDS
SOURCE Bradyrhizobium japonicum
ORGANISM Bradyrhizobium japonicum
REFERENCE 1
AUTHORS Grabowski,R. and Berghof,K.
TITLE Nucleic acid molecules for detecting bacteria and phylogenetic
units of bacteria
JOURNAL Patent: WO 0123606-A 366 05-APR-2001;
Biotecon Diagnostics GmbH (DE)
FEATURES
source
1..40
/organism="Bradyrhizobium japonicum"
/mol_type="unassigned DNA"
/db_xref="taxon:375"
ORIGIN

Alignment Scores:
Pred. No.: 1.29e+03 Length: 40
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX107547 (1-40)

Qy 4 ProValGluLysLeuLeuProLeuSer 12
Db 40 CCAATCGAACGATTAGTACCGGTAGC 14

RESULT 11
LOCUS AR036483 41 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5872218.
ACCESSION AR036483
VERSION AR036483.1 GI:5953151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
Williams,L.Thomas.
TITLE Human platelet-derived growth factor receptor extracellular domain
antibodies
JOURNAL Patent: US 5872218-A 16 16-FEB-1999;
FEATURES
Location/Qualifiers
source
1..41
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.32e+03 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR258638 (1-40)

Qy 3 ProProValGluLysLeuLeuProLeuSer 12
Db 3 CGCGCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 12
LOCUS AR069442 41 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 16 from patent US 5891652.
ACCESSION AR069442
VERSION AR069442.1 GI:7220330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
Williams,L.Thomas.
TITLE Methods of using domains of extracellular region of human
platelet-derived growth factor receptor polypeptides
JOURNAL Patent: US 5891652-A 16 06-APR-1999;
FEATURES
Location/Qualifiers
source
1..41
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.32e+03 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR069442 (1-41)

Qy 1 SerAsnProProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 13
LOCUS I73464 41 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 16 from patent US 5686572.
ACCESSION I73464
VERSION I73464.1 GI:3009605
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
Williams,L.Thomas.
TITLE Domains of extracellular region of human platelet derived growth
factor receptor polypeptides
JOURNAL Patent: US 5686572-A 16 11-NOV-1997;
FEATURES
Location/Qualifiers
source
1..41
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.32e+03 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2

```



Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x I73464 (1-41)

QY 1 SerAsnProValGluLysLeu 8  
DB 37 TCGATCCGCCAGTTAAGCACTT 14

## RESULT 14

BD243527

LOCUS

DEFINITION BD243527 48 bp DNA linear PAT 17-JUL-2003  
Nucleotide fragment, probe, primer, reagent, and method for  
detecting nucleotide sequence derived from replication origin of  
pBR322.

## ACCESSION

BD243527

VERSION BD243527.1 GI:33053297

KEYWORDS JP 2002537856-A/34.

SOURCE unidentified

ORGANISM unidentified

unclassified.

1 (bases 1 to 48)

REFERENCE

AUTHORS Lamy, D.

TITLE Nucleotide fragment, probe, primer, reagent, and method for  
detecting nucleotide sequence derived from replication origin of

JOURNAL Patent: JP 2002537856-A 34 12-NOV-2002;

TRANSGENE

OS pBR322 plasmid

PN JP 2002537856-A/34

PD 12-NOV-2002

PF 03-MAR-2000 JP 2000603424

PR 05-MAR-1999 FR 99/02968

PI DIDIER LAMY

PC C12N15/09,C12Q1/68,C12N15/00

CC Nucleotide fragment, probe, primer, reagent, and method for  
detecting

CC nucleotide sequence derived from replication origin of pBR322

CC Key Location/Qualifiers

FT source 1. .48

FT Location/Qualifiers

/organism='pBR322 plasmid'.

1. .48

/organism='unidentified'

/mol\_type='genomic DNA'

/db\_xref='taxon:32844'

## FEATURES

source

## ORIGIN

Alignment Scores:

Pred. No.: 1.53e+03 Length: 48  
Score: 34.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x BD243527 (1-48)

QY 3 ProProValGluLysLeuProLeuSer 12

DB 19 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 48

## RESULT 15

AX034950

LOCUS

DEFINITION AX034950 48 bp DNA linear PAT 15-NOV-2000  
Sequence 34 from Patent WO0053803.

ACCESSION AX034950

VERSION AX034950.1 GI:11190875

KEYWORDS

Cloning vector pBR322

SOURCE

artificial sequences; vectors.

REFERENCE

1

AUTHORS Lamy, D.  
TITLE Nucleotide fragment, probe, primer, reagent and method for  
detecting a nucleotide sequence derived from pBR322 replication

JOURNAL Patent: WO 0053803-A 34 14-SEP-2000;

FEATURES LAMY DIDIER (FR) ; TRANSGENE (FR)

source Location/Qualifiers

1. .48

/organism='Cloning vector pBR322'

/mol\_type='unassigned DNA'

/db\_xref='taxon:47470'

## ORIGIN

Alignment Scores:

Pred. No.: 1.53e+03 Length: 48  
Score: 34.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX034950 (1-48)

QY 3 ProProValGluLysLeuProLeuSer 12

DB 19 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 48

Search completed: October 26, 2004, 22:56:44

Job time : 1895 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 21:18:21 ; Search time 389 Seconds

(without alignments)  
188.925 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 4074946

Minimum DB seq length: 0

Maximum DB seq length: 57

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO spool\_p/US09980881/runat\_26102004\_083352\_5565/app\_query.fasta\_1.199  
-DB=N Geneseq 23Sep04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=57  
-USER=US09980881 @CGN 1.1.708 @runat\_26102004\_083352\_5565 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq\_23Sep04.\*

1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46	65.7	43	4	Aaf80298 PCR prime
C 2	37	52.9	41	6	Abz48454 Human org
C 3	57	52.9	51	2	Aat00624 Human (2'
4	36	51.4	36	10	Add69569 Food enri
C 5	36	51.4	36	10	Add69568 Food enri
6	36	51.4	51	4	Aal27400 Human SNP

C 7	35.5	50.7	39	2	AAQ36595	AaQ36595 PCR prime
C 8	35	50.0	45	2	AAZ33905	Aaz33905 Human PRO
C 9	35	50.0	45	3	AAC78611	Aac78611 Human PRO
C 10	35	50.0	45	6	ABK40321	Abk40321 Oligonuc1
C 11	35	50.0	45	8	ACA63473	Aca63473 Novel hum
C 12	35	50.0	45	8	ACA71637	Aca71637 Human PRO
C 13	35	50.0	45	8	ACB92277	Abx92277 Human PRO
C 14	35	50.0	45	8	ACA66018	AcA66018 Human sec
C 15	35	50.0	45	9	ADA24556	Ada24556 Secreterd
C 16	35	50.0	45	9	ACD29619	AcD29619 Novel hum
C 17	35	50.0	45	9	ADA12217	Ada12217 Human sec
C 18	35	50.0	45	9	ACD29034	AcD29034 Novel hum
C 19	35	50.0	45	10	ADB73523	AdB73523 Human PRO
C 20	35	50.0	45	10	ADB76239	AdB76239 Human PRO
C 21	35	50.0	45	10	ADC43665	AdC43665 Human PRO
C 22	35	50.0	45	10	ADC61425	AdC61425 Human PRO
C 23	35	50.0	45	10	ADC63389	AdC63389 Human PRO
C 24	35	50.0	45	10	ADC66489	AdC66489 Human PRO
C 25	35	50.0	45	10	ADC68613	AdC68613 Human PRO
C 26	35	50.0	45	10	ADC62673	AdC62673 Human PRO
C 27	35	50.0	45	10	ADC67738	AdC67738 Human PRO
C 28	35	50.0	45	10	ADC41058	AdC41058 Human PRO
C 29	35	50.0	45	10	ADC67113	AdC67113 Human PRO
C 30	35	50.0	45	10	ADC62049	AdC62049 Human PRO
C 31	35	50.0	45	10	ADC41682	AdC41682 Human PRO
C 32	35	50.0	45	10	ADE49051	Ade49051 Human PRO
C 33	35	50.0	45	10	ADE35105	Ade35105 Human PRO
C 34	35	50.0	45	10	ADE16219	Ade16219 Human PRO
C 35	35	50.0	45	10	ADD72834	AdD72834 Human PRO
C 36	35	50.0	45	10	ADD72192	AdD72192 Human PRO
C 37	35	50.0	45	10	ADF46857	AdF46857 Human PRO
C 38	35	50.0	45	10	ADG52614	AdG52614 Human PRO
C 39	35	50.0	45	10	ADG59934	AdG59934 Human PRO
C 40	35	50.0	45	10	ADI60694	AdI60694 Human PRO
C 41	35	50.0	45	10	ADJ37384	AdJ37384 Tumour th
C 42	35	50.0	45	10	ACD42438	AcD42438 Novel hum
C 43	35	50.0	45	12	ADE48351	Ade48351 Human PRO
C 44	35	50.0	45	12	ADE89452	Ade89452 Human PRO
C 45	35	50.0	45	12		

ALIGNMENTS

RESULT 1

AAF80298/c

ID AAF80298 standard; DNA; 43 BP.

XX

AC AAF80298;

XX

DT 29-JUN-2001 (first entry)

XX

DE PCR primer used to amplify the RK2 origin of replication.

XX

KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;

KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant;

KW PCR primer; ss.

XX

OS Escherichia coli.

PN FR2798139-A1.

XX

PD 09-MAR-2001.

XX

PF 03-SEP-1999; 99FR-00011112.

XX

PR 03-SEP-1999; 99FR-00011112.

XX

PA (MERI-) MERISTEM THERAPEUTICS SA.

XX

PI Gruber V, Comeau D;

XX

DR WPI; 2001-259847/27.

XX

PT New vector free from non-essential elements, useful for transforming  
 PT cells for protein production and for preparing transgenic plants.  
 XX  
 PS Example 1; Page 13; 180pp; French.  
 XX  
 CC The specification describes a synthetic vector containing only those  
 CC elements essential for its functionality and transgenesis of a cell  
 CC (especially a plant cell). The vector consists of at most one origin of  
 CC replication (ori), at most one sequence encoding a selection agent and a  
 CC trfA locus encoding a protein that increases the level of plasmid  
 CC replication. The vector particularly contains an RK2 ori, especially oriV  
 CC from pRK2 of *Escherichia coli* with a broad host range, an antibiotic  
 CC resistance gene (especially nptII conferring resistance to kanamycin in  
 CC bacteria) and a trfA locus from pRK2 encoding the proteins p285 and p382.  
 CC The vectors are used to prepare transgenic plants and transformed host  
 CC cells for production of a heterologous proteins, e.g. insulin,  
 CC interferon, lipase, blood proteins and anti-inflammatory agents. PCR  
 CC primers AAF80297-98 were used to amplify the RK2 ori, and the amplified  
 CC fragment was used to construct plasmids of the invention  
 XX  
 SQ Sequence 43 BP; 11 A; 6 C; 17 G; 9 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.67 Length: 43  
 Score: 46.00 Matches: 9  
 Percent Similarity: 90.91% Conservative: 1  
 Best Local Similarity: 81.82% Mismatches: 1  
 Query Match: 65.71% Indels: 0  
 DB: 4 Gaps: 0

US-09-980-881A-9 (1-14) x AAF80298 (1-43)

Qy 1 SerAnProProValGluLysLeuLeuProLeu 11  
 Db 38 TCGAACCTCCGCGAAGGCTTCTACCATTA 6

RESULT 2

ABZ48454/c  
 ID ABZ48454 standard; DNA; 41 BP.

XX AC ABZ48454;

XX DT 26-JUN-2003 (first entry)

XX DE Human organic cation transporter OCT1 gene polymorphic site, #5237.

XX KW Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
 KW drug evaluation; drug screening; genotyping; genetic profiling;  
 KW therapeutic customisation; adverse reaction; clinical trial;  
 KW drug approval; single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT variation replace(21,T)  
 FT /\*tag= a

FT /standard\_name= "single nucleotide polymorphism (SNP) "

XX WO200252044-A2.

XX PD 04-JUL-2002.

XX PF 27-DEC-2001; 2001WO-JP011592.

XX PR 27-DEC-2000; 2000JP-00399443.

XX PR 02-MAY-2001; 2001JP-00135256.

XX PR 27-AUG-2001; 2001JP-00256862.

XX FA (RIKE ) RIKEN KK.

XX FI Nakamura Y, Sekine A, Iida A, Saito S;

XX WPI; 2002-583571/62.

XX Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 XX

PS Claim 23; Page 166; 2785pp; English.

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy  
 XX

SQ Sequence 41 BP; 11 A; 11 C; 13 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 276 Length: 41  
 Score: 37.00 Matches: 7  
 Percent Similarity: 77.78% Conservative: 0  
 Best Local Similarity: 77.78% Mismatches: 2  
 Query Match: 52.86% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x ABZ48454 (1-41)

Qy 3 ProProValGluLysLeuLeuProLeu 11

Db 33 CCACCTGTGGAGCTTCTTCCATCCTG 7

RESULT 3

ID AAT00624

XX AAT00624 standard; DNA; 51 BP.

XX AC AAT00624;

XX DT 03-FEB-1996 (first entry)

XX DE Human (2'-5') oligo A synthetase antigenic peptide CDNA.

XX KW (2'-5') oligo A synthetase; interferon; antigenic peptide; ss.

XX OS Homo sapiens.

XX CA1337281-C.

PN

XX 10-OCT-1995.  
PD  
XX 18-APR-1985; 85CA-00479459.  
PF  
XX 18-APR-1984; 84US-00601782.  
PR  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA  
XX Revel M, Chebath J;  
PI  
XX WPI; 1995-366737/48.  
DR  
XX P-PSDB; AAR84190.  
DR  
XX New DNA encoding 2'-5' oligo A synthetase and related vectors -  
PT transformed microorganisms, proteins and antigenic peptide(s), useful for  
PT monitoring interferon activity in cells and body fluids.  
PT  
PS Claim 7; Fig 7a; 75pp; English.  
PS  
XX Enzyme AAR84186 has a mol.wt. of about 41,500 daltons. AA sequence  
CC AAR84186 is claimed. Also claimed is the antigenic peptide AAR84190 which  
CC is AAS 348-364 of AAR84186. A DNA molecule coding for a C-terminal  
CC heptadecapeptide of (2'-5') oligo A synthetase comprising nts 1075-1124  
CC of AAT00619 is claimed. This encodes AAR84190, and its sequence is given  
CC in AAT00624. For further information see AAR84186 and AAT00619  
XX  
SQ Sequence 51 BP; 7 A; 24 C; 6 G; 14 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 355 Length: 51  
Score: 37.00 Matches: 7  
Percent Similarity: 66.67% Conservative: 1  
Best Local Similarity: 58.33% Mismatches: 4  
Query Match: 52.86% Indels: 0  
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x AAT00624 (1-51)  
QY 3 ProValGluLysLeuLeuProLeuSerLeuLys 14  
| | | | |  
Db 14 CCTCCCTGCCATTTCATCCCTGCCCCCTCTCCATGAAG 49  
| | | | |  
RESULT 4  
ADD69569  
ID ADD69569 standard; DNA; 36 BP.  
XX  
AC ADD69569;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Food enrichment-related PCR primer QCR1 - SEQ ID 49.  
XX  
KW food; gamma-glutamyl cysteine; drink; seasoning; flavour improvement;  
KW PCR; primer; ss; QCR1.  
XX  
OS Unidentified.  
XX  
PN WO2003080832-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 26-MAR-2003; 2003WO-JP003715.  
XX  
PR 26-MAR-2002; 2002JP-00085058.  
XX  
PA (AJIN ) AJINOMOTO CO INC.  
XX  
XX Nishiuchi H, Nishimura Y, Kuroda M;  
PI  
XX WPI; 2003-833508/77.  
XX  
XX Genetically-modified Candida utilis for producing foods and drinks

PT enriched with gamma-glutamyl cysteine or cysteine, useful in food  
PT industry e.g. for seasoning, by culturing and processing to enhance  
PT flavor.  
XX  
PS Example 3; SEQ ID NO 49; 70pp; Japanese.  
XX  
CC The invention relates to a novel method for producing a food containing  
CC gamma-glutamyl cysteine or cysteine comprising culturing under  
CC appropriate conditions Candida utilis (Pichia jadinii) containing 1% or  
CC more by weight of gamma-glutamyl cysteine based on dry cells in the  
CC logarithmic growth phase when cultured in the minimum medium, adding the  
CC obtained culture, optionally after heating, to a food or drink material  
CC and processing. The yeast of the invention may be used for producing food  
CC and drink with enriched gamma-glutamyl cysteine or cysteine which is  
CC useful in food industry e.g. for seasoning. In this way, food and drink  
CC can be cheaply produced with improved flavour. The current sequence is  
CC that of the food enrichment-related PCR primer of the invention.  
XX  
SQ Sequence 36 BP; 16 A; 9 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 352 Length: 36  
Score: 26.00 Matches: 7  
Percent Similarity: 72.73% Conservative: 1  
Best Local Similarity: 63.64% Mismatches: 3  
Query Match: 51.43% Indels: 0  
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x ADD69569 (1-36)  
QY 4 ProValGluLysLeuLeuProLeuSerLeuLys 14  
| | | | |  
Db 4 CCTATTGAAATAATTACTACCCACCACCAAGAAAG 36  
| | | | |  
RESULT 5  
ADD69568/c  
ID ADD69568 standard; DNA; 36 BP.  
XX  
AC ADD69568;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Food enrichment-related PCR primer QCR1 - SEQ ID 48.  
XX  
KW food; gamma-glutamyl cysteine; drink; seasoning; flavour improvement;  
KW PCR; primer; ss; QCR1.  
XX  
OS Unidentified.  
XX  
PN WO2003080832-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 26-MAR-2003; 2003WO-JP003715.  
XX  
PR 26-MAR-2002; 2002JP-00085058.  
XX  
PA (AJIN ) AJINOMOTO CO INC.  
XX  
XX Nishiuchi H, Nishimura Y, Kuroda M;  
PI  
XX WPI; 2003-833508/77.  
XX  
XX Genetically-modified Candida utilis for producing foods and drinks  
PT enriched with gamma-glutamyl cysteine or cysteine, useful in food  
PT industry e.g. for seasoning, by culturing and processing to enhance  
PT flavor.  
XX  
PS Example 3; SEQ ID NO 48; 70pp; Japanese.  
XX  
CC The invention relates to a novel method for producing a food containing  
CC gamma-glutamyl cysteine or cysteine comprising culturing under  
CC appropriate conditions Candida utilis (Pichia jadinii) containing 1% or

CC more by weight of gamma-glutamyl cysteine based on dry cells in the  
 CC logarithmic growth phase when cultured in the minimum medium, adding the  
 CC obtained culture, optionally after heating, to a food or drink material  
 CC and processing. The yeast of the invention may be used for producing food  
 CC and drink with enriched gamma-glutamyl cysteine or cysteine which is  
 CC useful in food industry e.g. for seasoning. In this way, food and drink  
 CC can be cheaply produced with improved flavour. The current sequence is  
 CC that of the food enrichment-related PCR primer of the invention.  
 XX  
 SQ Sequence 36 BP; 7 A; 4 C; 9 G; 16 T; 0 U; 0 Other;

Alignment Scores: 352 Length: 36  
 Pred. No.: 36.00 Matches: 7  
 Score: 72.73% Conservative: 1  
 Percent Similarity: 63.64% Mismatches: 3  
 Best Local Similarity: 51.43% Indels: 0  
 Query Match: 10 Gaps: 0  
 DB:

US-09-980-881A-9 (1-14) x ADD69568 (1-36)

QY 4 ProValGluLysLeuLeuProLeuSerLeuLys 14  
 ID AAL27400 standard; DNA; 51 BP.  
 AC AAL27400;  
 XX  
 XX 24-JAN-2002 (first entry)  
 DT  
 XX Human SNP oligonucleotide #608.  
 DE

RESULT 6

AAL27400  
 ID AAL27400 standard; DNA; 51 BP.  
 AC AAL27400;  
 XX  
 XX 24-JAN-2002 (first entry)  
 DT  
 XX Human SNP oligonucleotide #608.  
 DE

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 KW amyloid protein; angiopeptide; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200147944-A2.  
 PN  
 XX 05-JUL-2001.  
 PD  
 XX 28-DEC-2000; 2000WO-US035498.  
 PF  
 XX 28-DEC-1999; 98US-0173419P.  
 PR  
 XX 27-DEC-2000; 2000US-00173419.  
 PR  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Shimkets RA, Leach M;  
 PI  
 XX WPI; 2001-465210/50.  
 DR  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 PS  
 XX Claim 1; Page 1561; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiopeptide,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
 CC protein coupled receptors and thioesterases. The present sequence is one

CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of the proteins listed above.  
 CC Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms  
 XX  
 SQ Sequence 51 BP; 11 A; 18 C; 9 G; 13 T; 0 U; 0 Other;

Alignment Scores: 525 Length: 51  
 Pred. No.: 36.00 Matches: 7  
 Score: 76.92% Conservative: 3  
 Percent Similarity: 53.85% Mismatches: 3  
 Best Local Similarity: 51.43% Indels: 0  
 Query Match: 4 Gaps: 0  
 DB:

US-09-980-881A-9 (1-14) x AAL27400 (1-51)

QY 1 SerAsnProProValGluLysLeuLeuProLeuSerLeu 13  
 ID AAL27400 standard; DNA; 39 BP.  
 AC AAL27400;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT  
 XX 28-MAY-1993 (first entry)  
 DT

RESULT 7

AAQ36595  
 ID AAL27400 standard; DNA; 39 BP.  
 AC AAL27400;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT  
 XX 28-MAY-1993 (first entry)  
 DT

XX PCR primer FH for construction of humanised Heavy chain anti IL-2 Ab.  
 DE antibody; monoclonal; chimaeric; grafted; humanised; IL-2; interleukin-2;  
 KW cytokines; interleukin-2 receptor; 55kD beta chain; activated T cells;  
 KW T cell mediated disease; graft versus host disease; transplant rejection;  
 KW autoimmune diseases; chemotherapy; immunosuppressants; T cell typing;  
 KW diagnosis; testing; detection; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9301289-A1.  
 PN  
 XX 21-JAN-1993.  
 PD  
 XX 10-JUL-1992; 92WO-GB001258.  
 PF  
 XX 11-JUL-1991; 91GR-00015010.  
 PR  
 XX (WELL) WELLCOME FOUND LTD.  
 PA  
 XX (WALD) WALDMANN H.  
 PA  
 XX Waldmann H, Winter GP, Crowe JS, Lewis AP;  
 PI  
 XX WPI; 1993-045493/05.  
 DR  
 XX Human interleukin-2 receptor antibodies - useful for treating and  
 PT preventing T-cell mediated diseases e.g. graft versus host disease,  
 PT transplant rejection etc.  
 PS  
 XX Example; Page 42; 48pp; English.

XX This PCR primer was used with AAQ36594 in the construction of a humanised  
 CC anti-IL-2 antibody. The initial template for the reaction was anti-CD4  
 CC heavy chain (on KOL framework; WO9205274). (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 XX Sequence 39 BP; 11 A; 12 C; 8 G; 8 T; 0 U; 0 Other;

Alignment Scores: 469 Length: 39  
Pred. No.: 35.50 Matches: 9  
Score: 83.33% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 50.71% Indels: 1  
DB: 2 Gaps: 1

US-09-980-881A-9 (1-14) x AAQ36595 (1-39)

QY 3 ProProValGluLysLeuProLeuSerLeuLys 14

Db 5 CCCCCGGTG--AAGCTGTACTCTTGACACAGAA 37

RESULT 8

AAZ33905/c

ID AAZ33905 standard; DNA; 45 BP.

XX AAZ33905;

XX 07-DEC-1999 (first entry)

XX Human PRO274 hybridisation probe.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-00040220.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 23-MAR-1998; 98US-0079294P.

PR 26-MAR-1998; 98US-0079656P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079689P.

PR 27-MAR-1998; 98US-0079728P.

PR 27-MAR-1998; 98US-0079786P.

PR 30-MAR-1998; 98US-0079920P.

PR 30-MAR-1998; 98US-0079923P.

PR 31-MAR-1998; 98US-0080105P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080165P.

PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080328P.

PR 01-APR-1998; 98US-0080333P.

PR 01-APR-1998; 98US-0080334P.

PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.

PR 08-APR-1998; 98US-0081071P.

PR 09-APR-1998; 98US-0081195P.

PR 09-APR-1998; 98US-0081203P.

PR 09-APR-1998; 98US-0081229P.

PR 15-APR-1998; 98US-0081817P.

PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082766P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084411P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086192P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.

(GETH ) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

XX New secreted and transmembrane polypeptides and their polynucleotides,  
XX useful for treating blood coagulation disorders, cancers and cellular  
XX adhesion disorders.

XX Example 4; Page 184; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides  
XX and their polynucleotides. The nucleotide sequences are useful as sources  
XX of probes, primers, for chromosome mapping, and for generation of  
XX antisense sequences. They can also be used to create transgenic animals.  
XX The proteins can be used to treat a variety of diseases and disorders,  
XX depending on their function. Diseases that may be treated include blood  
XX coagulation disorders, cancers and cellular adhesion disorders. They may

CC also be used to raise antibodies. AAC233891 to AAC234338, and AAY41685 to  
CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention

SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 672 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x AAC233905 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAGGCGTGTCTCCC 3

RESULT 9

AAC78611/c

ID AAC78611 standard; DNA; 45 BP.

XX AC AAC78611;

XX DT 08-FEB-2001 (first entry)

XX DE Human PRO274 hybridisation probe SEQ ID NO:17.

XX KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
XX expressed sequence tag; detection; cancer; PCR primer; probe; ss.

XX OS Homo sapiens.

XX PN WO200053756-A2.

XX PD 14-SEP-2000.

XX PF 18-FEB-2000; 2000WO-US004341.

XX PR 08-MAR-1999; 99WO-US005028.

XX PR 12-MAR-1999; 99US-0123957P.

XX PR 29-MAR-1999; 99US-0126773P.

XX PR 21-APR-1999; 99US-0130232P.

XX PR 28-APR-1999; 99US-0131445P.

XX PR 14-MAY-1999; 99US-0134287P.

XX PR 23-JUN-1999; 99US-0141037P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 29-OCT-1999; 99US-0162508P.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 02-DEC-1999; 99WO-US028551.

XX PR 02-DEC-1999; 99WO-US028565.

XX PR 16-DEC-1999; 99WO-US030095.

XX PR 30-DEC-1999; 99WO-US031243.

XX PR 30-DEC-1999; 99WO-US031274.

XX PR 05-JAN-2000; 2000WO-US000219.

XX PR 06-JAN-2000; 2000WO-US000277.

XX PR 06-JAN-2000; 2000WO-US000376.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
XX Stewart TA, Tumas D, Williams PM, Wood WI;

XX DR WPI; 2000-611443/58.

XX PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
XX target bioactive molecules to specific cells, and to modulate cellular  
XX activities.

XX Example 4; Page 235; 636pp; English.  
XX  
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
CC polynucleotides and polypeptides can be used for detecting the presence  
CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
CC and for modulating biological activities of cells, using the polypeptides  
CC for specific targeting. The polypeptide targeting can be used to kill the  
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
CC AAC78987 represent PCR primers and probes used in the isolation of the  
CC PRO polynucleotide sequences  
XX  
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 672 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x AAC78611 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAGGCGTGTCTCCC 3

RESULT 10

ABK40321/c

ID ABK40321 standard; DNA; 45 BP.

XX AC ABK40321;

XX DT 15-JUL-2002 (first entry)

XX DE Oligonucleotide probe for human PRO274 DNA.

XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
XX leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;  
XX inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;  
XX neuroprotective; probe; ss.

XX OS Homo sapiens.

XX PN WO200153486-A1.

XX PD 26-JUL-2001.

XX PF 11-FEB-2000; 2000WO-US003565.

XX PR 08-MAR-1999; 99WO-US005028.

XX PR 11-MAR-1999; 99US-0123972P.

XX PR 11-MAY-1999; 99US-0133459P.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 22-JUN-1999; 99US-0140650P.

XX PR 22-JUN-1999; 99US-0140653P.

XX PR 20-JUL-1999; 99US-0144758P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 28-JUL-1999; 99US-0146222P.

XX PR 17-AUG-1999; 99US-0149395P.

XX PR 31-AUG-1999; 99US-0151689P.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 01-DEC-1999; 99WO-US028301.

XX PR 01-DEC-1999; 99WO-US028634.

XX PR 05-JAN-2000; 2000WO-US000219.

XX PA (GETH ) GENENTECH INC.



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XX  Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillian KJ;
PI  Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI  Watanabe CK, Wood WI;
XX
DR  WPI; 2002-205567/26.
XX
PT  Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT  benign or malignant tumors, leukemias and lymphoid malignancies,
PT  inflammatory, angiogenic and immunologic disorders.
XX
XX  Example 10; Page 120; 302pp; English.
XX
CC  The present invention relates to the isolation of novel human PRO
CC  polypeptides (AAU86128-AAU86162) and the polynucleotide sequences
CC  encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO
CC  antibodies are useful for treating benign or malignant tumours (e.g.
CC  renal, kidney, bladder, breast, etc), leukaemias and lymphoid
CC  malignancies, other disorders such as neuronal, glial, astrocytal,
CC  hypothalamic, glandular, macrophagal, stromal and blastocoeleic disorders,
CC  inflammatory, immune and angiogenic disorders. The polynucleotide
CC  sequences are also useful in gene therapy. The present sequence
CC  represents a probe used in the methods of the present invention
XX
SQ  Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      672      Length:      45
Score:          35.00    Matches:      7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match:      50.00% Indels:      0
DB:               6      Gaps:      0

US-09-980-881A-9 (1-14) x ABK40321 (1-45)

Qy  1 SerAsnProProValGluLysLeuLeuPro 10
Db  32 AGCAATGCCCGGTTCAAGCCCTGCTCCCC 3

RESULT 11
ACA63473/c
ID  ACA63473 standard; DNA; 45 BP.
XX
AC  ACA63473;
XX
DT  16-JUN-2003 (first entry)
XX
DE  Novel human secreted and transmembrane protein related probe #2.
XX
KW  Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW  antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW  antidiabetic; gene therapy; inflammatory disease; organ failure;
KW  atherosclerosis; cardiac injury; infertility; birth defect;
KW  premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW  gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW  tissue typing; probe; ss.
XX
OS  Homo sapiens.
XX
PN  US2002192706-A1.
XX
PD  19-DEC-2002.
XX
XX  24-OCT-2001; 2001US-0099832.
XX
PR  17-OCT-1997; 97US-0062250P.
PR  03-NOV-1997; 97US-0064249P.
PR  13-NOV-1997; 97US-0065311P.
PR  21-NOV-1997; 97US-0066364P.
PR  10-MAR-1998; 98US-0077450P.
PR  11-MAR-1998; 98US-0077632P.
PR  11-MAR-1998; 98US-0077641P.

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PR  11-MAR-1998; 98US-0077649P.
PR  12-MAR-1998; 98US-0077791P.
PR  13-MAR-1998; 98US-0078004P.
PR  17-MAR-1998; 98US-00040220.
PR  20-MAR-1998; 98US-0078886P.
PR  20-MAR-1998; 98US-0078910P.
PR  20-MAR-1998; 98US-0078936P.
PR  20-MAR-1998; 98US-0078939P.
PR  25-MAR-1998; 98US-0079294P.
PR  26-MAR-1998; 98US-0079656P.
PR  27-MAR-1998; 98US-0079663P.
PR  27-MAR-1998; 98US-0079664P.
PR  27-MAR-1998; 98US-0079689P.
PR  27-MAR-1998; 98US-0079728P.
PR  27-MAR-1998; 98US-0079786P.
PR  30-MAR-1998; 98US-0079920P.
PR  30-MAR-1998; 98US-0079923P.
PR  31-MAR-1998; 98US-0080105P.
PR  31-MAR-1998; 98US-0080107P.
PR  31-MAR-1998; 98US-0080165P.
PR  31-MAR-1998; 98US-0080194P.
PR  01-APR-1998; 98US-0080327P.
PR  01-APR-1998; 98US-0080338P.
PR  01-APR-1998; 98US-0080333P.
PR  01-APR-1998; 98US-0080334P.
PR  08-APR-1998; 98US-0081049P.
PR  08-APR-1998; 98US-0081070P.
PR  08-APR-1998; 98US-0081071P.
PR  09-APR-1998; 98US-0081195P.
PR  09-APR-1998; 98US-0081203P.
PR  09-APR-1998; 98US-0081229P.
PR  15-APR-1998; 98US-0081817P.
PR  15-APR-1998; 98US-0081819P.
PR  15-APR-1998; 98US-0081838P.
PR  15-APR-1998; 98US-0081952P.
PR  15-APR-1998; 98US-0081953P.
PR  21-APR-1998; 98US-0082568P.
PR  21-APR-1998; 98US-0082569P.
PR  22-APR-1998; 98US-0082700P.
PR  22-APR-1998; 98US-0082704P.
PR  22-APR-1998; 98US-0082797P.
PR  22-APR-1998; 98US-0082804P.
PR  23-APR-1998; 98US-0082796P.
PR  07-OCT-1998; 98WO-US021141.
PR  20-NOV-1998; 98WO-US024855.
PR  05-JAN-1999; 99WO-US000106.
PR  08-MAR-1999; 99WO-US005028.
PR  10-MAR-1999; 99WO-US005190.
PR  14-MAY-1999; 99WO-US010733.
PR  02-JUN-1999; 99WO-US012252.
PR  30-NOV-1999; 99WO-US028313.
PR  02-DEC-1999; 99WO-US028551.
PR  02-DEC-1999; 99WO-US028565.
PR  16-DEC-1999; 99WO-US030095.
PR  30-DEC-1999; 99WO-US031243.
PR  30-DEC-1999; 99WO-US031274.
PR  05-JAN-2000; 2000WO-US000219.
PR  06-JAN-2000; 2000WO-US000277.
PR  06-JAN-2000; 2000WO-US000376.
PR  11-FEB-2000; 2000WO-US003565.
PR  18-FEB-2000; 2000WO-US004341.
PR  24-FEB-2000; 2000WO-US005004.
PR  02-MAR-2000; 2000WO-US005841.
PR  10-MAR-2000; 2000WO-US006319.
PR  21-MAR-2000; 2000WO-US007532.
PR  30-MAR-2000; 2000WO-US008439.
PR  17-MAY-2000; 2000WO-US013705.
PR  22-MAY-2000; 2000WO-US014042.
PR  30-MAY-2000; 2000WO-US014941.
PR  02-JUN-2000; 2000WO-US015264.
PR  28-JUL-2000; 2000WO-US020710.
PR  24-AUG-2000; 2000WO-US023328.
PR  01-DEC-2000; 2000WO-US032678.

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PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 27-NOV-2000; 2000US-00723749.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 22-MAR-2001; 2001US-00816920.  
 PR 22-MAR-2001; 2001WO-US009552.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 30-JUL-2001; 2001US-00918585.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-328499/31.  
 XX  
 XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as  
 PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying  
 PT modulators of receptor-ligand interactions.  
 XX  
 PS Disclosure; SEQ ID NO 17; 55pp; English.  
 XX  
 CC The invention relates to an isolated secreted and transmembrane  
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful  
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for  
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an  
 CC antibody against it is useful for modulating a biological activity of a  
 CC cell. The PRO polypeptide is useful in industrial applications including  
 CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO  
 CC polypeptide is also useful as a thrombolytic agent, interferon,  
 CC interleukin, erythropoietin, colony stimulating factor and other  
 CC cytokines. The PRO polypeptide is useful for treating disease such as  
 CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,  
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,  
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,  
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and  
 CC myocardial ischaemia; kidney disease e.g. renal failure and  
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial  
 CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory  
 CC bowel disease; reproductive disorders e.g. premature labour and  
 CC preeclampsia; carcinogenesis. The present sequence represents a PRO  
 CC polypeptide associated oligonucleotide of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?docID=20020177553  
 XX  
 SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 672 Length: 45  
 Score: 35.00 Matches: 7  
 Percent Similarity: 80.00% Conservative: 1

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 RESULT 13  
 ABX92277/c  
 ID ABX92277 standard; DNA; 45 BP.  
 XX AC ABX92277;  
 XX  
 DT 08-MAY-2003 (first entry)  
 XX  
 DE Human PRO DNA probe SEQ ID No 17.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
 KW cardiac insufficiency; nervous system disorder; kidney disorder;  
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;  
 KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;  
 KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;  
 KW cardiant; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002169284-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 16-OCT-2001; 2001US-00978697.  
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 PR 26-MAY-1981; 81US-00267213.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 03-NOV-1997; 97US-0064249P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 21-NOV-1997; 97US-0066364P.  
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 PR 11-MAR-1998; 98US-0077632P.  
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 PR 12-MAR-1998; 98US-0077791P.  
 PR 13-MAR-1998; 98US-0078004P.  
 PR 17-MAR-1998; 98US-00040220.  
 PR 20-MAR-1998; 98US-0078886P.  
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 PR 27-MAR-1998; 98US-0079689P.  
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 PR 27-MAR-1998; 98US-0079786P.  
 PR 30-MAR-1998; 98US-0079920P.  
 PR 30-MAR-1998; 98US-0079923P.  
 PR 26-JUN-1998; 98US-00105413.  
 PR 07-OCT-1998; 98US-00168978.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 02-NOV-1998; 98US-00184216.  
 PR 06-NOV-1998; 98US-00187368.  
 PR 20-NOV-1998; 98WO-US024855.  
 PR 07-DEC-1998; 98US-00202054.  
 PR 22-DEC-1998; 98US-00218517.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 05-MAR-1999; 99US-00254465.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 10-MAR-1999; 99US-00265686.



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PR 26-MAR-1998; 98US-0079656P.
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PR 27-MAR-1998; 98US-0079668P.
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PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
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PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 05-JAN-2000; 2000WO-US000277.
PR 05-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
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PR 05-JUN-2001; 2001US-00874503.
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PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

PR 30-JUL-2001; 2001US-00918585.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-341189/32.
XX New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX Example 4; Page 121; 460pp; English.
XX The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence is a probe used in the isolation of a cDNA
CC encoding a PRO polypeptide
XX SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 672 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Gaps: 0
DB: 8

US-09-980-881A-9 (1-14) x ACA66018 (1-45)

QY 1 SerAsnProValGluLysLeuLeuPro 10
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ID ADA24556 standard; DNA; 45 BP.
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AC ADA24556;
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KW chromosome identification; vaccine; cancer; retinal disorder;  
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;  
KW wound healing; obesity; diabetes; hearing loss;  
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;  
KW haemoglobin associated disorder; probe; ss.  
XX  
OS Homo sapiens.  
XX  
XX US2003050241-A1.  
XX  
XX 13-MAR-2003.  
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XX 16-OCT-2001; 2001US-00978564.  
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PR 13-NOV-1997; 97US-0065311P.  
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PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
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PR 11-MAR-1998; 98US-0077649P.  
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PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
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PR 31-MAR-1998; 98US-0080103P.  
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PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
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PR 08-APR-1998; 98US-0081049P.  
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PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
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PR 01-JUL-1998; 98US-0091359P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
PR 07-OCT-1998; 98WO-US021141.  
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PR 22-DEC-1998; 98US-0113296P.  
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PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 12-MAR-1999; 99US-0123957P.  
PR 29-MAR-1999; 99US-0126773P.  
PR 21-APR-1999; 99US-0130232P.  
PR 26-APR-1999; 99US-0131022P.  
PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 16-JUN-1999; 99US-0139557P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0142680P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 30-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 05-JAN-2000; 99WO-US031274.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.

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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006550.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
XX
XX
XX New isolated PRO polypeptides for example extracellular, secreted and
XX membrane bound proteins, useful for modulating the biological activities
XX of cells and for treating, for example diabetes, cancer, rheumatoid
XX arthritis, and hearing loss.
XX
XX Example 4; Page 132; 461pp; English.
XX
XX
XX The invention describes an isolated secreted and transmembrane (PRO)
XX polypeptide (1). PRO337 polypeptide is useful for detecting PRO4993
XX polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
XX useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
XX useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
XX useful for linking a bioactive molecule to a cell expressing a PRO337
XX polypeptide, and PRO337 is useful for linking a bioactive molecule to a
XX cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
XX bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739
XX polypeptide, and PRO735, PRO700 and PRO739 polypeptides are useful for
XX
XX
XX Alignment Scores:
XX Pred. No.: 672 Length: 45
XX Score: 35.00 Matches: 7
XX Percent Similarity: 80.00% Conservative: 1
XX Best Local Similarity: 70.00% Mismatches: 2
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XX Db 32 AGCAATGCCCGGTTCGAAGCGTCTGCTCCC 3

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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	34	48.6	40	US-08-675-502-127	Sequence 127, App
4	34	48.6	40	US-09-245-802-127	Sequence 127, App
5	34	48.6	41	US-08-168-917-16	Sequence 16, Appl
6	34	48.6	41	US-08-460-510-16	Sequence 16, Appl
7	34	48.6	41	US-08-460-490-16	Sequence 16, Appl
8	34	48.6	41	PCT-US92-00730-16	Sequence 16, Appl
9	34	48.6	41	PCT-US92-10430-11	Sequence 11, Appl
10	34	48.6	51	US-08-350-260A-287	Sequence 287, App
11	34	48.6	51	US-09-104-337A-287	Sequence 287, App
12	33	47.1	36	US-08-816-155B-38	Sequence 38, Appl

13	33	47.1	36	3	US-08-815-809-23	Sequence 23, Appl
14	33	47.1	36	3	US-09-079-587-38	Sequence 38, Appl
15	33	47.1	41	1	US-08-168-917-18	Sequence 18, Appl
16	33	47.1	41	2	US-08-460-510-18	Sequence 18, Appl
17	33	47.1	41	2	US-08-460-490-18	Sequence 18, Appl
18	33	47.1	41	5	PCT-US92-00730-18	Sequence 18, Appl
19	33	47.1	41	5	PCT-US92-10430-13	Sequence 13, Appl
20	32	45.7	33	4	US-09-566-420-2	Sequence 2, Appl
21	32	45.7	33	4	US-10-201-764-2	Sequence 2, Appl
22	32	45.7	47	4	US-08-422-978-2745	Sequence 2745, Ap
23	32	45.7	54	1	US-08-373-124A-2192	Sequence 2192, Ap
24	32	45.7	54	1	US-08-435-628-2192	Sequence 2192, Ap
25	31	44.3	43	3	US-08-832-985-52	Sequence 52, Appl
26	31	44.3	43	4	US-09-410-903-33	Sequence 33, Appl
27	31	44.3	43	4	US-08-835-159-52	Sequence 52, Appl
28	31	44.3	47	1	US-08-093-884-31	Sequence 31, Appl
29	30	42.9	39	4	US-09-548-797B-151	Sequence 151, App
30	30	42.9	39	4	US-09-548-797B-152	Sequence 152, App
31	30	42.9	45	2	US-08-494-151-2	Sequence 2, Appl
32	30	42.9	47	4	US-09-422-978-522	Sequence 522, App
33	30	42.9	47	4	US-09-422-978-2073	Sequence 2073, Ap
34	30	42.9	50	2	US-08-709-368-2	Sequence 2, Appl
35	30	42.9	52	4	US-08-956-171E-2252	Sequence 2252, Ap
36	30	42.9	54	1	US-08-781-986A-2252	Sequence 2252, Ap
37	30	42.9	54	1	US-08-366-953A-23	Sequence 23, Appl
38	30	42.9	54	1	US-08-311-486C-1099	Sequence 29728, A
39	30	42.9	56	4	US-09-270-767-29728	Sequence 9, Appl
40	29.5	42.1	44	3	US-08-865-960-9	Sequence 70, Appl
41	29.5	42.1	55	2	US-08-850-049-70	Sequence 71, Appl
42	29.5	42.1	55	2	US-08-850-049-74	Sequence 74, Appl
43	29.5	42.1	55	2	US-08-050-478-70	Sequence 70, Appl
44	29.5	42.1	55	2	US-08-050-478-70	Sequence 71, Appl
45	29.5	42.1	55	2	US-08-050-478-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
5256545-42  
; Patent No. 5256545  
; APPLICANT: BROWN, MICHAEL S.; GOLDSTEIN, JOSEPH L.; RUSSELL,  
; DAVID W.; SUDHOF, THOMAS C.  
; TITLE OF INVENTION: STEROL REGULATORY ELEMENTS  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/425,852  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 33,330  
; FILING DATE: 30-MAR-1987  
; APPLICATION NUMBER: 33,081  
; FILING DATE: 30-MAR-1987  
; SEQ ID NO:42:  
; LENGTH: 34  
5256545-42

Alignment Scores:  
Pred. No.: 61.2 Length: 34  
Score: 34.00 Matches: 7  
Percent Similarity: 70.00% Conservative: 0  
Best Local Similarity: 70.00% Mismatches: 3  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x 5256545-42 (1-34)

Qy 2 AsnProValGluLysLeuLeuProLeu 11  
|||  
Db 4 ATACCCCACTGCACAACTCTCCCTG 33  
|||||

RESULT 2  
US-08-425-684-127  
; Sequence 127, Application US/08425684

```
; Patent No. 5934252
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN ESO., TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528J-015400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-425-684-127

Alignment Scores:
Pred. No.: 75.3 Length: 40
Score: 34.00 Matches: 5
Percent Similarity: 90.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 48.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-425-684-127 (1-40)
Qy 3 ProProValGluLysLeuLeuProLeuSer 12
Db 3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 3
US-08-675-502-127
; Sequence 127, Application US/08675502
; Patent No. 5928905
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; Patent No. 5934252
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESO., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-675-502-127

Alignment Scores:
Pred. No.: 75.3 Length: 40
Score: 34.00 Matches: 5
Percent Similarity: 90.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 48.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-675-502-127 (1-40)
Qy 3 ProProValGluLysLeuLeuProLeuSer 12
Db 3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 4
US-09-245-802-127
; Sequence 127, Application US/09245802
; Patent No. 6489146
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

NAME: MURPHY, ESQ., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 165283-015410US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular

US-09-245-802-127  
Alignment Scores:  
Pred. No.: 75.3 Length: 40  
Score: 34.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 48.57% Indels: 0  
DB: 4 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-245-802-127 (1-40)  
Qy 3 ProProValGluLysLeuLeuProLeuSer 12  
Db 3 CCGCCTTTCAGTGCCTGATACGCTCGCC 32

RESULT 5  
US-08-168-917-16/c  
Sequence 16, Application US/08168917  
Patent No. 5686572  
GENERAL INFORMATION:  
APPLICANT: Wolf, David  
APPLICANT: Tomlinson, James E.  
APPLICANT: Fretto, Larry J.  
APPLICANT: Giese, Neill A.  
APPLICANT: Escobedo, Jaime A.  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND  
STREET: Steuart Street Tower, 20th Floor \ One Market  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105

COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/168,917  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/650,793  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: 12418-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
STRAIN: lambda gt10  
US-08-168-917-16

Alignment Scores:  
Pred. No.: 77.7 Length: 41  
Score: 34.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 48.57% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-168-917-16 (1-41)

Qy 1 SerAsnProValGluLysLeu 8  
Db 37 TCGAATCCGCCAGTTAAGGAATT 14

RESULT 6  
US-08-460-510-16/c  
Sequence 16, Application US/08460510  
Patent No. 5872218  
GENERAL INFORMATION:  
APPLICANT: Wolf, David  
APPLICANT: Tomlinson, James E.  
APPLICANT: Fretto, Larry J.  
APPLICANT: Giese, Neill A.  
APPLICANT: Escobedo, Jaime A.  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW  
STREET: One Market Plaza, Steuart Street Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,510  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 012418-001430  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
STRAIN: lambda gt10

```
US-08-460-510-16
Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-460-510-16 (1-41)
Qy 1 SerAsnProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 7
; Sequence 16, Application US/08460490
; Patent No. 5891852
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
US-08-460-510-16
Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0

US-09-980-881A-9 (1-14) x US-08-460-510-16 (1-41)
Qy 1 SerAsnProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 8
PCT-US92-00730-16/c
; Sequence 16, Application PC/TUS9200730
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00730
; FILING DATE: 19920128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
PCT-US92-00730-16
Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 5 Gaps: 0

US-09-980-881A-9 (1-14) x PCT-US92-00730-16 (1-41)
Qy 1 SerAsnProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14
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RESULT 9
PCT-US92-10430-11
; Sequence 11, Application PC/TUS9210430
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: Methods for Production of Purified
; TITLE OF INVENTION: Soluble Type B and Type A Human Platelet-D
; TITLE OF INVENTION: Factor Receptor Fragments
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10430
; FILING DATE: 19921201
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,794
; FILING DATE: 02-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 12418-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US92-10430-11

Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.0 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 5 Gaps: 0

US-09-960-881A-9 (1-14) x PCT-US92-10430-11 (1-41)

Qy 1 SerAenProValGluLysLeu 8
|||||
Db 5 TCGAATCCGCAGTTAAGGAACTT 28
|||||

RESULT 10
US-08-350-260A-287
; Sequence 287, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs

```

```
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Wetherhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-09-104-337A-287

Alignment Scores:
Pred. No.: 103 Length: 51
Score: 34.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 48.57% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-104-337A-287 (1-51)
Qy 3 ProProValGluLysLeuProLeu 11
Db 11 CCGCGATACGACGAGTCTCCACTG 37

RESULT 12
US-08-816-155B-38
; Sequence 38, Application US/08816155B
; Patent No. 5990091
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```
; GENERAL INFORMATION:
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; APPLICANT: GETTIG, RUSSELL R.
; APPLICANT: MARTINEZ, HECTOR
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: PINCUS, STEVEN E.
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
; METHODS OF MAKING AND USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
; STREET: 745 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10151
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,155B
; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-588-0800
; TELEFAX: 212-588-0500
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-816-155B-38

Alignment Scores:
Pred. No.: 101 Length: 36
Score: 33.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 47.14% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-816-155B-38 (1-36)
Qy 3 ProProValGluLysLeuLeuPro 10
Db 1 CCCCCTGCAGAAAAATTAGGCC 24

RESULT 13
US-08-815-809-23
; Sequence 23, Application US/08815809
; Patent No. 6004777
; GENERAL INFORMATION:
; APPLICANT: TARTAGLIA, James
; APPLICANT: GOEBEL, Scott J.
; APPLICANT: COX, William I.
; APPLICANT: GETTIG, Russell R.
; APPLICANT: PINCUS, Steven E.
; APPLICANT: PAOLETTI, Enzo
; APPLICANT: JACOBS, Bertram L.
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF
; MAKING AND USES THEREOF
; FILE REFERENCE: 454310-3010
; CURRENT APPLICATION NUMBER: US/08/815,809
; CURRENT FILING DATE: 1997-03-12
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Vaccinia virus
US-08-815-809-23

Alignment Scores:
Pred. No.: 101 Length: 36
Score: 33.00 Matches: 6
Percent Similarity: 75.00% Conservatives: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 47.14% Indels: 0
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-815-809-23 (1-36)
QY 3 ProProValGluLysLeuLeuPro 10
Db 1 CCCCTGCAGAAAAATTAGGCC 24

RESULT 14
US-09-079-587-38
; Sequence 38, Application US/09079587
; Patent No. 6130066
; GENERAL INFORMATION:
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; APPLICANT: GETTIG, RUSSELL R.
; APPLICANT: MARTINEZ, HECTOR
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: PINCUS, STEVEN E.
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
; METHODS OF MAKING AND USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
; STREET: 745 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10151
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,587
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/816,155
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-588-0800
; TELEFAX: 212-588-0500
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-079-587-38
Alignment Scores:
Pred. No.: 101 Length: 36
Score: 33.00 Matches: 6
Percent Similarity: 75.00% Conservatives: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 47.14% Indels: 0
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-815-809-23 (1-36)
QY 3 ProProValGluLysLeuLeuPro 10
Db 1 CCCCTGCAGAAAAATTAGGCC 24

RESULT 15
US-08-168-917-18/c
; Sequence 18, Application US/08168917
; Patent No. 5686572
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,917
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,793
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
US-08-168-917-18
Alignment Scores:
Pred. No.: 119 Length: 41
Score: 33.00 Matches: 7
Percent Similarity: 77.78% Conservatives: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 47.14% Indels: 0
DB: 3 Gaps: 0
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DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-168-917-18 (1-41)

Qy 1 SerAsnProProValGluLysLeu 9

Db 37 TCGAATCCGCCAGTTATGATGTTGCTT 11

Search completed: October 26, 2004, 22:59:49  
Job time : 86 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 22:59:55 ; Search time 349 Seconds  
(without alignments)  
205.544 Million cell updates/sec

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Perfect score: 70  
Sequence: 1 SNPPVKLLPLSLK 14

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 1965782

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-TRANS-human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=57 -USER=US0980881@cgn\_1\_1\_723@runat\_26102004\_083355\_5681 -NCPU=6  
-ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:
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- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:
- 18: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:
- 19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:
- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
C 1	46	65.7	43	10	US-09-845-064-24
C 2	37	52.9	41	16	US-10-035-833A-5237
C 3	35	50.0	45	9	US-09-978-295A-17
C 4	35	50.0	45	9	US-09-978-697-17
C 5	35	50.0	45	9	US-09-978-192A-17
C 6	35	50.0	45	9	US-09-999-832A-17
C 7	35	50.0	45	10	US-09-978-189-17
C 8	35	50.0	45	10	US-09-978-608A-17
C 9	35	50.0	45	10	US-09-978-585A-17
C 10	35	50.0	45	10	US-09-978-191A-17
C 11	35	50.0	45	10	US-09-978-403A-17
C 12	35	50.0	45	10	US-09-978-564A-17
C 13	35	50.0	45	10	US-09-999-833A-17
C 14	35	50.0	45	10	US-09-981-915A-17
C 15	35	50.0	45	10	US-09-978-824-17
C 16	35	50.0	45	10	US-09-918-585A-17
C 17	35	50.0	45	10	US-09-999-834A-17
C 18	35	50.0	45	10	US-09-978-423A-17
C 19	35	50.0	45	10	US-09-978-193A-17
C 20	35	50.0	45	10	US-09-999-830A-17
C 21	35	50.0	45	10	US-09-978-757A-17
C 22	35	50.0	45	10	US-09-978-187B-17
C 23	35	50.0	45	10	US-09-978-643A-17
C 24	35	50.0	45	10	US-09-978-375A-17
C 25	35	50.0	45	10	US-09-978-298A-17
C 26	35	50.0	45	10	US-09-978-188A-17
C 27	35	50.0	45	10	US-09-978-681A-17
C 28	35	50.0	45	10	US-09-978-194A-17
C 29	35	50.0	45	10	US-09-999-829A-17
C 30	35	50.0	45	10	US-09-978-544A-17
C 31	35	50.0	45	10	US-09-978-665A-17
C 32	35	50.0	45	10	US-09-978-802A-17
C 33	35	50.0	45	10	US-09-999-831A-17
C 34	35	50.0	45	11	US-09-999-831A-17
C 35	35	50.0	45	14	US-10-017-081A-17
C 36	35	50.0	45	14	US-10-167-749-17
C 37	35	50.0	45	14	US-10-013-921A-17
C 38	35	50.0	45	14	US-10-013-929A-17
C 39	35	50.0	45	14	US-10-016-177A-17
C 40	35	50.0	45	15	US-10-166-709A-17
C 41	35	50.0	45	15	US-10-143-031A-17
C 42	35	50.0	45	15	US-10-002-967A-17
C 43	35	50.0	45	15	US-10-017-083A-17
C 44	35	50.0	45	15	US-10-145-128A-17
C 45	35	50.0	45	15	US-10-145-128A-17

ALIGNMENTS

RESULT 1  
US-09-845-064-24/c  
; Sequence 24, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 43  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Oligo  
; OTHER INFORMATION: Desoxynucleotide containing Stul restriction site

US-09-845-064-24

## Alignment Scores:

Pred. No.:	4.15	Length:	43
Score:	46.00	Matches:	9
Percent Similarity:	90.91%	Conservative:	1
Best Local Similarity:	81.82%	Mismatches:	1
Query Match:	65.71%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-845-064-24 (1-43)

Qy 1 SerAnProValGluLysLeuProLeu 11

Db 38 TCGAACCTCCGCGTAAGGCTTCTTACCATTA 6

## RESULT 2

US-10-035-833A-5237/c

; Sequence 5237, Application US/10035833A

; Publication No. US20040072156A1

; GENERAL INFORMATION:

; APPLICANT: Nakamura, Yuho

; APPLICANT: Sekine, Akihiro

; APPLICANT: Iida, Aritoshi

; APPLICANT: Saito, Osamu

; TITLE OF INVENTION: Detection of Genetic Polymorphisms

; FILE REFERENCE: FORS-06904

; CURRENT APPLICATION NUMBER: US/10/035,833A

; CURRENT FILING DATE: 2001-12-27

; NUMBER OF SEQ ID NOS: 7669

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5237

; LENGTH: 41

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-035-833A-5237

## Alignment Scores:

Pred. No.:	153	Length:	41
Score:	37.00	Matches:	7
Percent Similarity:	77.78%	Conservative:	0
Best Local Similarity:	77.78%	Mismatches:	2
Query Match:	52.86%	Indels:	0
DB:	16	Gaps:	0

US-09-980-881A-9 (1-14) x US-10-035-833A-5237 (1-41)

Qy 3 ProProValGluLysLeuProLeu 11

Db 33 CCACCTGTGGAGMCTTCTTACCACTG 7

## RESULT 3

US-09-978-295A-17/c

; Sequence 17, Application US/09978295A

; Patent No. US20020156006A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
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; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
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; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
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; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01

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/	PRIOR FILING DATE:	1998-05-15
/	PRIOR APPLICATION NUMBER:	60/085697

  

Alignment Scores:	
Pred. No.:	382
Score:	35.00
Percent Similarity:	80.00%
Best Local Similarity:	70.00%
Query Match:	50.00%
DB:	9

  

US-09-980-881A-9 (1-14) x US-09-978-295A-17 (1-45)
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RESULT 4

US-09-978-697-17/C

; Sequence 17, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

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; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tunes, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
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;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores: 45  
Pred. No.: 382 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-697-17 (1-45)

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RESULT 5

US-09-978-192A-17/c

Sequence 17, Application US/09978192A

Patent No. US2002017553A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Saton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
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;; APPLICANT: Goddard, Audrey  
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;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James;  
;; APPLICANT: Peoni, Nicholas F.

;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C9  
;; CURRENT APPLICATION NUMBER: US/09/978,192A  
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Alignment Scores: 382 Length: 45  
Pred. No.: 35.00 Matches: 7  
Score: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-192A-17 (1-45)

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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
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; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Shelton, David L.

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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
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PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598

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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:      382      Length:      45
Score:          35.00    Matches:      7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match:      50.00% Indels:      0
DB:               9      Gaps:      0

US-09-980-881A-9 (1-14) x US-09-999-832A-17 (1-45)

Qy      1 SerAnProValGlutylLeuPro 10
Db      32 ACRAATGCCCGTTCAAGGCTGCTCC 3

RESULT 7
US-09-978-189-17/c
; Sequence 17, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gutney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 382  
Score: 35.00  
Percent Similarity: 80.00%  
Best Local Similarity: 70.00%  
Query Match: 50.00%  
DB: 10

Length: 45  
Matches: 7  
Conservative: 1  
Mismatches: 2  
Indels: 0  
Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-189-17 (1-45)  
Qy 1 SerAsnProValGluLysLeuLeuPro 10  
Db 32 AGCANTGCCCGTTCACAGGCTGCTCCCC 3

RESULT 8  
US-09-978-608A-17/c  
; Sequence 17, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 17
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-608A-17

Alignment Scores:
Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-608A-17 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 9
US-09-978-585A-17/c
; Sequence 17, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 17
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-585A-17

Alignment Scores:
Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-585A-17 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 10
US-09-978-191A-17/c
; Sequence 17, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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US-09-980-881A-9 (1-14) x US-09-978-191A-17 (1-45)

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 ; APPLICANT: Botstein, David  
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 ; APPLICANT: Eaton, Dan  
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 ; APPLICANT: Roy, Margaret Ann  
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 ; APPLICANT: Tumas, Daniel  
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 ; APPLICANT: Wood, William I.  
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54	PRIOR FILING DATE: 1998-05-13
55	PRIOR APPLICATION NUMBER: 60/085579
56	PRIOR FILING DATE: 1998-05-15
57	PRIOR APPLICATION NUMBER: 60/085582
58	PRIOR FILING DATE: 1998-05-15
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61	PRIOR APPLICATION NUMBER: 60/085689
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63	PRIOR APPLICATION NUMBER: 60/085579
64	PRIOR FILING DATE: 1998-05-15
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66	PRIOR FILING DATE: 1998-05-15
67	PRIOR APPLICATION NUMBER: 60/085573
68	PRIOR FILING DATE: 1998-05-15
69	PRIOR APPLICATION NUMBER: 60/085704
70	PRIOR FILING DATE: 1998-05-15
71	PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:

382

382  
35.00

**Length:**

45  
7

Length:  
Matches:

45  
7

Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 10 Indels: 0  
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-564A-17 (1-45)

QY 1 SerAnProValCluLysLeuPro 10  
DB 32 AGCAATGCCCGGTTCAGGCGCTGCTCCCC 3

RESULT 13

US-09-999-833A-17/c

Sequence 17, Application US/09999833A

Publication No. US20030054405A1

GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi
- APPLICANT: Baker Kevin P.
- APPLICANT: Botstein, David
- APPLICANT: Desnoyers, Luc
- APPLICANT: Eaton, Dan
- APPLICANT: Ferrara, Napoleon
- APPLICANT: Filvaroff, Ellen
- APPLICANT: Fong, Sherman
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Hillan, Kenneth J
- APPLICANT: Kiljavin, Ivar J.
- APPLICANT: Kuo, Sophia S.
- APPLICANT: Napier, Mary A.
- APPLICANT: Pan, James;
- APPLICANT: Paoni, Nicholas F.
- APPLICANT: Roy, Margaret Ann
- APPLICANT: Shelton, David L.
- APPLICANT: Stewart, Timothy A.
- APPLICANT: Tumas, Daniel
- APPLICANT: Williams, P. Mickey
- APPLICANT: Wood, William I.
- TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
- FILE REFERENCE: P26301C65
- CURRENT APPLICATION NUMBER: US/09/999,833A
- CURRENT FILING DATE: 2001-10-24
- PRIOR APPLICATION NUMBER: 09/918585
- PRIOR FILING DATE: 2001-07-30
- PRIOR APPLICATION NUMBER: 60/062250
- PRIOR FILING DATE: 1997-10-17
- PRIOR APPLICATION NUMBER: 60/064249
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- PRIOR FILING DATE: 1998-03-20
- PRIOR APPLICATION NUMBER: 60/078939
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 382  
Score: 35.00  
Percent Similarity: 80.00%  
Best Local Similarity: 70.00%  
Length: 45  
Matches: 7  
Conservative: 1  
Mismatch: 2

Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0  
US-09-980-881A-9 (1-14) x US-09-999-833A-17 (1-45)  
Qy 1 SerAsnProValGluLysLeuLeuPro 10  
Db 32 AGCAATCCCGGTTCAAGGCGCTGCTCCCC 3  
RESULT 14  
US-09-981-915A-17/c  
; Sequence 17, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Hillan, Kenneth J.  
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; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Sheiton, David L.  
; APPLICANT: Stewart, Daniel  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC12  
; CURRENT APPLICATION NUMBER: US/09/981.915A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

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US-09-980-881A-9 (1-14) x US-09-981-915A-17 (1-45)
Qy 1 SerAnProValGluLysLeuPro 10
Db 32 AGCAATGCCCGTTCAAGGCTGCTCCC 3

RESULT 15
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; Sequence 17, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
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; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
```





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OM protein - protein search, using sw model

Run on: October 27, 2004, 00:51:05 ; Search time 39 Seconds  
(without alignments)  
34,539 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3436

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: Pirl:\*

2: Pirl2:\*

3: Pirl3:\*

4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	41.4	13	2	B35245 histone H1.c - mou
2	28	40.0	19	2	S59485 hydroxyproline-rich
3	26	37.1	13	2	A35245 histone H1a - mous
4	26	37.1	14	2	C33098 223K exoantigen -
5	26	37.1	14	2	D61308 hemocyanin chain 5
6	25	35.7	14	2	S65392 cytochrome-c oxida
7	24.5	35.0	18	2	I52614 u-plasminogen acti
8	24	34.3	12	2	PA0098 ribosomal protein
9	23	32.9	10	2	S65715 aryl hydrocarbon (
10	23	32.9	18	2	S09026 carboxylesterase (
11	22	31.4	13	2	PT0331 Ig heavy chain CRD
12	22	31.4	15	2	S27248 pseudogargin - whe
13	22	31.4	15	2	PD0444 coupling factor 6
14	21	30.0	11	1	XASNBA bradykinin-potent
15	21	30.0	11	2	I33098 173K exoantigen -
16	21	30.0	11	2	F33098 214K exoantigen (v
17	21	30.0	13	2	B19434 probable sex-speci
18	21	30.0	14	2	PA0111 protein QA100054 -
19	21	30.0	18	2	S56715 hydroxymethylgluta
20	20	28.6	8	2	S16324 hydrothetical prote
21	20	28.6	9	2	S66419 tetrameric protein
22	20	28.6	10	2	S18396 probable glucose-6
23	20	28.6	10	2	C35389 urease (EC 3.5.1.5
24	20	28.6	10	2	B61218 alpha-gliadin 6Ha
25	20	28.6	13	2	A40207 cell surface glyco
26	20	28.6	14	4	I52618 hemoglobin beta ch
27	20	28.6	15	2	S05700 insulin-like growt
28	20	28.6	15	2	S20410 protein kinase (EC
29	20	28.6	15	2	G24417 interphotoreceptor

protein Pfl - gold  
insulin-like growt  
hypothetical COI1/  
beta-Gliadine 13 -  
H4-transporing tw  
24K protein - List  
RNA polymerase bet  
N4-(beta-N-acetyl)  
MHC class I histoc  
crabrolin - Europe  
hemocyanin chain 2  
phosphoprotein, 80  
unidentified 22K p  
gene c-fms protein  
protein p12E - Pri  
blaz protein - Sta

ALIGNMENTS

RESULT 1

B35245  
Histone H1.c - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997

C:Accession: B35245

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A>Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ-

A:Reference number: A35245; MUID:90202935; PMID:1690730

A:Accession: B35245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <AWI>

C:Superfamily: histone H1

C:Keywords: chromosomal protein; nucleosome

Query Match 41.4%; Score 29; DB 2; Length 13;  
Best Local Similarity 55.6%; Pred. No. 75;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPPVEKLL 9  
DB 3 SGPPVSELI 11

RESULT 2

S59485

hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C>Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C:Accession: S59485; S59484; S59483

R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A>Title: Specificity in the immobilisation of cell wall proteins in response to differ-

A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59485

A:Molecule type: protein

A:Residues: 1-19 <WOJ>

A:Cross-references: UNIPROT:Q7M1M8

A>Note: hydroxyproline-rich cell wall glycoprotein, 42K

A:Accession: S59484

A:Molecule type: protein

A:Residues: 1-15 <WOW>

A>Note: hydroxyproline-rich cell wall glycoprotein, 84K

A:Accession: S59483

A:Molecule type: protein

A:Residues: 1-14 <WOF>

A>Note: hydroxyproline-rich cell wall glycoprotein, 136K, minor component

C:Superfamily: proline-rich protein 3

C:Keywords: glycoprotein; hydroxyproline

F;6,11,16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 40.0%; Score 28; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEK 7  
 Db 5 PPVEK 9  
 |||||  
 |||||

RESULT 3  
 A35245  
 histone H1a - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997  
 C:Accession: A35245  
 R:Ajiro, K.; Shibata, K.; Nishikawa, Y.  
 J. Biol. Chem. 265, 6494-6500, 1990  
 A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differentially phosphorylated serines  
 A:Reference number: A35245; PMID:1690730  
 A:Accession: A35245  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-13 <AJI>  
 C:Superfamily: histone H1  
 C:Keywords: chromosomal protein; nucleosome

Query Match 37.1%; Score 26; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNPPVEKLL 9  
 Db 3 TGPPVSELI 11  
 : ||| : ||  
 : ||| : ||

RESULT 4  
 C33098  
 223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: C33098  
 R:Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: C33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <NIC>

Query Match 37.1%; Score 26; DB 2; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPVEKL 8  
 Db 3 PPQEK 8  
 |||||  
 |||||

RESULT 5  
 D61308  
 hemocyanin chain 5A - Sahara scorpion (fragment)  
 C:Species: Androctonus australis (Sahara scorpion)  
 C>Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 09-Jul-2004  
 C:Accession: D61308  
 R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
 FEBS Lett. 106, 289-291, 1979  
 A:Title: Structural characterization of seven different subunits in Androctonus australis  
 A:Reference number: A61308; PMID:80047238; PMID:499512  
 A:Accession: D61308  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <JOL>

A:Cross-references: UNIPROT:Q7M486

Query Match 37.1%; Score 26; DB 2; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EKLPL 11  
 Db 7 ERLPL 12  
 |:||||  
 |:||||

RESULT 6

S65392

cytochrome-c oxidase (EC 1.9.3.1) chain VIII-L - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 07-May-1999

C:Accession: S65392; S65393; S65391

R:Schaeffer, H.; Noack, H.; Halanck, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term

A:Reference number: S65372; PMID:95324529; PMID:7601105

A:Accession: S65392

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SCH>

A:Accession: S65393

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SC2>

A:Accession: S65391

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SC3>

C:Keywords: oxidoreductase

Query Match 35.7%; Score 25; DB 2; Length 14;

Best Local Similarity 62.5%; Pred. No. 4.1e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNPPVEKL 8

Db 3 SKPPREQL 10

||| |||

RESULT 7

I52614

u-plasminogen activator receptor precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004

C:Accession: I52614

R:Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.

Blood 86, 624-635, 1995

A:Title: A conserved TATA-less proximal promoter drives basal transcription from the uro

A:Reference number: I52614; PMID:95329719; PMID:7605992

A:Accession: I52614

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-18 <RES>

A:Cross-references: UNIPROT:Q03405; GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g426198

C:Genetics:

A:Gene: uPAR

C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 35.0%; Score 24.5; DB 2; Length 18;

Best Local Similarity 58.3%; Pred. No. 6.6e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 2 NPPVEKLPLSL 13

Db 3 HPP---LLPLLL 11

:|| |||||

RESULT 8

PA0098  
ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: PA0098  
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi  
A:Reference number: PA0051  
A:Accession: PA0098  
A:Molecule type: protein  
A:Residues: 1-12 <CHO>  
A:Cross-references: UNIPROT:Q7M4X9

Query Match 34.3%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPPVEKLPL 11  
|:|:|:|:|  
Db 3 SPPVPTFGL 12

RESULT 9  
S65715  
aryl hydrocarbon (benzo[a]pyrene) hydroxylase (EC 1.14.14.-) cytochrome P450 K(Ah) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 29-Oct-1999  
C:Accession: S65715  
R:Ohgiya, N.; Yokota, H.; Takahashi, M.; Komoro, S.; Yuasa, A.  
Biochim. Biophys. Acta 1209, 122-130, 1996  
A:Title: Purification and properties of a new beta-naphthoflavone inducible cytochrome P  
A:Reference number: S65715; MUID:96195850; PMID:8605221  
A:Accession: S65715  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <OHG>  
C:Keywords: monooxygenase; oxidoreductase

Query Match 32.9%; Score 23; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 6.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLPL 10  
|:|:|:|  
Db 4 PVXLLPL 10

RESULT 10  
S09026  
carboxylesterase (EC 3.1.1.1) MK1, microsomal - crab-eating macaque (fragment)  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S09026  
R:Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A:Reference number: S09021; MUID:90179180; PMID:2310190  
A:Accession: S09026  
A:Molecule type: protein  
A:Residues: 1-18 <HOS>  
A:Cross-references: UNIPROT:Q7M2Q1  
C:Keywords: carboxylic ester hydrolase

Query Match 32.9%; Score 23; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPPV 5  
|:|:|:|  
Db 3 SSPPV 7

RESULT 11  
PT0331  
Ig heavy chain CRD3 region (clone J2-121) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0331  
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0331  
A:Molecule type: DNA  
A:Residues: 1-13 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPPVE 6  
|:|:|:|  
Db 8 NNPPFQ 13

RESULT 12  
S27248  
pseudogerm - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 29-Aug-1997  
C:Accession: S27248  
R:Lane, B.G.; Cuming, A.C.; Fregeau, J.; Carpita, N.C.; Harkman, W.J.; Bernier, F.; Drat  
Eur. J. Biochem. 209, 961-969, 1992  
A:Title: Germ in isoforms are discrete temporal markers of wheat development. Pseudogerm  
ated embryos, it is incorporated into cell walls.  
A:Reference number: S27247; MUID:93049354; PMID:1425703  
A:Accession: S27248  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <LAN>

Query Match 31.4%; Score 22; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 NPPVEKLPL 10  
|:|:|:|  
Db 7 NPPVTPXXP 15

RESULT 13  
PD0444  
coupling factor 6 mitochondrial - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 05-Feb-1999  
C:Accession: PD0444  
R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPID, August 1998  
A:Description: Proteome analysis of mouse brain.  
A:Reference number: PD0441  
A:Contents: Striatum  
A:Accession: PD0444  
A:Molecule type: protein  
A:Residues: 1-15 <KAW>  
C:Keywords: mitochondrion

Query Match 31.4%; Score 22; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVEKL 8  
|:|:|:|  
Db 6 PVQKL 10

```
RESULT 14
XASNBA
bradykinin-potentiating peptide B - mamushi
C:Species: Agkistrodon blomhoffi (mamushi)
C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C:Accession: A01254
R:Kato, H.; Suzuki, T.
Proc. Jpn. Acad. 46, 176-181, 1970
A:Reference number: A01254
A:Accession: A01254
A:Molecule type: protein
A:Residues: 1-11 <NA>
A:Cross-references: UNIPROT:P01021
A>Note: the sequence of the natural peptide was confirmed by the synthesis and analysis
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; vena
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      30.0%; Score 21; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 PPVEKLLP 10
      |||
DB      4 PPRPKIPP 11

RESULT 15
I33098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: I33098
R:Nichols, J. H.; Hager, L. P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: I33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NIC>

Query Match      30.0%; Score 21; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPVEKLLPL 11
      |||
DB      3 PPELPLFPI 11

Search completed: October 27, 2004, 01:06:06
Job time : 43 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 22:25:16 ; Search time 2863 Seconds  
(without alignments)  
178.189 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 214274

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DBV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US09980881/runat\_26102004\_083353\_5586/app\_query.fasta\_1.199  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=57  
-USER=US09980881@cgn\_1\_15180@runat\_26102004\_083353\_5586 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gssi:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	40	57.1	55	9 CR221258	Forward s
C 2	38	54.3	50	1 AU107009	AU107009 AU107009
C 3	35	50.0	56	8 AZ808573	AZ808573 2M0072K08
C 4	33	47.1	43	1 A1655018	A1655018 wb66b02.x
C 5	33	47.1	43	9 TA279C01P	AL487206 T. brucei
C 6	33	47.1	44	9 CL675662	CL675662 PRI0115C
C 7	33	47.1	49	1 AA482011	AA482011 zu98c07.s
C 8	33	47.1	52	1 AA897173	AA897173 am09d08.s
C 9	33	47.1	53	9 CR026397	CR026397 Forward s

10	33	47.1	56	6 CF314148	CF314148 HD--02-J0
11	33	47.1	56	7 CF866287	CF866287 tr1c086xc
12	32.5	46.4	50	7 CN869022	CN869022 001202AAO
C 13	32	45.7	31	1 A1760292	A1760292 wg59f03.x
C 14	32	45.7	38	8 A2964138	A2964138 2M0233N11
C 15	32	45.7	43	9 CL654491	CL654491 PRI0120C
C 16	32	45.7	45	9 AU590579	AU590579 Arabidops
C 17	32	45.7	48	8 BH790348	BH790348 SALK_0568
C 18	32	45.7	49	1 AA865390	AA865390 oh49f11.s
C 19	32	45.7	50	1 AU107993	AU107993 AU107993
C 20	32	45.7	51	1 AV528824	AV528824 AV528824
C 21	32	45.7	53	1 AL965914	AL965914 AL965914
C 22	31	44.3	41	9 BX943466	BX943466 Arabidops
C 23	31	44.3	50	6 CD029909	CD029909 mgmk016xm
C 24	31	44.3	50	8 A2805497	A2805497 2M0066K19
C 25	31	44.3	50	9 CR148320	CR148320 Forward s
C 26	31	44.3	53	9 BX891907	BX891907 Arabidops
C 27	31	44.3	54	7 CN756377	CN756377 ID0AAA18C
C 28	31	44.3	55	1 AU789274	AU789274 AU789274
C 29	31	44.3	57	7 CR429117	CR429117 CR429117
C 30	30	42.9	34	8 A2832181	A2832181 2M0112K19
C 31	30	42.9	43	4 BI460424	BI460424 603200910
C 32	30	42.9	45	9 BX945468	BX945468 Arabidops
C 33	30	42.9	45	9 CR356909	CR356909 Arabidops
C 34	30	42.9	48	8 BH627451	BH627451 100707180
C 35	30	42.9	48	8 BH904904	BH904904 SALK_1053
C 36	30	42.9	50	1 A1174165	A1174165 vz84f07.r
C 37	30	42.9	50	1 AU107434	AU107434 AU107434
C 38	30	42.9	50	8 A2767297	A2767297 1M0566G21
C 39	30	42.9	51	8 BH218345	BH218345 1006078E0
C 40	30	42.9	52	7 CN750625	CN750625 ApDT-XX-H
C 41	30	42.9	52	9 AG248432	AG248432 Lotus cor
C 42	30	42.9	53	6 CA840659	CA840659 MCT039H07
C 43	30	42.9	54	8 A2579138	A2579138 1M0363C03
C 44	30	42.9	55	1 AA937358	AA937358 ci08e10.s
C 45	30	42.9	55	9 CL293365	CL293365 02S0349-0

ALIGNMENTS

RESULT 1  
CR221258/c

LOCUS  
DEFINITION

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL

FEATURES  
source

CR221258 55 bp DNA linear GSS 06-JUL-2004  
Forward strand read from insert in 5'HPRT insertion targeting and  
chromosome engineering clone MHPN238119, genomic survey sequence.

CR221258.1 GI:50000107  
GSS; Genome survey sequence; MICER.  
Mus musculus (house mouse)  
Mus musculus

1 (bases 1 to 55)  
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
Rogers,J. and Bradley,A.

Direct Submission  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

Location/Qualifiers  
1..55  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN238119"  
/clone\_lib="MHPN"

ORIGIN

Alignment Scores:

Pred. No.: 681 Length: 55  
Score: 40.00 Matches: 8  
Percent Similarity: 81.82% Conservative: 1  
Best Local Similarity: 72.73% Mismatches: 2

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Query Match: 57.14% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CR221258 (1-55)

Qy 3 ProProValGlulysLeuLeuProLeuSerLeu 13
Db 50 CCCCCAGCAATCCCTACTCTCTCTCACTC 18

RESULT 2
LOCUS AU107009 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU107009 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV6C668, mRNA sequence.
ACCESSION AU107009
VERSION AU107009.1 GI:13556530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., See,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,F., Nakamura,F., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ZRV6C668"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Alignment Scores:
Pred. No.: 1.37e+03 Length: 50
Score: 38.00 Matches: 8
Percent Similarity: 90.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 1
Query Match: 54.23% Indels: 0
Gaps: 0
DB: 1

US-09-980-881A-9 (1-14) x AU107009 (1-50)
Qy 3 ProProValGlulysLeuLeuProLeuSer 12
Db 15 CCGTGTGTGGAGAACTGCTGCGGTGTCA 44

RESULT 3
LOCUS AZ808573 56 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0072K08F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0072K08 F, genomic survey sequence.
ACCESSION AZ808573
VERSION AZ808573.1 GI:12974037
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 56)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: K column: 08
Seq Primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 56.
FEATURES
source
1..56
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0072K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.: 5.33e+03 Length: 56
Score: 35.00 Matches: 7
Percent Similarity: 64.29% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 50.00% Indels: 0
Gaps: 0
DB: 8

US-09-980-881A-9 (1-14) x AZ808573 (1-56)
Qy 1 SerAsnProProValGlulysLeuLeuProLeuSerLeuLys 14
Db 15 TCAAAATCCCCCCCCACATATAAAATCATCCCTCATCTGCCTCAAA 56

RESULT 4
LOCUS AI655018 43 bp mRNA linear EST 04-MAY-1999
DEFINITION wb66b02.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2310603 3',
similar to TR:O35295 O35295 VASCULAR ACTIN SINGLE-STRANDED
DNA-BINDING FACTOR 2 P44 COMPONENT. 1, mRNA sequence.

```

ACCESSION AI655018  
 VERSION AI655018.1 GI:4738997  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 43)  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

#### FEATURES

source

1..43  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2310603"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP GC6"  
 /notes="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
 from the normalized library NCI-CGAP GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneIDs  
 1257096-125831, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

Alignment Scores:  
 Pred. No.: 8.75e+03 Length: 43  
 Score: 33.00 Matches: 6  
 Percent Similarity: 70.00% Conservatve: 1  
 Best Local Similarity: 60.00% Mismatches: 3  
 Query Match: 47.14% Indels: 0  
 DB: 1 Gaps: 0

US-09-980-881a-9 (1-14) x AI655018 (1-43)

QY 3 ProProValGlutylsLeuLeuProLeuSer 12  
 ||||| :|||  
 Db 3 CCGCGCTCGTGGCGCTCGCTGCGCTGTGTG 32

RESULT 5  
 TA279C01P 43 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 279c01, forward sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL487206  
 VERSION AL487206.1 GI:11852258  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

#### REFERENCE

AUTHORS

#### TITLE

JOURNAL

#### COMMENT

1 (bases 1 to 43)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genomic Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

#### FEATURES

source

1..43  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="279c01"

#### ORIGIN

Alignment Scores:  
 Pred. No.: 8.75e+03 Length: 43  
 Score: 33.00 Matches: 6  
 Percent Similarity: 75.00% Conservatve: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 47.14% Indels: 0  
 DB: 9 Gaps: 0

US-09-980-881a-9 (1-14) x TA279C01P (1-43)

QY 3 ProProValGlutylsLeuLeuPro 10

||||| :|||  
 Db 13 CCCCCCTTTTCAAAACTCTCCCT 36

#### RESULT 6

CL675662/c

LOCUS

DEFINITION

CL675662

PRIO115C.B08.2 - PRIO115C.BR (44) Mixed stage fosmid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic

survey sequence.

CL675662

CL675662.1 GI:50180358

GSS.

KEYWORDS

ORGANISM

Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

1 (bases 1 to 44)

Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer, R.J.

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

```

FEATURES
source
Location/Qualifiers
1..44
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strains="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
./note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 9e+03 Length: 44
Score: 33.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 47.14% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CL675662 (1-44)

QY 1 SerAsnProValGluLysLeuLeuProLeuSer 12
||| |||||::: ||||| ||| |||
Db 38 TCCCCCCCCCCTAAATAAAGCTCAGTCTCGATCA 3

RESULT 7
AA482011 49 bp mRNA linear EST 14-AUG-1997
LOCUS zu98c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746028 3'
DEFINITION similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN);, mRNA
sequence.
ACCESSION AA482011
VERSION AA482011.1 GI:2209689
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtrp/image.html

Trace considered overall poor quality
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Homo sapiens"
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/db_xref="GDB:5945466"
/db_xref="taxon:9606"
/clone_lib="IMAGE:746028"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
./note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman

FEATURES
source
Location/Qualifiers
1..44
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strains="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
./note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 9e+03 Length: 44
Score: 33.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 47.14% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CL675662 (1-44)

QY 1 SerAsnProValGluLysLeuLeuProLeuSer 12
||| |||||::: ||||| ||| |||
Db 38 TCCCCCCCCCCTAAATAAAGCTCAGTCTCGATCA 3

RESULT 7
AA482011 49 bp mRNA linear EST 14-AUG-1997
LOCUS zu98c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746028 3'
DEFINITION similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN);, mRNA
sequence.
ACCESSION AA482011
VERSION AA482011.1 GI:2209689
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtrp/image.html

Trace considered overall poor quality
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5945466"
/db_xref="taxon:9606"
/clone_lib="IMAGE:746028"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
./note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman

FEATURES
source
Location/Qualifiers
1..44
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strains="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
./note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 9e+03 Length: 44
Score: 33.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 47.14% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CL675662 (1-44)

QY 1 SerAsnProValGluLysLeuLeuProLeuSer 12
||| |||||::: ||||| ||| |||
Db 38 TCCCCCCCCCCTAAATAAAGCTCAGTCTCGATCA 3

RESULT 7
AA482011 49 bp mRNA linear EST 14-AUG-1997
LOCUS zu98c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746028 3'
DEFINITION similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN);, mRNA
sequence.
ACCESSION AA482011
VERSION AA482011.1 GI:2209689
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtrp/image.html

Trace considered overall poor quality
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5945466"
/db_xref="taxon:9606"
/clone_lib="IMAGE:746028"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
./note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman

FEATURES
source
Location/Qualifiers
1..44
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strains="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
./note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 9e+03 Length: 44
Score: 33.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 47.14% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CL675662 (1-44)

QY 1 SerAsnProValGluLysLeuLeuProLeuSer 12
||| |||||::: ||||| ||| |||
Db 38 TCCCCCCCCCCTAAATAAAGCTCAGTCTCGATCA 3

RESULT 7
AA482011 49 bp mRNA linear EST 14-AUG-1997
LOCUS zu98c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746028 3'
DEFINITION similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN);, mRNA
sequence.
ACCESSION AA482011
VERSION AA482011.1 GI:2209689
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtrp/image.html

Trace considered overall poor quality
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5945466"
/db_xref="taxon:9606"
/clone_lib="IMAGE:746028"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
./note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman

FEATURES
source
Location/Qualifiers
1..44
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strains="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
./note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 9e+03 Length: 44
Score: 33.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 47.14% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CL675662 (1-44)

QY 1 SerAsnProValGluLysLeuLeuProLeuSer 12
||| |||||::: ||||| ||| |||
Db 38 TCCCCCCCCCCTAAATAAAGCTCAGTCTCGATCA 3

RESULT 7
AA482011 49 bp mRNA linear EST 14-A
```

I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Donaldo.

## ORIGIN

Alignment Scores:  
Pred. No.: 1.1e+04 Length: 52  
Score: 33.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 47.14% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x AA897173 (1-52)

Qy 6 GluLyLeuLeuProLeuSerLeu 13

Db 24 GAGAAATTTCTTCCTTTATCCCTC 1

## RESULT 9

CR026397/c 53 bp DNA linear GSS 05-JUL-2004  
LOCUS Forward strand read from insert in 3'HPRT insertion targeting and  
DEFINITION chromosome engineering clone MHPPI35d08, genomic survey sequence.

ACCESSION CR026397

VERSION CR026397.1 GI:49759452

KEYWORDS GSS; genome survey sequence; MICR.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 53)  
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
Rogers,J., and Bradley,A.

TITLE Direct Submission

JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICR

## FEATURES

source  
1..53  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPPI35d08"  
/clone\_lib="MHP"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.13e+04 Length: 53  
Score: 33.00 Matches: 5  
Percent Similarity: 80.00% Conservative: 3  
Best Local Similarity: 50.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CR026397 (1-53)

Qy 3 ProProValGluLyLeuLeuProLeuSer 12

Db 47 CCCCCCTTGACTCTCTTGTCCCATATCA 18

## RESULT 10

CF314148 56 bp mRNA linear EST 15-AUG-2003  
LOCUS HD-02-J02.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD-02-J02, mRNA sequence.

ACCESSION CF314148

VERSION CF314148.1 GI:33685909

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 56)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1..56

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="HD-02-J02"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr- Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.2e+04 Length: 56  
Score: 33.00 Matches: 5  
Percent Similarity: 60.00% Conservative: 1  
Best Local Similarity: 50.00% Mismatches: 4  
Query Match: 47.14% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x CF314148 (1-56)

Qy 2 AnProProValGluLyLeuLeuProLeu 11

Db 22 AATCCCCCAATCCGATCTCGCTTCTCTT 51

## RESULT 11

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CF886287 56 bp mRNA linear EST 31-OCT-2003  
tric086xc09.g1 T-reesei mycelial culture, Version 6 October 2003  
Hypocrea jecorina cDNA clone tric086xc09, mRNA sequence.

CF886287

CF886287.1 GI:38140969

EST.

Hypocrea jecorina (anamorph: Trichoderma reesei)

Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 56)

Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,

Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,

Ward,M. and Dean,R.A.

Characterization of the protein processing and secretion pathways

in a comprehensive set of expressed sequence tags from Trichoderma

reesei

FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: ralph\_dean@ncsu.edu  
Seq primer: Lt-R1 primer.  
Location/Qualifiers

FEATURES  
source

1..56  
/organism="Hypocrea jecorina"  
/mol\_type="mRNA"  
/strain="QM6a"  
/db\_xref="taxon:51453"  
/clone="tric086xc09"  
/dev\_stage="mycelia"  
/clone\_lib="T.reesei mycelial culture, Version 6 October 2003"  
/notes="Vector: pREP3Y; Site\_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Alignment Scores:  
Pred. No.: 1.2e+04 Length: 56  
Score: 33.00 Matches: 5  
Percent Similarity: 88.89% Conservative: 3  
Best Local Similarity: 55.56% Mismatches: 1  
Query Match: 47.14% Indels: 0  
DB: Gaps: 0

US-09-980-881A-9 (1-14) x CF886287 (1-56)

Qy 2 AenProValGlulysLeuLeuPro 10  
|||||:|::|||:|::|||  
Db 9 AATCCGCCTATAAAAAAATAGGTGCT 35

RESULT 12  
CN869022 50 bp mRNA linear EST 03-JUN-2004  
LOCUS CN869022  
DEFINITION clone AA0A004091HT (AAOA) Royal Gala phloem Malus x domestica cDNA  
ACCESSION CN869022  
VERSION CN869022.1 GI:48126603  
KEYWORDS EST.  
SOURCE Malus x domestica (cultivated apple)  
ORGANISM Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE  
1 (bases 1 to 50)  
Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janesen,B.,  
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.,  
HortResearch Apple EST Project  
Unpublished (2004)  
Contact: Gleave,A.  
Sequencing Facility  
The Horticulture and Food Research Institute of New Zealand Ltd  
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand  
Tel: 00 64 09 815 4200  
Fax: 00 64 09 815 4201  
Email: est@hortresearch.co.nz.

FEATURES  
source

1..50  
/organism="Malus x domestica"  
/mol\_type="mRNA"  
/db\_xref="taxon:3750"  
/clone="AA0A004091"  
/tissue\_type="Phloem, scrapings from inside of bark mature wood"  
/clone\_lib="(AAOA) Royal Gala phloem"  
/notes="Vector: pBluescript SK(-); Library sequenced by Genesis Research & Development"

ORIGIN

Alignment Scores:  
Pred. No.: 1.29e+04 Length: 50  
Score: 32.50 Matches: 6  
Percent Similarity: 91.67% Conservative: 5

```

Query Match: 45.71% Indels: 0
DB: Gaps: 0

US-09-980-881A-9 (1-14) x AZ964138 (1-38)

QY 6 GluLysLeuLeuProLeuSerLeu 13
   ::|||::|||
DB 1 CAGAAATATTACCTCTCTCTC 24

RESULT 15
CL654491/c linear GSS 09-JUL-2004
LOCUS PRI0120c_H04 - PRI0120c_B21 (43) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL654491
VERSION CL654491.1 GI:50133440
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES             Location/Qualifiers
     source            1..43
     /organism="Pristionchus pacificus"
     /mol_type="genomic DNA"
     /strain="California"
     /db_xref="taxon:54126"
     /clone_lib="Mixed stage fosmid library of P. pacificus
     var. California"
     /notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores: 1.31e+04 Length: 43
Pred. No.: 32.00 Matches: 7
Score: 66.67% Conservative: 1
Percent Similarity: 58.33% Mismatches: 4
Best Local Similarity: 45.71% Indels: 0
Query Match: 9 Gaps: 0
DB:

US-09-980-881A-9 (1-14) x CL654491 (1-43)

QY 2 AsnProValGluLysLeuLeuProLeuSerLeu 13
   ::|||
DB 39 TCCCTCTCTCTCTCCACTCTCTCTCTCTCTC 4

Search completed: October 26, 2004, 23:47:45
Job time : 2867 secs

```

Search completed: October 26, 2004, 23:47:45  
Job time : 2867 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 23:47:55 ; Search time 134 Seconds  
(without alignments)  
60.114 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 12441

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	40.0	14	2	Q16232 homo sapien
2	28	40.0	19	2	Q7M1M8 phaseolus v
3	28	40.0	19	2	Q9S8G9 psophocarpu
4	26.5	37.9	19	2	Q94106 brassica na
5	26	37.1	14	2	Q7M486 androctonus
6	25	35.7	10	1	Q7M486 canis fami
7	25	35.7	10	1	Q8CJEO rattus norv
8	25	35.7	11	2	Q8IVG8 homo sapien
9	25	35.7	11	2	Q47604 escherichia
10	25	35.7	11	2	Q47604 escherichia
11	25	35.7	11	2	Q47604 escherichia
12	25	35.7	15	2	Q714T7 prionitis 1
13	25	35.7	15	2	Q714T7 prionitis 1
14	24	34.3	12	2	Q8KXP2 clostridium
15	24	34.3	16	2	Q9QYF8 cricetus
16	24	34.3	16	2	Q6WV37 simian t-ly
17	24	34.3	16	2	Q6WV42 simian t-ly
18	24	34.3	16	2	Q6WV42 simian t-ly
19	24	34.3	16	2	Q6WV42 simian t-ly
20	24	34.3	16	2	Q6WV42 simian t-ly
21	24	34.3	18	1	Q8CJEO rattus norv
22	24	34.3	18	1	Q8CJEO rattus norv
23	24	34.3	19	1	Q8CJEO rattus norv
24	23	32.9	15	2	Q8RKN0 escherichia
25	23	32.9	16	2	Q79034 emericella
26	23	32.9	18	2	Q7M201 macaca fasc
27	23	32.9	18	2	Q41588 human immu
28	23	32.9	19	2	Q9BDX2 macaca mula
29	23	32.9	19	2	Q33755 streptococ
30	22	31.4	14	2	Q35917 rattus norv
31	22	31.4	15	1	UC17_MAIZE

Q61ail drosophila  
Caa76424 drosophil  
Caa76430 drosophil  
Caa76436 drosophil  
Caa76442 drosophil  
Caa76448 drosophil  
Caa76454 drosophil  
Caa76460 drosophil  
Caa76466 drosophil  
Caa76476 drosophil  
Q8J696 human t-lym  
Q8J697 human t-lym  
Q8J698 human t-lym  
Q8J699 human t-lym

## ALIGNMENTS

RESULT 1  
Q16232 PRELIMINARY; PRT; 14 AA.  
AC Q16232  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE NF2 protein (Fragment).  
GN Name=NF2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94348501; PubMed=8069299;  
RA Arakawa H., Hayashi N., Nagase H., Ogawa M., Nakamura Y.;  
RT "Alternative splicing of the NF2 gene and its mutation analysis of  
RT breast and colorectal cancers.";  
RL Hum. Mol. Genet. 3:565-568(1994).  
DR EMBL, S73855; AAD14139.1; -;  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1513 MW; 82766855653CBB2A CRC64;

Query Match 40.0%; Score 28; DB 2; Length 14;  
Best Local Similarity 58.3%; Pred. No. 8.1e+02;  
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 PPVEKLLPLSLK 14  
| | | | |  
Db 3 PKAEDLSALSLSK 14

## RESULT 2

Q7M1M8 PRELIMINARY; PRT; 19 AA.  
AC Q7M1M8  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hydroxyproline-rich cell wall glycoprotein (42k and others)  
DE (Fragment).  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3885;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96011753; PubMed=7548825;  
RA Wojtaszek P., Trehowan J., Bolwell G.P.;  
RT "Specificity in the immobilisation of cell wall proteins in response  
RT to different elicitor molecules in suspension-cultured cells of French  
RT bean (Phaseolus vulgaris L.).";

RL Plant Mol. Biol. 28:1075-1087(1995).

DR PIR; S59485; S59485.

FT NON\_TER 1

FT NON\_TER 19

SQ SEQUENCE 19 AA; 2225 MW; 53AB9D0984A87E0A CRC64;

Query Match 40.0%; Score 28; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7

|||||

5 PPVEK 9

RESULT 3

Q9S8G9

ID Q9S8G9 PRELIMINARY; PRT; 19 AA.

AC Q9S8G9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE Proline-rich protein (Fragment).

OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

OC Psophocarpus.

OX NCBI\_TaxID=3891;

RN [1]

RP SEQUENCE.

RX MEDLINE=95277008; PubMed=7757337;

RA Esaka M., Hayakawa H.;

RT "Specific secretion of proline-rich proteins by salt-adapted winged

bean cells.";

RL Plant Cell Physiol. 36:441-446(1995).

SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match 40.0%; Score 28; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7

|||||

5 PPVEK 9

RESULT 4

Q94L06

ID Q94L06 PRELIMINARY; PRT; 19 AA.

AC Q94L06;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Isopropyl malate synthase (Fragment).

GN Name=Mt24-1-BN-7;

OS Brassica napus (Rape).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucosids II; Brassicales; Brassicaceae; Brassica.

OX NCBI\_TaxID=3708;

RN [1]

RP SEQUENCE FROM N.A.

RA Fourmann M., Proger N., Brunel D.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF258256; AAK49052.1; --

FT NON\_TER 1

FT NON\_TER 19

SQ SEQUENCE 19 AA; 1989 MW; A41FC1E46CFC0E6D CRC64;

Query Match

Best Local Similarity 46.2%; Score 26.5; DB 2; Length 19;

Matches 6; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2 NPPVEKLLPLSLK 14

|||||

3 NAPLEKVV-MALK 14

RESULT 5

Q7M486

ID Q7M486 PRELIMINARY; PRT; 14 AA.

AC Q7M486;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hemocyanin chain SA (Fragment).

OS Androctonus australis (Sahara scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Buthida; Buthoidea; Buthidae; Androctonus.

OX NCBI\_TaxID=6858;

RN [1]

RP SEQUENCE.

RA Jolles J., Jolles P., Lamy J., Lamy J.;

RT "Structural characterization of seven different subunits in

Androctonus australis haemocyanin.";

RL FEBS Lett. 106:289-291(1979).

DR PIR; D61308; D61308.

FT NON\_TER 1

FT NON\_TER 14

SQ SEQUENCE 14 AA; 1658 MW; 6FA4342770FEAF0B CRC64;

Query Match 37.1%; Score 26; DB 2; Length 14;

Best Local Similarity 83.3%; Pred. No. 1.8e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 EKLLPL 11

|||||

7 ERLPL 12

RESULT 6

CK82\_CANFA

ID CK82\_CANFA STANDARD; PRT; 10 AA.

AC P61905;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cytochrome c oxidase polypeptide VIII-liver (EC 1.9.3.1) (Cytochrome c

oxidase subunit 8-2) (Fragment).

GN Name=COX8A;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=96092035; PubMed=8529022;

RA Linder D., Freund R., Kadenbach B.;

RT "Species-specific expression of cytochrome c oxidase isozymes.";

Comp. Biochem. Physiol. 112B:461-469(1995).

CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide

chains of cytochrome c oxidase, the terminal oxidase in

mitochondrial electron transport.

CC -!- CATALYTIC ACTIVITY: 4 ferrocyanide c + O(2) = 4 ferricyanide

c + 2 H(2)O.

CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -!- TISSUE SPECIFICITY: Liver specific isoform.

CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.

KW Direct protein sequencing; Inner membrane; Mitochondrion;

FT NON\_TER 10

FT NON\_TER 10

SQ SEQUENCE 10 AA; 1204 MW; 9304F6041776325 CRC64;

Query Match

35.7%; Score 25; DB 1; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPPVEKL 8  
Db 3 SKPPREQL 10

RESULT 7  
ID Q8CJEO PRELIMINARY; PRT; 10 AA.  
AC Q8CJEO;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Resistin (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Nohira T., Hisatomi H.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB093559; BAC21195.1; -.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1079 MW; 34EA46D326DDC777 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPVEKL 10  
Db 3 PPAQKAQP 10

RESULT 8  
ID Q8IVG8 PRELIMINARY; PRT; 11 AA.  
AC Q8IVG8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Low density lipoprotein receptor related protein 1 (Lipoprotein receptor-related protein) (Fragment).  
GN Name=LRP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Glaeser C.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Schulz S.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RX MEDLINE=90089395; PubMed=2597675;  
RA Kuett H.C., Herz J., Stanley K.K.;  
RT "Structure of the low-density lipoprotein receptor-related protein (LRP) promoter.";  
RL Biochim. Biophys. Acta 1009:229-236 (1989).  
DR EMBL; Y18524; CAD57169.1; -.  
DR EMBL; X15424; CAA33464.1; -.

DR CO; GO:0004872; F:receptor activity; IEA.  
KW Lipoprotein; Receptor.  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 2.1e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPVEKL 10  
Db 4 PPLL 11

RESULT 9  
ID Q47604 PRELIMINARY; PRT; 11 AA.  
AC Q47604;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE REase protein (Fragment).  
GN Name=REase;  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-modification systems.";  
RT J. Bacteriol. 173:1367-1375 (1991).  
RL EMBL; M63621; AAA24560.1; -.  
FT NON\_TER 11  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 55.6%; Pred. No. 2.1e+03;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPPVEKL 9  
Db 2 SHEDLNKL 10

RESULT 10  
ID CAA33464 PRELIMINARY; PRT; 11 AA.  
AC CAA33464;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Lipoprotein receptor-related protein (Fragment).  
GN LRP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RA Kuett H.C., Herz J., Stanley K.K.;  
RT "Structure of the low-density lipoprotein receptor-related protein (LRP) promoter.";  
RL Biochim. Biophys. Acta 1009:229-236 (1989).  
DR EMBL; X15424; CAA33464.1; -.  
KW Receptor.  
FT NON\_TER 11  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 11;

Best Local Similarity 62.5%; Pred. No. 2.1e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVEKLLP 10  
||: |||  
Db 4 PELLLLP 11

## RESULT 11

Q714T7 PRELIMINARY; PRT; 15 AA.  
AC Q714T7; (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE tRNA proteolysis tag (Fragment).  
GN Name=s8rA;  
OS Prionitis lanceolata.  
OG Chloroplast.  
OC Eukaryota; Rhodophyta; Florideophyceae; Halymeniales; Halymeniaceae;  
OC Prionitis.  
OX NCBI\_TaxID=31457;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14681369;  
RA Gueneau de Novoa P., Williams K.P.;  
RT "The tRNA website: reductive evolution of tRNA in plastids and other endosymbionts.";  
RL Nucleic Acids Res. 32:D104-D108(2004).  
DR EMBL; AF550353; AAQ12669.1; --  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1659 MW; 44990BB95D14E2B2 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. No. 3e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 KLLPLSLK 14  
||: |||  
Db 4 QILPLSRK 11

## RESULT 12

AAQ12669 PRELIMINARY; PRT; 15 AA.  
AC AAQ12669;  
DT 02-MAR-2004 (TREMBlrel. 27, Created)  
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
DE tRNA proteolysis tag (Fragment).  
GN SSRA.  
OS Prionitis lanceolata.  
OG Chloroplast.  
OC Eukaryota; Rhodophyta; Florideophyceae; Halymeniales; Halymeniaceae;  
OC Prionitis.  
OX NCBI\_TaxID=31457;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14681369;  
RA Gueneau de Novoa P., Williams K.P.;  
RT "The tRNA website: reductive evolution of tRNA in plastids and other endosymbionts.";  
RL Nucleic Acids Res. 32:D104-D108(2004).  
DR EMBL; AF550353; AAQ12669.1; --  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1659 MW; 44990BB95D14E2B2 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. No. 3e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 KLLPLSLK 14

Db 4 QILPLSRK 11  
||: |||  
||: |||

## RESULT 13

Q7M4X9 PRELIMINARY; PRT; 12 AA.  
AC Q7M4X9; (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Ribosomal protein S3 (Fragment).  
OS Fusarium sporotrichioides.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
OX NCBI\_TaxID=5514;  
RN [1]  
RP SEQUENCE.  
RA Chow L.P., Fukaya N., Sugiura Y., Ueno Y., Tabuchi K., Taugita A.;  
RL Submitted (OCT-1994) to the PIR data bank.  
DR PIR; PA0098; PA0098.  
FT NON\_TER 1  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1242 MW; 227BFCBA7C2772D7 CRC64;

Query Match 34.3%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 3.5e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPPVEKLLPL 11  
||: |||  
Db 3 SPPVPKTFGL 12

## RESULT 14

Q8KPF2 PRELIMINARY; PRT; 16 AA.  
AC Q8KPF2;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Putative glycosyl transferase (Fragment).  
OS Clostridium perfringens.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1502;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=ATCC 10543;  
RX MEDLINE=22194081; PubMed=12204375;  
RA Calcutt M.J., Hsieh H.-Y., Chapman L.F., Smith D.S.;  
RT "Identification, molecular cloning and expression of an alpha-N-acetylglactosaminidase gene from Clostridium perfringens.";  
RL FEMS Microbiol. Lett. 214:77-80(2002).  
DR EMBL; AY121611; AAM55478.1; --  
DR GO; GO:0016740; F:transferase activity; IEA.  
KW Transferase.  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1828 MW; C8C94354576B7B8F CRC64;

Query Match 34.3%; Score 24; DB 2; Length 16;  
Best Local Similarity 27.3%; Pred. No. 4.8e+03;  
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 PVEKLLPLSLK 14  
||: ||: |||  
Db 6 PIDTWIKIELK 16

## RESULT 15

Q9QUY8 PRELIMINARY; PRT; 16 AA.  
ID Q9QUY8  
AC Q9QUY8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Histone H1 (Fragment).  
OS Cricetulus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96070893; PubMed=7499230;  
RA Gurley L.R., Valdez J.G., Buchanan J.S.;  
RT "Characterization of the mitotic specific phosphorylation site of  
RT histone H1. Absence of a consensus sequence for the p34cdc2/cyclin B  
RT kinase.";  
RL J. Biol. Chem. 270:27653-27660(1995).  
SQ SEQUENCE 16 AA; 1479 MW; 75EB488737288C8A CRC64;  
  
Query Match 34.3%; Score 24; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 4.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 PPVEK 7  
Db 12 PPAEK 16  
  
Search completed: October 27, 2004, 01:05:16  
Job time : 139 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: October 27, 2004, 09:22:01 ; Search time 30.5 Seconds  
(without alignments)  
4696.619 Million cell updates/sec

Title: US-09-980-881A-1\_COPY\_18\_1097  
Perfect score: 1932  
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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 478139 seqs, 66318000 residues  
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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilesl.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1852.5	95.9	386	4	US-09-813-133A-2
2	1835	95.0	423	1	US-07-649-591B-3
3	1835	95.0	423	1	US-08-277-540-3
4	1835	95.0	423	1	US-08-430-787A-3
5	1835	95.0	423	2	US-08-869-057-2
6	1824	94.4	423	4	US-09-813-133A-4
7	640.5	33.2	404	1	US-08-696-139-2
8	639.5	33.1	415	2	US-08-860-882A-57
9	639.5	33.1	415	4	US-09-011-769A-39
10	638	33.0	417	1	US-07-649-591B-7
11	638	33.0	417	1	US-08-277-540-7
12	638	33.0	417	1	US-08-430-787A-7

13	635	32.9	417	1	US-07-649-591B-6
14	635	32.9	417	1	US-08-277-540-6
15	635	32.9	417	1	US-08-430-787A-6
16	635	32.9	417	4	US-09-917-254-66
17	632	32.7	424	4	US-09-011-769A-56
18	623	32.2	716	3	US-09-171-945-125
19	613.5	31.8	437	4	US-09-675-305-10
20	613.5	31.8	437	4	US-10-200-344-10
21	604	31.3	307	2	US-08-782-760-6
22	604	31.3	307	5	PCT-US96-00995-6
23	603.5	31.2	396	1	US-07-649-591B-4
24	603.5	31.2	396	1	US-08-277-540-4
25	603.5	31.2	396	1	US-08-430-787A-4
26	576	29.8	306	1	US-08-696-139-4
27	561	29.0	329	4	US-09-011-769A-51
28	561	29.0	349	4	US-09-011-769A-47
29	560	29.0	613	3	US-09-171-945-113
30	554	28.7	349	4	US-09-011-769A-60
31	553	28.6	349	4	US-09-011-769A-64
32	553	28.6	417	1	US-07-649-591B-8
33	553	28.6	417	1	US-08-277-540-8
34	553	28.6	417	1	US-08-430-787A-8
35	546	28.3	399	4	US-09-710-099-8
36	546	28.3	399	4	US-10-200-910-8
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44	513	26.6	417	3	US-08-640-906-4
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ALIGNMENTS

RESULT 1  
US-09-813-133A-2

; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

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Score: 1852.50 Matches: 354  
Percent Similarity: 94.16% Conservative: 1  
Best Local Similarity: 93.90% Mismatches: 5  
Query Match: 95.89% Indels: 18  
DB: 4 Gaps: 1

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Db	1	McLysBueCySerLeuValProIleValPheCysGluGlnHieVal	20
QY	61	TTTCGGCTTCAGAGTGGCGAAGTCTTAGTCTTCTTAGAACCTCTAGGCAAGTTCAA	120

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Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Qy 121 GTTCTACAGAATCTTACTACACATATGAGATTGTTCTCGCAGCCGGTAACAGCTGAC 180
Db 41 ValLeuGlnAenLeuThrThrThrTyrGluileValLeuTrpGlnProValThrAlaAsp 60
Qy 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGATCTGATGTCGACAAATGTG 240
Db 61 LeuileVallyLysLysGlnValHisPhePheValAenAlaSerAspValAspAenVal 80
Qy 241 AAAGCCCATTTAAATGTGAGCGGAATCCATGTCAGTGTCTTCTGGCAGAGCTGCAAGAT 300
Db 81 LysAlaHisLeuAenValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp 100
Qy 301 CTTATTCAACAGCAGATTTCACAGACACAGTACGCCCCCGAGCCTCGCATCGTACTAT 360
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Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAenAlaIleTrpIleAspCysGlyIle 180
Qy 541 CATGCCAGAGATGATCTCTCTGCTTCCTGCTTCTGCTGTTTCATAGGCGCAATCGCATG 600
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAenArgMet 200
Qy 601 TGGAGAAAGAACCGTTCTTTCTATCGCAACATCATTCATCGGAACAGACTCAATAGC 660
Db 201 TrpArgLysAenArgSerPheTyrAlaAenAenHisCysIleGlyThrAspLeuAenArg 220
Qy 661 AACTTTGTCTCAACACTGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAC 720
Db 221 AenPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 240
Qy 721 TACTGTGACATTTATCTGAGTCAAGACAGACAGTGAAGTGGCTGAGTCTTCTGAGA 780
Db 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaAlaLaserPheLeuArg 260
Qy 781 AGAATATCAACAGATTAAGCATACATCATCATGATGCAATTCATCTCCAGCATATAGT 840
Db 261 ArgAenIleAenGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
Qy 841 TTTCCATATTCCTATACACGAGTAAAGCAAGCAACCATGAGGAACCTGCTCTAGTAGCC 900
Db 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
Qy 901 AGTGAGCAGTTCGTGCTTATCACAAACTAGTAAATAATACAGTATACACATGGCCAT 960
Db 301 SerGluAlaValArgAlaIleGluLysIleSerLysAenThrArgTyrThrHisGlyHis 320
Qy 961 GCCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGACGATGATGATCTATGATTTGGC 1020
Db 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340
Qy 1021 ATCAAAATTCGTT----- 1034
Db 341 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 360
Qy 1035 -----TACATCAACCCACTGTAGAGACGTTTTTGCCTGCTCTCTAAA 1079
Db 361 GluArgTyrIleLysProThrCysArgGluAlaPheAlaAlaValSerLys 377

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RESULT 2

US-07-649-591B-3

; Sequence 3, Application US/07649591B

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; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-649-591B-3

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Alignment Scores:

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Pred. No.: 2,49e-206 Length: 423
Score: 1835.00 Matches: 356
Percent Similarity: 86.23% Conservative: 1
Best Local Similarity: 85.99% Mismatches: 3
Query Match: 94.98% Indels: 55
DB: 1 Gaps: 2

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US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-07-649-591B-3 (1-423)

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Qy 1 ATGAGAGCTTTGACAGCTTGTGAGTCCCTTGTACCCATTTGTTCTTCTGTGAGCAGCATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Qy 61 TTCGCGTTCCAGAGTGCCCAAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Qy 121 GTTCTACAGAATCTTACTACAAATATGAGATTGTTCTTCTGGCAGCCGGTAACAGCTGAC 180
Db 41 ValLeuGlnAenLeuThrThrThrTyrGluileValLeuTrpGlnProValThrAlaAsp 60
Qy 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGATCTGATGTCGACAAATGTG 240
Db 61 LeuileVallyLysLysGlnValHisPhePheValAenAlaSerAspValAspAenVal 80
Qy 241 AAAGCCCATTTAAATGTGAGCGGAATCCATGTCAGTGTCTTCTGGCAGAGCTGCAAGAT 300
Db 81 LysAlaHisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Qy 301 CTTATTCAACAGCAGATTTCACAGACACAGTACGCCCCCGAGCCTCGCATCGTACTAT 360
Db 101 LeuileGlnGlnGlnIleSerAenAspThrValSerProArgAlaSerAlaSerTyrTyr 120

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QY 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGATAGAAATTTTAACTCAGAGCAT 420
DB 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTTACAAAATCCACATTCGATCCTCATTTGAGAAGTACCACCTCTATGTT 480
DB 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAGGTTCTCGAAGAAGAACACAGCCCAAAATGCCATATGCTGATTCACCTGTGGAATC 540
DB 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 541 CATGCCAGAAATGGAATCTCTCTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
DB 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 ----- 591
DB 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----AATCGAATGTGGAGAAAG 609
DB 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTTCTATCGCAACATCATTCATCGGAACAGACCTGAATAGCAACTTGTGTC 669
DB 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGA 729
DB 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTATCCTGAGTCAGAACCCAGACGAGGAGGAGTGGCTAGTCTTCTTGAGAGAAATATC 789
DB 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
QY 790 AACCAATTAAGCATACATCAGCATGCATCTTCTACTCCAGCATATAGTGTTCATAT 849
DB 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCTATACAGAAAGTAAAGCAAGAACCATGAGGAATCTGTCTCTAGTACCGAGTGAAGA 909
DB 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTACAAACTAGTAAATATACAGGTATACATGCGCATGCGCTCAGAA 969
DB 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATACCTAGTCTCTGAGGTGGGACGATGATGATCTATGATTTGGGCATCAATAT 1029
DB 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCCTT-----TAC 1037
DB 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCAGCTGAGAGAGCTTTGCGCTGCTCTAAA 1079
DB 401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLys 414

RESULT 3
US-08-277-540-3
; Sequence 3, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Dravna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
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; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-277-540-3

Alignment Scores:
Pred. No.: 2,49e-206 Length: 423
Score: 1835.00 Matches: 356
Percent Similarity: 86.23% Conservative: 1
Best Local Similarity: 85.99% Mismatches: 3
Query Match: 94.98% Indels: 55
DB: 1 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-277-540-3 (1-423)

QY 1 ATGACGCTTTGACAGCTTCAGCTCCTGTGACCATGTTCTCTCTGTCAGCAGCATGTC 60
DB 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 120
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGAACTTACTACACATATGAGATGTTCTTCTGGCAGCGCGTAAACAGCTGAC 180
DB 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTCAAGAAAACCAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACAATGTG 240
DB 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGTCAGACGCTGGAAGAT 300
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTCCACAGACACAGTCAGCCCCCGAGCTCCGATCTGCTACTAT 360
DB 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGATAGAAATTTTAACTCAGAGCAT 420
DB 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
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QY 421 CCTGATATGCTTACAAAATCCACATTCGATCCTCATTTGAGAGTACCCTCTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAAGGTTTCTGGAAGAGACAAACAGCAGCAAAATGCCATATGATGATGCTGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAspCysGlyIle 180
QY 541 CATGCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
Db 181 HisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheIleGlyHisIleThrGln 200
QY 591 ----- 591
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----AATCGAATGTGGAGAAAG 609
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTyrLysAsnArgMetTyrArgLys 240
QY 610 AACCGTTCTTTCTATGCGAACAATCATTCGACGAGACAGACCTGAATAGCACTTGTCTC 669
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCACAACTGTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGA 729
Db 261 SerLysHisTyrCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCTGAGTTCAGAACCAAGTGAAGGAGGAGTGTCTCTCTCTCTCTCTCTCTCT 789
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 300
QY 790 AACCAAGATTAAAGCATACATCAGCATGATTCATATCTCCAGCATATAGTGTTCATAT 849
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACAGCAAGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 909
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTGCAAAACTAGTAAATACCAATACCAATACCAATACCAATACCAAT 969
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATACCTAGCTCTGAGGTGGGAGCAATGATGATGATGATGATGATGATGATGAT 1029
Db 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTyrPheTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAA 1079
Db 401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLys 414

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RESULT 4

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US-08-430-787A-3
; Sequence 3, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-430-787A-3

Alignment Scores:
Pred. No.: 2,49e-206 Length: 423
Score: 1835.00 Matches: 356
Percent Similarity: 86.23% Conservative: 1
Best Local Similarity: 85.99% Mismatches: 3
Query Match: 94.98% Indels: 55
DB: 1 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-430-787A-3 (1-423)

QY 1 ATGAAGCTTTTCAGGCTTGCAGTCTCTTACCCATTGTTCTCTCTGAGCAGCATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGTTTCCAGAGTGGCCAAAGTTCTAGTCTCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaIleLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGATCTTACTACAAATATAGATGTTGTTCTCTGCGAGCCCGGTACAGCTGAC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
QY 181 CTTATTGTGAAGAAAACACAGTCCATTTTGTAAATGCATCTGTGTCGACAAATGTG 240
Db 61 LeuIleValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTCTGCGCAGAGCTGGAAGAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTCCAAACAGACAGTACAGCCCGGAGCTCCGATCGTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATACTGAGAGGAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTyrPheIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTACAAAATCCACATTCGATCCTCATTTGAGAGTACCCTCTATGTT 480

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Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTyrVal 160
QY 481 TTAAGGTTCTTGGAAGAAACAAACAGCCAAAATGTCATATGATGACTGTGGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 541 CATGCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 ----- 591
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----AATCGAATGTGGGAAG 609
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTCTATCGCAACATCATTCATCGGACAGACTGAATAGCAACTTTGTC 669
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCCAAACACTGGTGCAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGA 729
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCTCTGAGTCAGAACACAGAGTGAAGGAGTGGCTAGTTTCTTGAGAGAAATATC 789
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
QY 790 AACCATTAAGCATACATCAGCATGCTTCTACTCCAGCATATAGTTTCCATAT 849
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACAGAAAGTAAAGCAAGACCATGAGAACTGTCTCTAGTACGACGAGCA 909
Db 321 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTCAAAACACTAGTAAATAACAGGTATACATGCGCATGCTCAGAA 969
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATCTACTCTCTGAGTGGGAGCATGATGATCTATCATTTGGGCATCAATAT 1029
Db 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTTAAA 1079
Db 401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLys 414

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RESULT 5

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US-08-869-057-2
; Sequence 2, Application US/08869057
; Patent No. 5985562
; GENERAL INFORMATION:
; APPLICANT: Morser, Michael J
; APPLICANT: Nagashima, Mariko
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease
; TITLE OF INVENTION: Risk
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Berlex Biosciences Legal Department
; STREET: 15049 San Pablo Avenue
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804-0099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,057
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Washtien, Wendy L
; REGISTRATION NUMBER: 36,301
; REFERENCE/DOCKET NUMBER: 51509AUSM1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-262-5411
; TELEFAX: 510-262-7095
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Plasma
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 23..401
; US-08-869-057-2

Alignment Scores:
Pred. No.: 2,49e-206 Length: 423
Score: 1835.00 Matches: 356
Percent Similarity: 86.23% Conservativity: 1
Best Local Similarity: 85.99% Mismatches: 3
Query Match: 94.98% Indels: 55
DB: 2 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-869-057-2 (1-423)

QY 1 ATGAGCTTTTGAGCTTGCAGCTTGCAGTCTTGTACCATTTGTTCTTCTGTGAGCAGCATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCCGGCTTCCAGAGTGGCCAACTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGAACTTACTACAACTATGAGATTGTTCTTCTGCGCCGGGTACAGCTGAC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTCAAGAAAACAAAGTCCATTTTTTTGTAATGTCATCTGATGCGACAATGTG 240
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTCACAGACAGACAGTCCGCCCCGAGCTCCGCTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATGAAATTTTAACTGAGAGGCAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTATTGAGAGTACCACCTCTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAGGTTTCTCGAAAAGAAACAAACAGCCAAAATGTCATATGATGACTGTGGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180

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QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCAT----- 591
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 ----- 591
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----ATCGAATGTGGAGAAAG 609
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTTCTATGCGAACCAATCATTCGATCGGAACAGACCTCAATAGCAACTTGTGTC 669
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCCAAACACTGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACACTTACTGTGGA 729
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCCTGACTCAGAACCAAGTGAAGGAGTGGCTAGTTTCTTGTAGAGAAATATC 789
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
QY 790 ACCAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 849
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACAGAAAGTAAAGCAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 909
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTCTATTGACAAACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGAA 969
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATACCTAGCTCCTGGAGTGGGACGATCGATCTATGATTTCGGCATCAAAAT 1029
Db 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCACTGTAGAGAACCTTTGCCGCTGTCTCTAA 1079
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414
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RESULT 6

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US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Alignment Scores:
Pred. No.: 4,876-205 Length: 423
Score: 1824.00 Matches: 354
Percent Similarity: 85.75% Conservative: 1
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Best Local Similarity: 85.51% Mismatches: 5
Query Match: 94.41% Indels: 55
Db: 4 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-09-813-133A-4 (1-423)

QY 1 ATGAAGCTTTTCAGCCTTGAGCTCTTGATCCCATTTGTTCTCTCTGAGCAGCATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGCGTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTAGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGATCTTACTACACATATGAGATTTCTCTGCGACGCGGTAAACAGCTCAC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTCTAAATGCATCTGATGTGCAAAATGTG 240
Db 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTAGCGGAATTCATGTCAGTGTCTTGTGGCAGAGCTGGAAGAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTCCACACACAGTCAGCCCCGAGCCTCGGCATCTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGATTTATACTAGAGAGCAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 421 CCTCATATGCTTACAAAAATCCACATTTGATTCCTATTGAGAGTACCCACTCTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAGGTTTCTGAAAAGAACACACAGCCAAAATGCCATATGGATTGACTGTGGAAATC 540
Db 161 LeuLysValSerGlyLysGluGlnAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCAT----- 591
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 ----- 591
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----ATCGAATGTGGAGAAAG 609
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTTCTATGCGAACCAATCATTCGATCGGAACAGACCTCAATAGCAACTTGTGTC 669
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCCAAACACTGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACACTTACTGTGGA 729
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCCTGACTCAGAACCAAGTGAAGGAGTGGCTAGTTTCTTGTAGAGAAATATC 789
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
QY 790 ACCAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 849
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACAGAAAGTAAAGCAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 909
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
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QY 910 GTTCGTGCTATTGACAAACTAGTAAATACCAAGTATACACATGGCCATGGCTCAGAA 969  
 DB 341 ValArgAlaIleGluLysSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360  
 QY 970 ACCTTATACCTAGCTCCTCGAGGTGGGACGATTGGATCTATGATTGGGCAATCAATAT 1029  
 DB 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrrIleTyrAspLeuGlyIleLysTyr 380  
 QY 1030 TCGTT-----TAC 1037  
 DB 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400  
 QY 1038 ATCAACCCACCTGTAGAAAGCTTTGGCGTGTCTCTAAA 1079  
 DB 401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLys 414

## RESULT 7

US-08-696-139-2  
 ; Sequence 2, Application US/08696139  
 ; Patent No. 5672496  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fayerman, Jeffrey T.  
 ; APPLICANT: Greenen, David P.  
 ; APPLICANT: Hersberger, Charles L.  
 ; APPLICANT: Larson, Jeffrey L.  
 ; APPLICANT: Sterner, Jane L.  
 ; APPLICANT: Zhang, Haichao  
 ; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Eli Lilly and Company  
 ; STREET: Lilly Corporate Center  
 ; CITY: Indianapolis  
 ; STATE: Indiana  
 ; COUNTRY: United States of America  
 ; ZIP: 46285  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/696,139  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/153,258  
 ; FILING DATE: 16-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Gaylo, Paul J.  
 ; REGISTRATION NUMBER: 36,808  
 ; REFERENCE/DOCKET NUMBER: X-8681  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (317) 276-0756  
 ; TELEFAX: (317) 276-3861  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 404 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-696-139-2

Alignment Scores:  
 Pred. No.: 4,42e-66  
 Score: 640.50  
 Percent Similarity: 54.29%  
 Best Local Similarity: 37.67%  
 Query Match: 33.15%  
 DB: 1  
 Length: 404  
 Matches: 136  
 Conservative: 60  
 Mismatches: 122  
 Indels: 43  
 Gaps: 6

US-09-980-881a-1\_COPY\_18\_1097 (1-1080) x US-08-696-139-2 (1-404)  
 QY 67 TTCAGAGTGCAGGTTCTAGTGTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTTA 126  
 DB 10 PheGluGlyGluLysValPheArgValAsnValGluAspGluAsnAspIleSerLeuLeu 29  
 QY 127 CAGAACTCTTACTCAACATATGAGATTGTTCTCTGGCAGCCGGTAAACAGCTGACCTTATT 186  
 DB 30 HisGluLeuAlaSerThrArgGlnIleAspPheTrpLysProAspSerValThrGlnIle 49  
 QY 187 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAGCC 246  
 DB 50 LysProHisSerThrValAspPheArgValLysAlaGluAspIleLeuAlaValGluAsp 69  
 QY 247 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTGTGGCAGACGCTGGAAGATCTTATT 306  
 DB 70 PheLeuGluGlnAsnGluLeuGlnTyrGluValLeuIleAsnAsnLeuArgSerValLeu 89  
 QY 307 CAACAGCAGATTTCACACGACACAGTCCAGCCCCGCGCTCCGCATCTGCTACTATGAACAG 366  
 DB 90 GluAlaGlnPheAspSerArgVal-----ArgThrThrGlyHisSerTyrGluLys 106  
 QY 367 TATCACTCACTAAATGAAATCTATCTCTGGATAGAAATTTATAACTGAGAGGCATCCTGAT 426  
 DB 107 TyrAsnAsnTrpGluThrIleGluAlaTrpThrLysGlnValThrSerGluAsnProasp 126  
 QY 427 ATGCTTACAAAAATCCACATGTCATTCATTGAGAAAGTACCCACTCTATGTTTAAAG 486  
 DB 127 LeuIleSerArgThrAlaIleGlyThrThrPheLeuGlyAsnAsnIleTyrLeuLeuLys 146  
 QY 487 GTTCTCGAAAAGAAACAAACAGCCAAAATGCCATATGCCATATGCTGGAATTCATGCC 546  
 DB 147 Val---GlyLysProGlyProAsnLysProAlaIlePheMetAspCysGlyPheHisAla 165  
 QY 547 AGAAGATGATCTCTCCTGCTTTCGCTGTGGTTCATA----- 585  
 DB 166 ArgGluTrpIleSerHisAlaPheCysGlnTrpPheValArgGluAlaValLeuThrTyr 185  
 QY 585 ----- 585  
 DB 186 GlyTyrGluSerHisMetThrGluPheLeuAsnLysLeuAspPheTyrValLeuProVal 205  
 QY 586 -----GGCCAT-----AATCGAATGTGGAGAAAGAACCGT 615  
 DB 206 LeuAsnIleAspGlyTyrIleTyrThrTrpThrLysAsnArgMetTrpArgLysThrArg 225  
 QY 616 TCTTCTATGCGAACAAATCAITTCATCGAACAGACCTGAATAGCAACTTTGCTCCAAA 675  
 DB 226 SerThrAsnAlaGlyThrThrCysIleGlyThrAspProAsnArgAsnPhe---AspAla 244  
 QY 676 CACTGTGTGAGGAAGGTGCATCCAGTTCCTCATGTCGAAACCTACTGTGACTTTAT 735  
 DB 245 GlyTrpCysThrThrGlyAlaSerThrAspProCysAspGluThrTyrCysGlySerAla 264  
 QY 736 CCTGAGTCAGAACCAAGTGAAGCAGTGGGTAGTTCTTGAGAGAAATATCAACCCAG 795  
 DB 265 AlaGluSerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnAsnLeuSerSer 284  
 QY 796 ATTAAGCATATCATCAGCATGTCATCTCCAGCATATAGTGTTCCTATTCCTAT 855  
 DB 285 IleLysAlaTyrLeuThrIleHisSerTyrSerGlnMetIleLeuTyrProTyrSerTyr 304  
 QY 856 ACACGAAGTAAAAAGCAAGACCATGAGAACTGTCTAGTAGCCAGTGAAGCAGTTCGT 915  
 DB 305 AspTyrLysLeuProGluAsnAsnAlaGluLeuAsnAsnLeuAlaLysAlaValLys 324  
 QY 916 GCTATTGACAAAACCTAGTAAAAATACCAAGTATACATGGCCATGGCTCAGAAACCTTA 975  
 DB 325 GluLeu---AlaThrLeuTyrGlyThrLysTyrThrTyrGlyProGlyAlaThrThrIle 343  
 QY 976 TACCTAGTCTCTGGAGGTGGGACGATTGAGTATGATGTTGGGCATCAATATTCGTTT 1035  
 DB 344 TyrProAlaAlaGlyGlySerAspAspTrpAlaTyrAspGlnGlyIleLysTyrSerPhe 363

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QY 1036 ACA 1038
Db 364 Thr 364

RESULT 8
US-08-860-882A-57
; Sequence 57, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGLESE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM, JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HOW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-882A-57

Alignment Scores:
Pred. No.: 5,87e-66 Length: 415
Score: 639.50 Matches: 140
Percent Similarity: 51.72% Conservative: 71
Best Local Similarity: 34.31% Mismatches: 136
Query Match: 33.10% Indels: 62
DB: 2 Gaps: 8

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-860-882A-57 (1-415)
QY 16 CTTGAGCTCTTGTACCCATTGTTCTTCTGTGAGCAGCATGTTCTTCGCG---TTCCAG 72
Db 2 LeuLeuValLeuValThrValAlaLeuAlaSerAlaHisHisGlyGlyGluHisPheGlu 21
QY 73 AGTGCCAAAGTTCTAGCTCTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAA 132
Db 22 GlyGluLysValPheArgValAsnValGluAspGluAsnHisAlaAsnIleIleArgGlu 41
QY 133 CTTACTACAAATATGAGATTGTTCTCTGCGCCGGTAAACAGCTGACCTTATTGTGAAG 192

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Db 396 CysGluGluThrPheLeuAlaIle 403

RESULT 9

US-09-011-769A-39

Sequence 39, Application US/09011769A

Patent No. 6436691

GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.

BLAKE, David C.

DAVIES, David H.

HENNAM, John F.

HENNEQUIN, Laurent F.A.

MARSHAM, Peter R.

DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 415 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-011-769A-39

Alignment Scores:

Pred. No.: 5.87e-66 Length: 415

Score: 639.50 Matches: 140

Percent Similarity: 51.72% Conservative: 71

Best Local Similarity: 34.31% Mismatches: 136

Query Match: 33.10% Indels: 62

DB: 4 Gaps: 8

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-09-011-769A-39 (1-415)

QY 16 CTTGACGCTCTGTACCATGTCTCTCTGTGACGAGCATCTCTCGCG---TTCCAG 72

Db 2 LeuLeuValValThrValAlaLeuAlaSerAlaHisGlyGlyGluHisPheGlu 21

QY 73 AGTGGCCAGTCTTAGCTGTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAA 132

Db 22 GlyGluValPheArgValAsnValGluAspGluAsnHisIleAsnIleIleArgGlu 41

QY 133 CTTACTACAAATATAGATGTCTCTGCGACCGGTAAACGCTGACCTTATGTGAAG 192

Db 42 LeuAlaSerThrThrGlnIleAspPheThrLysProAspSerValThrGlnIleLysPro 61

QY 193 AAAAAACAAGTCCATTTTTTTGTAATGCACTCTGATGTCGACAAATGTGAAAGCCCATTTA 252

Db 62 HisSerThrValAspPheArgValLysAlaGluAspThrValThrValGluAsnValLeu 81

QY 253 AATGTGACGGAAATTCATGCAAGTCTCTGTCGCGACAGCTGGAAGATCTTATTCAACAG 312

Db 82 LysGlnAsnGluLeuGlnThrLysValLeuIleSerAsnLeuArgAsnValValGluAla 101

QY 313 CAGATTTCCAAACGACACAGTCAGCCCGAGCTCCGATCGCTACTATGAAACAGTATCAC 372

Db 102 GlnPheAspSerArgVal-----ArgAlaThrGlyHisSerThrGluLysThrAsn 118

QY 373 TCACATAATGAAATCTATTCTTGGATAGAAATTTATACTAGAGAGCATCTCTATATGCTT 432

Db 119 LysTrpGluThrIleGluAlaTrpThrGlnGlnValAlaThrGluAsnProAlaLeu 138

QY 433 ACAAAAATCCACATGTCATCTTCAGAGTACCCACATCTATGTTTAAAGGTTTCT 492

Db 139 SerArgSerValIleGlyThrThrPheGluGlyArgAlaIleThrLeuLeuLysVal 157

QY 493 GGAAGAAGAACAAACAGCCCAAAATGCCATATGATGATGATGATGATGATGATGATGAT 552

Db 158 GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHisAlaArgGlu 177

QY 553 TGGATCTCTCTGCTTTCTGCTTGTGTTTCATA----- 585

Db 178 TrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThrThrGlyArg 197

QY 585 ----- 585

Db 198 GluIleGlnValThrGluLeuAspLysLeuAspPheThrValLeuProValLeuAsn 217

QY 586 -----GGCCAT-----AATCCAATGTGGAGAAAGAACCGTCTCTTTC 621

Db 218 IleAspGlyThrIleThrTrpThrLysSerArgPheTrpArgLysThrArgSerThr 237

QY 622 TATGCGAAACAATTCATTGTCATCGGAACACAGACCTGAATAGCACTTGTCTCCAAACACTGG 681

Db 238 HisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---AspAlaGlyTrp 256

QY 682 TGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCTCTGAG 741

Db 257 CysGluIleGlyAlaSerArgAsnProCysAspGluThrThrCysGlyProAlaAlaGlu 276

QY 742 TCAGAACCAAGAGTGAAGCGTGTCTTCTTGAGAAAGAAATATCAACAGATATAA 801

Db 277 SerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSerSerIleLys 296

QY 802 GCATACATCAGCATGTCATCTATCTCCAGCATATAGTGTTCCTATATCTTATATACACGA 861

Db 297 AlaThrLeuThrIleHisSerThrSerGlnMetIleThrProThrSerThrAlaThr 316

QY 862 AGTAAAGCAAGACCATGAGCACTGTCTTAGTAGCCAGTCAGTCAGTTCGTGTATT 921

Db 317 LysLeuGlyGluAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrValLysGluLeu 336

QY 922 GACAAACTAGTAAAAAATACAGGTATACACATGCGCATGCGTTCAGAAAACCTTATACCTA 981

Db 337 ---AlaSerLeuHisGlyThrLysThrThrThrGlyProGlyAlaThrThrIleThrPro 355

QY 982 GCTCTGAGGAGTGGGACGATTGGATCTATGATTTGGGCATCAAAATTCGTTTACATC- 1040

Db 356 AlaAlaGlyGlySerAspAspTrpAlaThrAspGlnGlyIleArgThrSerPheThrPhe 375

QY 1041 -----AAACCACC 1049

Db 376 GluLeuArgAspThrGlyArgThrGlyPheLeuLeuProGluSerGlnIleArgAlaThr 395

QY 1050 TGTAGAGAACTTTTCCCGCTGTC 1073

Db 396 CysGluGluThrPheLeuAlaIle 403

RESULT 10

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US-07-649-591B-7
; Sequence 7, Application US/07649591B
; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; CITY: 460 Point San Bruno Blvd
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-649-591B-7

Alignment Scores:
Pred. No.:      8,838-66      Length:      417
Score:          638.00      Matches:     147
Percent Similarity: 51.23%      Conservative: 62
Best Local Similarity: 36.03%      Mismatches: 135
Query Match:      33.02%      Indels:      65
DB:                1          Gaps:        9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-07-649-591B-7 (1-417)
QY 16 CTGTCAGTCTGTATCCCATTTCTCTCTCTGTGAGCAGCATGTCTTCGCGTTCAGAGT 75
Db 7 MetAlaValIleTyr-ThrThrLeuAlaIleAlaProValHis-----PheAspArg 23
QY 76 GCGCAAGTTCTAGCTGCTCTTCTAGAACCTCTAGCAGAGTTCAGTTCACAGATCTT 135
Db 24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43
QY 136 ACTACACATATGAGATGTTCTCTGCGCAGCGGTAACAGCTGACCTATTGTGAAGAA 195
Db 44 ThrGlnSerIleGluLeuAspPheThrPyrProAspAlaIleHisAspIleAlaValAsn 63
QY 196 AAACAAGTCCATTTTTTTGTAATGCATCTGTGACAAATGTGAAAGCCCATTTAAAT 255
Db 64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83
QY 256 GTGACGGGAATCCATGCAGTCTCTGTCGACAGAGTGGAGGATCTTATTCACAGCAG 315
Db 84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluGluIleLysGln 103
QY 316 ATTTC---AAGCAGACAGTACGCCCCGAGCGCTCGCATCTGTACTATGACAGTATCAC 372
Db 316 ATTTC---AAGCAGACAGTACGCCCCGAGCGCTCGCATCTGTACTATGACAGTATCAC 372

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Db 104 PheAspValLysAspGluIleAlaGlyArgHisSer-----TyrAlaLysTyrAsn 120
QY 373 TCACATAAATGAATCTATTCTTTGGATAGAAATTTATAACTGAGAGCATCTCTGATATGTT 432
Db 121 AspTrpAspLysIleValSerThrGluLysMetLeuGluLysHisProGluMetVal 140
QY 433 ACAAAATCCACATTCATCTCATTTGAGNAGTACCCACTCTATGTTTAAAGGTTTCT 492
Db 141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159
QY 493 GGAAGAAGAACAAACAGCCAAATATGCCATATGATGATGATGATGATGATGATGATGAT 552
Db 160 GlyLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179
QY 553 TGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
Db 180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199
QY 592 AAT----- 594
Db 200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219
QY 595 -----CGAATGTGAGAGAAACCGTTCTTTC 621
Db 220 ValAspGlyTyrIleTrpSerThrGlnAspArgMetTrpArgLysAsnArgSerArg 239
QY 622 TATCGAACATCATTCATCGAACAGACCTGAATAGCACTTTGTCTCCAAACACTGG 681
Db 240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258
QY 682 TGTGAGAGAGTGCATCCAGTTCCTCATCTCGGAAACCTACTGTGCACTTTATCTCTGAG 741
Db 259 AspSerSerProAsnThrAsnLysProCysLeuAsnValTyrArgGlyProAlaProGlu 278
QY 742 TCAGAACAGAGTGAAGGAGTGGCTAGTTCTTGTGAGAGAAATATCAACAGCATTA 801
Db 279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298
QY 802 GCATCATCAGCATGCTATTCATCTCCAGCATATAGTGTTCATATTCCTATATACAGCA 861
Db 299 AlaTyrIleThrPheHisSerTyrSerGlnMetLeuLeuIleProTyrGlyTyrThrPhe 318
QY 862 AGTAAAGCAAGACCATGAGGAAGTCTCTCTAGTACGAGTGAAGAGTTCGCTGCTATT 921
Db 319 LysLeuProProAsnHisGlnAspLeuLysValAlaArgIleAlaThrAspAlaLeu 338
QY 922 GACAAACTAGTAAAAATACCCAGGTATACATGCGCATGCCATGCCCTCAGAAACCTTATACCTA 981
Db 339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357
QY 982 GCTCCTGAGAGTGGGAGCATTCATGATTCATGATTTGGCATCAATATTCGTTTAC----- 1037
Db 358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyIleLysHisThrPheAlaPhe 377
QY 1038 -----ATCAAAACCCACC 1049
Db 378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397
QY 1050 TGTAGAGAAGCTTTTGGCGCTGTC 1073
Db 398 CysLysGluThrMetLeuSerVal 405

RESULT 11
US-08-277-540-7
; Sequence 7, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd

```



CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277,540  
 FILING DATE: 19-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/167727  
 FILING DATE: 15-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/959944  
 FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/649591  
 FILING DATE: 01-FEB-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689D1C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 417 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-277-540-7

Alignment Scores:  
 Pred. No.: 8,83e-66 Length: 417  
 Score: 638.00 Matches: 147  
 Percent Similarity: 51.23% Conservative: 62  
 Best Local Similarity: 36.03% Mismatches: 135  
 Query Match: 33.02% Indels: 65  
 DB: 1 Gaps: 9

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-08-277-540-7 (1-417)

QY 16 CTTCAGCTCTGTACCCATGTCTCTGTGAGCAGCATGTCTTCGCGTTCACAGT 75  
 Db 7 MetAlaValIleTyrThrLeuAlaIleAlaProValHis-----PheAspArg 23  
 QY 76 GGCCAAAGTTCTAGCTGTCTCTCTAGAACCTCTAGGCAAGTTCAGTTCACAGATCTT 135  
 Db 24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43  
 QY 136 ACTACACATATGAGATTGTCTCTGCACGCGGTAAACAGCTGACCTTATTGGAAGAAA 195  
 Db 44 ThrGlnSerIleGluLeuAspPheTyrProAspAlaIleHisAspIleAlaValAsn 63  
 QY 196 AAACAAGTCCATTTTTTGTAAATCATCTGATCTGCACAAATGTGAAGCCCATTTAAAT 255  
 Db 64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83  
 QY 256 GTGAGCCGAATTCATCAGTGTCTCTCTGCGAGACCTGGAAGATCTTATCAACAGCAG 315  
 Db 84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluIleGluLysGln 103  
 QY 316 ATTTC---AACGACAGTCAGCCCGGAGCCCTCCGATCGTACTATGAACAGTATCAC 372  
 Db 104 PheAspValLysAspGluIleAlaGlyArgHisSer-----TyrAlaLysTyrAsn 120  
 QY 373 TCACATAAATAAATCTTCTTGTGATAGAAATTTATACTGAGAGGCACTCTGATATGCTT 432

Db 121 AspTrpAspLysIleValSerTrpThrGluLysMetLeuGluLysHisPheProGluMetVal 140  
 QY 433 ACAGAAATCCACATTTGGATCTCTATTCGAGAAGTACCCACTCTATGTTTAAAGGTTTCT 492  
 Db 141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159  
 QY 493 GGAAAGAACAAACAGCCCAAAATGCTATGATGGATTGATGCTGGAAATCCATCCAGAGAA 552  
 Db 160 GlyLysLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179  
 QY 553 TGGATCTCTCTGCTTTCTGCTTGGTTGCTCATA-----GGCCAT 591  
 Db 180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199  
 QY 592 RAT----- 594  
 Db 200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219  
 QY 595 -----CGAATGTGGAGAAAGAACCGTCTTCTTTC 621  
 Db 220 ValAspGlyTyrIleTrpSerTrpThrGlnAspArgMetTrpArgLysAsnArgSerArg 239  
 QY 622 TATGCGAACATCATTCGGAACAGACCTGAATAGCAACTTGTCTCCAAACACTGG 681  
 Db 240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258  
 QY 682 TGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTTATCTCTAG 741  
 Db 259 AspSerSerProAsnThrAsnLysProCysLeuAsnValTyrArgGlyProAlaProGlu 278  
 QY 742 TCAGAACCCAGAAAGTGAAGCAGTGTCTTCTTGGAGAAATATCAACAGATATAA 801  
 Db 279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298  
 QY 802 GCATCATCAGCATGATTCATCTCCAGCATATAGTGTTCATATTCCTATATACACGA 861  
 Db 299 AlaTyrIleThrPheHisSerTyrSerGlnMetLeuLeuIleProTyrGlyTyrThrPhe 318  
 QY 862 ACTAAAGCAAGACCATGAGCACTGTCTCTAGTAGCCAGTGAACAGTTCGTGCTATT 921  
 Db 319 LysLeuProAsnHisGlnAspLeuLeuLysValAlaArgIleAlaThrAspAlaLeu 338  
 QY 922 GACAAACTAGTAAATAACAGGTATACATGCGCATGGCTCGAGAAACCTTATACCTA 981  
 Db 339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357  
 QY 982 GCTCTGAGGTGGGACGATTCGATCTATGATTTGGGCATCAAAATATTCGTTTAC---- 1037  
 Db 358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyLysHisThrPheAlaPhe 377  
 QY 1038 -----ATCAAAACCCACC 1049  
 Db 378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397  
 QY 1050 TGTAGAGAGCTTTTCCCGCTGTC 1073  
 Db 398 CysLysGluThrMetLeuSerVal 405

RESULT 12

US-08-430-787A-7  
 ; Sequence 7, Application US/08430787A  
 ; Patent No. 5593674  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080



```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-649-591B-6

Alignment Scores:
Pred. No.: 1,99e-65 Length: 417
Score: 635.00 Matches: 139
Percent Similarity: 52.31% Conservative: 76
Best Local Similarity: 33.82% Mismatches: 132
Query Match: 32.87% Indels: 65
DB: 9 Gaps: 9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-07-649-591B-6 (1-417)

QY 16 CTTGAGTCTGTGACCACTGTTCTCTCTGTGAGCAGCATGTTCTTCGCG----- 66
DB 1 MetArgLeuLeuLeuProValGlyLeuLeuAlaThrLeuAlaLeuProValArg 20

QY 67 TTCCAGAGTGGCAAGTCTTCTGCTCTCTCTGAGCACTCTAGGCAAGTTCAGATTCTA 126
DB 21 PheAspArgGluLysValPheArgValLysProGlnAspGluLysGlnAlaAspIle 40

QY 127 CAGATCTTACTACACATATGAGATTGTTCTCTGCGAGCCGGTACACCTGACCTATT 186
DB 41 LysAspLeuAlaLysThrAsnGluLeuAspPheTrpTyrProGlyAlaThrHisVal 60

QY 187 GTGAGAAAAACAAGTCCATTTTGTAAATGTCATCTGATCGACAAATGTGAAGCC 246
DB 61 AlaAlaAsnMetMetValAspPheArgValSerGluLysGluSerGlnAlaLeuGlnSer 80

QY 247 CATTAAATGTGAGCGAATTCATGCTGCTCTGTCGACAGCTGGAAGATCTTATT 306
DB 81 AlaLeuAspGlnAsnLysMetHisTyrGluLeuIleHisAspLeuGlnGluIle 100

QY 307 CAACAGCAGATTTC---AACGACACAGTCAGCCCGGAGCCCTCCGATCGTACTATGA 363
DB 101 GluLysGlnPheAspValLysGluAspIleProGlyArgHisSer-----TyrAla 117

QY 364 CAGTATCACTCACTAAATGAATTTCTTGTGATAGATTTATTAAGTGGAGCATCT 423
DB 118 LysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLysMetMetAspLysTyrPro 137

QY 424 GATATGCTTACAAAAATCCCATTTGATGTCCTCTATTTGAGAAGTACCCTCTATGTTTA 483
DB 138 GluMetValSerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeu 157

QY 484 AGGTTTCTGGAAGAACAAACAGCCAAATGCCATATGATGATGATGATGATGATGAT 543
DB 158 LysIle---GlyGluLysAsnGluArgGlyAlaIlePheMetAspCysGlyIleHis 176

QY 544 GCCAGAAATGGATCTCTCTGCTGTTCTGTTGTTTCATA----- 585

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177 AlaArgGluTrpValSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysThr 196
585 ----- 585

197 TyrGlyArgAsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrIleLeuPro 216
586 -----GGCCAT-----AATCGAATGTGAGAAAGAAC 612
217 ValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsnArgMetTrpArgLysAsn 236
613 CGTTCTTCTATGCAACATCATTGTCGGAACAGACCTGAATAGCACTTCTCTCTCC 672
237 ArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeuAsnArgAsnPhe---Asn 255
673 AACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTGCTCGCAACCTACTGTGGACTT 732
256 AlaSerTrpAsnSerIleProAsnThrAsnAspProCysAlaAspAsnTyrArgGlySer 275
733 TATCTGAGTCAGAACCCAGAGTGAAGCAGTGGCTAGTTCTTCTGAGAGAAATATCAAC 792
276 AlaProGluSerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsn 295
793 CAGATTAAAGCATATCATCAGCATGATCTCCAGCATATAGTCTTCTCCATATTC 852
296 GluIleLysValTyrIleThrPheHisSerTyrSerGlnMetLeuLeuPheProTyrGly 315
853 TATACACGAAGTAAAGCAAGACCATGAGCAACTGTCTCTAGTAGGACGAGTGAAGCAGTT 912
316 TyrThrSerLysLeuProProAsnHisGluAspLeuAlaLysValAlaLysIleGlyThr 335
913 CGTCTATTGACAAAACCTAGTAAAAATACCAAGGTATACACATGGCCATGGCTCAGAAACC 972
336 AspValLeu---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleGluSerThr 354
973 TTATACCTAGCTCTCTGAGAGTGGGACCATGAGTCTATGATTTGGCATCAATATTCG 1032
355 IleTyrProIleSerSerGlySerSerLeuAspTrpAlaTyrAspLeuGlyIleLysHisThr 374
1033 TTATAC-----ATC 1040
375 PheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeuLeuProGluSerArgIle 394
1041 AAACCCACCTGTAGAGAAAGCTTTTCCCGCTGTC 1073
395 LysProThrCysArgGluThrMetLeuAlaVal 405

RESULT 14
US-08-277-540-6
; Sequence 6, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-277-540-6

Alignment Scores:
Pred. No.: 1,996-65 Length: 417
Score: 635.00 Matches: 139
Percent Similarity: 52.31% Conservative: 76
Best Local Similarity: 33.82% Mismatches: 132
Query Match: 32.87% Indels: 65
DB: 1 Gaps: 9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-277-540-6 (1-417)
QY 16 CTTCAGTCCTGTACCAATGTTCTCTCTGTGAGCAGCATGCTTCGCG----- 66
DB 1 MetArgLeuLeuProValGlyLeuLeuAlaThrLeuAlaLeuAlaProValArg 20
QY 67 TTCCAGAGTGGCAAGTCTAGCTCTCTCTAGCACTCTAGCAAGTTCAGTCTCTA 126
DB 21 PheAspArgGluValPheArgValLysProGlnAspGluLysGlnAlaSpille 40
QY 127 CAGAACTTCTACCAATATGAGATGTTCTCTGCGACCGGTAAACAGCTGACCTTAT 186
DB 41 LysAspLeuAlaLysThrAsnGluLeuAspPheTyrProGlyAlaThrHisVal 60
QY 187 GTGAGAAAAACAAGTCCATTTTCTTAATGATCTGATGTCGCAATGTGAAGCC 246
DB 61 AlaAlaAsnMetMetValAspPheArgValSerGluLysGluSerGlnAlaLeuGlnSer 80
QY 247 CATTTAAATGTGACGGGAATTCATGCTGCTGCTGCGCAGCTGGAAGATCTTATT 306
DB 81 AlaLeuAspGlnAsnLysMethHisTyrGluLeuLeuLeuHisAspLeuGlnGluLeu 100
QY 307 CAACAGCAGATTTC---AACGACAGCTGACGCCCGGCTCCGCATCGTACTATGAA 363
DB 101 GluLysGlnPheAspValLysGluAspPheProGlyArgHisSer-----TyrAla 117
QY 364 CAGTATCACTCAATAAGAAATCTTCTTGGATAGATTTATTAACCTGAGGGCATCCT 423
DB 118 LysTyrAsnAsnTrpGluLysLeuValAlaThrThrGluLysMetMetAspLysTrpPro 137
QY 424 GATATGCTTACAAAAACACATTTGGATCCCTCATTTGAGAGTACCCTCTATGTTTAA 483
DB 138 GluMetValSerArgLeuLysLeuGlySerThrValGluAspAsnProLeuTyrValLeu 157
QY 484 AAGTTTCTGGAAGAAAGACAAACAGCCAAATATGATGATGATGATGATGATGATGAT 543
DB 158 Lysile---GlyGluLysAsnGluArgLysAlaLeuPheMetAspCysGlyLeuHis 176
QY 544 CCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 585
DB 177 AlaArgGluTrpValSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysThr 196
QY 585 ----- 585

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Db 197 TyrGlyArgAsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrIleLeuPro 216
QY 586 -----GCCAT-----AATCGAATGTGAGAAAGAAC 612
Db 217 ValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsnArgMetTrpArgLysAsn 236
QY 613 CGTTCTTTCTATGCGAAACAATCATTGTCAGAACAGACCTGGAATAGCACTTTGTCTCC 672
Db 237 ArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeuAsnArgAsnPhe---Asn 255
QY 673 AACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCTCGGAACCTACTGTGGACTT 732
Db 256 AlaSerTrpAsnSerIleProAsnThrAsnAspProCysAlaAspAsnTyrArgGlySer 275
QY 733 TATCTGAGTCAGAACCAAGAGTAGTGAAGCAGTGTAGTTCTTCTGAGAGAAATATCAAC 792
Db 276 AlaProGluSerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsn 295
QY 793 CAGATTAAAGCATACATCAGCATGCTTCTACTCTCCAGCATATAGTGTTCCTATATTC 852
Db 296 GluLeuLysValTyrIleThrPheHisSerTyrSerGlnMetLeuLeuPheProTyrGly 315
QY 853 TATACAGAGTAAAAGCAAGACCATCAGGAAGTCTCTCTAGTAGCCAGTGAAGCAGTT 912
Db 316 TyrThrSerLysLeuProProAsnHisGluAspLeuAlaLysValAlaLysIleGlyThr 335
QY 913 CGTCTATTGCAAAACTAGTAAAATACAGGTATACACATGCGCCATGGCTCAGAACC 972
Db 336 AspValLeu---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleGluSerThr 354
QY 973 TTATACCTAGTCTCCTGAGGTGGGAGCATGATGATGATGATGATGATGATGATGATGAT 1032
Db 355 IleTyrProLysSerGlySerSerLeuAspTrpAlaTyrAspLeuGlyIleLysHisThr 374
QY 1033 TTTAC-----ATC 1040
Db 375 PheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeuLeuProGluSerArgIle 394
QY 1041 AAACCCACCTGTAGAGAGCTTTTGGCGCTGTC 1073
Db 395 LysProThrCysArgGluThrMetLeuAlaVal 405

RESULT 15
US-08-430-787A-6
; Sequence 6, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674e1 Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944

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; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA: 07/649591
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1CID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-430-787A-6

Alignment Scores:
Pred. No.: 1,99e-65 Length: 417
Score: 635.00 Matches: 139
Percent Similarity: 52.31% Conservative: 76
Best Local Similarity: 33.82% Mismatches: 132
Query Match: 32.87% Indels: 65
DB: Gaps: 9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-430-787A-6 (1-417)
QY 16 CTTCAGTCTCTGACCATGTTCTCTCTGAGCAGCATGCTCTCGCG----- 66
Db 1 MetArgLeuLeuLeuProValGlyLeuLeuAlaThrLeuAlaLeuAlaProValArg 20
QY 67 TTCCAGAGTGGCAAGTTCTAGTCTCTCTCTAGAACCTCTAGCAAGTTCAAGTTCTA 126
Db 21 PheAspArgGluLysValPheArgValLysProGlnAspGluLysGlnAlaAspLeuLeu 40
QY 127 CAGAACTTCTACTACACATATGATTTCTCTGCGAGCCGGTACACGCTGACCTTATT 186
Db 41 LysAspLeuAlaLysThrAsnGluLeuAspPheTrpTyrProGlyAlaThrHisHisVal 60
QY 187 GTCAAGAAAAACAAGTCCATTTTGTAAATGTCATCTGTCGACAAATGGAAGCC 246
Db 61 AlaAlaAsnMetMetValAspPheArgValSerGluLysGluSerGlnAlaLeuGlnSer 80
QY 247 CATTTAAATGTGAGCGGAATTCATGCAGTGTCTCTGCGACAGCTGGAAGATCTTATT 306
Db 81 AlaLeuAspGlnAsnLysMetHisTyrGluLeuLeuLeuHisAspLeuGlnGluLeu 100
QY 307 CAACAGCAGATTTC---AACGACACAGTCAGCCCGGAGCCCTCCGCATCGTACTATGAA 363
Db 101 GluLysGlnPheAspValLysGluAspIleProGlyArgHisSer-----TyrAla 117
QY 364 CAGTATCACTCACTAAATGAATCTATTCTGTGATAGATTATTAAGTGAAGGCATCCT 423
Db 118 LysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLysMetMetAspLysTyrPro 137
QY 424 GATATGCTTACAAAAATCCATTGGATCCTCTCTGAGAAAGTACCACCTCTATGTTTA 483
Db 138 GluMetValSerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeu 157
QY 484 AAGTTTCTGGAAAGAACAAACAGCCAAATATGCCATATGGATTGACTGTGGAATCCAT 543
Db 158 LysIle---GlyGluLysAsnGluArgGlyAlaIlePheMetAspCysGlyIleHis 176
QY 544 GCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 585
Db 177 AlaArgGluTrpValSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysThr 196
QY 585 ----- 585
Db 197 TyrGlyArgAsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrIleLeuPro 216

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QY 586 -----GGCCAT-----AATCGAATGTGGAGAAAGAAC 612
Db 217 ValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsnArgMetTrpArgLysAsn 236
QY 613 CGTTCTTTCTATGCGAACAACTATTCATTCGGAACAGACCTGAATAGCAACTTTCTCTCC 672
Db 237 ArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeuAsnArgAsnPhe---Asn 255
QY 673 AAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCGGAACCTTACTGTGCACTT 732
Db 256 AlaSerTrpAsnSerIleProAsnThrAsnAspProCysAlaAspAsnTyrArgLysSer 275
QY 733 TATCTGAGTCTGAGAACCAAGAGTGAAGCAGTGGTCTAGTTCTTCTGAGAAAGAAATATCAAC 792
Db 276 AlaProGluSerGluLysAlaValThrAsnPheIleArgSerHisLeuAsn 295
QY 793 CAGATTAAGCATACATCAGCATGCAATTCATCTACTCCAGCATATAGTGTTCATATTC 852
Db 296 GluIleLysValTyrIleThrPheHisSerTyrSerGlnMetLeuLeuPheProTyrGly 315
QY 853 TATACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAGTCAAGCAGTT 912
Db 316 TyrThrSerLysLeuProAsnHisGluAspLeuAlaLysValAlaLysIleGlyThr 335
QY 913 CGTGTCTATTGACAAAACCTAGTAAAAAATACCAAGTATACACATGGCCATGGCTCAGAAACC 972
Db 336 AspValLeu---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleGluSerThr 354
QY 973 TTATACCTAGTCTCTGAGGAGTGGGACGATTCGATCTATGATTTGGGCATCAAAATATTCG 1032
Db 355 IleTyrProIleSerGlySerSerLeuAspTrpAlaTyrAspLeuGlyIleLysHisThr 374
QY 1033 TTTTAC-----ATC 1040
Db 375 PheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeuLeuProGluSerArgIle 394
QY 1041 AAACCCACCTGTAGAGAAAGCTTTTGGCGCTGTC 1073
Db 395 LysProThrCysArgGluThrMetLeuAlaVal 405

Search completed: October 27, 2004, 10:41:12
Job time : 43.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: October 27, 2004, 10:30:15 ; Search time 535.5 Seconds  
(without alignments)  
1307.761 Million cell updates/sec

Title: US-09-980-881A-1\_COPY\_18\_1097  
Perfect score: 1932  
Sequence: 1 atgaagcttgacgttcg.....ttttgcgcgtgtctctaaaa 1080

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1370721 seqs, 324215800 residues  
Total number of hits satisfying chosen parameters: 2741442

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=Published Applications AA -QFMT=Eastan -SUFFIX=rapb -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:  
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15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubppa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

Alignment Scores: 9.79e-184 Length: 386  
Pred. No.: 386

No.	Score	Match	Length	DB	ID	Description
1	1852.5	95.9	386	9	US-09-813-133A-2	Sequence 2, Appli
2	1852.5	95.9	386	14	US-10-212-877-2	Sequence 2, Appli
3	1835	95.0	423	14	US-10-379-836-17	Sequence 17, Appli
4	1824	94.4	423	9	US-09-813-133A-4	Sequence 4, Appli
5	1824	94.4	423	14	US-10-212-877-4	Sequence 4, Appli
6	1811.5	93.8	428	15	US-10-115-479-68	Sequence 68, Appli
7	1811.5	93.8	428	15	US-10-115-479-70	Sequence 70, Appli
8	1746	90.4	423	14	US-10-379-836-2	Sequence 2, Appli
9	1550.5	80.3	422	14	US-10-379-836-18	Sequence 18, Appli
10	1522.5	78.8	422	14	US-10-379-836-16	Sequence 16, Appli
11	1442.5	74.7	322	15	US-10-115-479-64	Sequence 64, Appli
12	1396.5	72.3	354	15	US-10-115-479-66	Sequence 66, Appli
13	839	43.4	211	9	US-09-925-302-467	Sequence 467, App
14	839	43.4	211	10	US-09-925-302-467	Sequence 467, App
15	646	33.4	416	15	US-10-074-978A-269	Sequence 269, App
16	641	33.2	417	15	US-10-074-978A-267	Sequence 267, App
17	641	33.2	417	15	US-10-074-978A-268	Sequence 268, App
18	641	33.2	417	16	US-10-477-515-3	Sequence 3, Appli
19	635	32.9	417	14	US-10-229-546-2	Sequence 2, Appli
20	635	32.9	417	14	US-10-229-546-9	Sequence 9, Appli
21	635	32.9	417	14	US-10-341-434-188	Sequence 188, App
22	635	32.9	417	15	US-10-282-511-72	Sequence 72, Appli
23	632	32.7	402	14	US-10-379-836-20	Sequence 20, Appli
24	627.5	32.5	416	15	US-10-074-978A-270	Sequence 270, App
25	623	32.2	716	9	US-09-910-059-125	Sequence 125, App
26	622	32.2	416	15	US-10-074-978A-266	Sequence 266, App
27	613.5	31.8	434	16	US-10-477-515-2	Sequence 2, Appli
28	613.5	31.8	437	13	US-10-200-344-10	Sequence 10, Appli
29	613.5	31.8	437	14	US-10-274-639-12	Sequence 12, Appli
30	613.5	31.8	437	15	US-10-333-574-12	Sequence 12, Appli
31	611.5	31.7	437	17	US-10-757-262-128	Sequence 128, App
32	564.5	29.2	374	9	US-09-888-615-61	Sequence 61, Appli
33	563	29.1	444	14	US-10-176-306-74	Sequence 74, Appli
34	560	29.0	613	9	US-09-910-059-113	Sequence 113, App
35	560	29.0	613	16	US-10-608-710-4	Sequence 4, Appli
36	546	28.3	399	14	US-10-200-910-8	Sequence 8, Appli
37	546	28.3	399	17	US-10-403-130-8	Sequence 8, Appli
38	533.5	27.6	419	15	US-10-072-012-788	Sequence 788, App
39	528.5	27.4	350	13	US-10-200-344-12	Sequence 12, Appli
40	524.5	27.1	286	16	US-10-408-765A-1959	Sequence 1959, Ap
41	522	27.0	286	15	US-10-072-012-887	Sequence 887, App
42	519.5	26.9	419	15	US-10-257-174-40	Sequence 40, Appli
43	519.5	26.9	436	14	US-10-200-910-6	Sequence 6, Appli
44	519.5	26.9	436	15	US-10-072-012-316	Sequence 316, App
45	519.5	26.9	436	15	US-10-072-012-784	Sequence 784, App

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2  
Alignment Scores: 9.79e-184 Length: 386  
Pred. No.: 386

Score: 1852.50 Matches: 354  
Percent Similarity: 94.16% Conservative: 1  
Best Local Similarity: 93.90% Mismatches: 5  
Query Match: 95.89% Indels: 18  
DB: 9 Gaps: 1

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QY 1 ATGAAGCTTTGCAGCTTGCAGCTTGTACCTTGTACCAATGTTCTCTCTGTGAGCAGCATGTC 60  
DB 1 MetLysLeuCySerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
QY 61 TTCGGGTTCCAGAGTGGCCAACTTCTAGCTGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120  
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
QY 121 GTTCTACAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 180  
DB 41 ValLeuGlnAsnLeuThrThrThrTyrrGluIleValLeuTrpGlnProValThrAlaAsp 60  
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTTGTAAATGCATCTGATGTCGACAATGTG 240  
DB 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80  
QY 241 AAAGCCCATTTAAATGTAGCCGAATTCATGACAGTTCCTGCTGGCAGAGCTGGAAGAT 300  
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
QY 301 CTTATTCAACAGCAGATTCCAAACACACAGTCAGCTGCTTCTGGCAGAGCTGGAAGAT 360  
DB 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrr 120  
QY 361 GAACAGTATCACTCACTAAATCAATCTATTCTGGATAGAAATTTATACTGAGAGGCAT 420  
DB 121 GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluPheIleThrGluArgHis 140  
QY 421 CCTGATATGCTTACAAATCCACATTTGGATTCCTCATTTGAGAAAGTACCCACTCTATGTT 480  
DB 421 CCTGATATGCTTACAAATCCACATTTGGATTCCTCATTTGAGAAAGTACCCACTCTATGTT 480

DB 321 GlySerGluThrLeuTyrrLeuAlaProGlyGlyGlyAspAspTrpIleTyrrAspLeuGly 340  
QY 1021 ATCAAAATATTCGTT----- 1034  
DB 341 IleLysTyrrSerPheThrIleGluLeuArgAspThrGlyThrTyrrGlyPheLeuLeuPro 360  
QY 1035 -----TACATCAAAACCCACCTGTAGAGAACCTTTTCCGCTGCTCTCTAAA 1079  
DB 361 GluArgTyrrIleLysProThrCysArgGluAlaPheAlaValSerLys 377

RESULT 2  
US-10-212-877-2  
; Sequence 2, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinui et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173DIV  
; CURRENT APPLICATION NUMBER: US/10/212.877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-212-877-2

Alignment Scores:  
Pred. No.: 9,79e-184 Length: 386  
Score: 1852.50 Matches: 354  
Percent Similarity: 94.16% Conservative: 1  
Best Local Similarity: 93.90% Mismatches: 5  
Query Match: 95.89% Indels: 18  
DB: 14 Gaps: 1

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-10-212-877-2 (1-386)

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DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
QY 121 GTTCTACAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 180  
DB 41 ValLeuGlnAsnLeuThrThrThrTyrrGluIleValLeuTrpGlnProValThrAlaAsp 60  
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTTGTAAATGCATCTGATGTCGACAATGTG 240  
DB 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80  
QY 241 AAAGCCCATTTAAATGTAGCCGAATTCATGACAGTTCCTGCTGGCAGAGCTGGAAGAT 300  
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
QY 301 CTTATTCAACAGCAGATTTCACACACACAGTCAGCTGAGCCCCGAGCTCCGCTATCGTACTAT 360  
DB 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrr 120  
QY 361 GAACAGTATCACTCACTAAATCAATCTATTCTGGATAGAAATTTATACTGAGAGGCAT 420  
DB 121 GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluPheIleThrGluArgHis 140  
QY 421 CCTGATATGCTTACAAATCCACATTTGGATTCCTCATTTGAGAAAGTACCCACTCTATGTT 480  
DB 421 CCTGATATGCTTACAAATCCACATTTGGATTCCTCATTTGAGAAAGTACCCACTCTATGTT 480



Db	141	ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal	160
QY	481	TTAAAGGTTTCTGGAAGAAACAAACAGCAGCAAAATGCGATATGATTCACCTGGATC	540
Db	161	LeuLysValSerGlyLysGluGlnAlaLysAsnAlaIleTrpIleAspCysGlyIle	180
QY	541	CATGCCAGAGATGGATCTCTCTGCTTTCTGCTGCTTCATAGGCCATTAATCGAATG	600
Db	181	HisAlaArgGluTrpLysProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet	200
QY	601	TGGAGAAAGACCGTTCTTTCTATGCGAAACAATTCATTCGGAACAGACCTGGAATAGC	660
Db	201	TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg	220
QY	661	AACTTTGCTCCAAACACATGGTGTGAGGAAGGTGCATCCAGTCCCTCATCGGAAACC	720
Db	221	AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr	240
QY	721	TACTGTGGACTTTATCTCTGAGTCAGAACAGACAGAGTGAAGCGCAGTGGCTAGTTCTTGAGA	780
Db	241	TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg	260
QY	781	AGAAATATCAACAGATTAAGCATACATCAGCATGCATTCATTCACCCAGCATATAGTG	840
Db	261	ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal	280
QY	841	TTTCCATATCTCATACAGAAAGTAAAGCAAGACCATGAGCAACTGCTCTAGTAGCC	900
Db	281	PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla	300
QY	901	AGTGAAGCAGTTCGTCTATTGACAAACCTAGTAAATAATACCAAGGTATACACATGGCCAT	960
Db	301	SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis	320
QY	961	GGCTCAGAACCTTATACCTAGTCTCTGGAGGTGGGACGATTCGATCTATGATTTGGGC	1020
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QY	1021	ATCAATATATCGTT-----	1034
Db	341	IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro	360
QY	1035	-----TACATCAAAACCCACTCTAGAGAGCTTTTGGCGCTGCTCTAA 1079	
Db	361	GluArgTyrIleLysProThrCysArgGluAlaPheAlaValSerLys	377

RESULT 3

US-10-379-836-17  
 ; Sequence 17, Application US/10379836  
 ; Publication No. US20030215850A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
 ; TITLE OF INVENTION: TAFI  
 ; FILE REFERENCE: D0214NP  
 ; CURRENT APPLICATION NUMBER: US/10/379, 836  
 ; CURRENT FILING DATE: 2003-03-04  
 ; PRIOR FILING DATE: 2002-03-04  
 ; PRIOR FILING DATE: 2002-03-04  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 17  
 ; LENGTH: 423  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-379-836-17

Alignment Scores:  
 Pred. No.: 6,71e-182 Length: 423  
 Score: 1835.00 Matches: 356  
 Percent Similarity: 86.23% Conservative: 1  
 Best Local Similarity: 85.99% Mismatches: 3  
 Query Match: 94.98% Indels: 55

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QY	61	TTCCGGTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTCTTAGAACCTCTAGGCAAGTTCAA	120
Db	21	PheAlaPheGlnSerGlyGlnValLeuAlaLaleuProArgThrSerArgGlnValGln	40
QY	121	GTTCTACAGAACTTTACTACAACATATGAGATTTGTTCTCTGCAGCCCGTAAACAGCTGAC	180
Db	41	ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp	60
QY	181	CTTATTGTGAGAAAAACAAGTCCATTTTGTAAATGTCATCTGATGTCACATGTC	240
Db	61	LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal	80
QY	241	AAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTCTGTCGACAGCTGGAAGAT	300
Db	81	LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp	100
QY	301	CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCTCCGCATCTGACTAT	360
Db	101	LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr	120
QY	361	GAACAGTATCATCTAAATGAAATCTATCTCTGATAGATTTTATACTGAGGCGAT	420
Db	121	GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis	140
QY	421	CCTGATATGCTTTACAAAATCCACATTTGGATCCTCATTTTGAGAAGTACCACCTCTATGT	480
Db	141	ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal	160
QY	481	TTAAAGGTTTCTGAAAAAGAACAAACAGCAAAATGCCATATGATTCAGTGTGAAATC	540
Db	161	LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle	180
QY	541	CATGCCAGAGATGATCTCTCTGCTTCTGCTGTTGTTGTTTATAGGCCAT	591
Db	181	HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln	200
QY	591	-----	591
Db	201	PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet	220
QY	592	-----AATCGAATGTGGAGAAAG	609
Db	221	ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys	240
QY	610	AACGGTTCTTTCTATGCGAAACAATTCATTCATCGGACAGACCTGATAGCACTTTGTC	669
Db	241	AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla	260
QY	670	TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAAACCTACTGTGA	729
Db	261	SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly	280
QY	730	CTTTATCTCTGAGTCAGAACCCAGAGTGAAGCGAGTGGCTAGTTTCTTTGAGAAATATC	789
Db	281	LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle	300
QY	790	AACAGATTAAGCATACATCAGCATGATTCATCTACTCCAGCATATAGTTTCCATAT	849
Db	301	AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr	320
QY	850	TCCTATACAGAAAGTAAAGCAAAAGACCATGAGGAACCTGCTCTCTAGTAGCCAGTGAAGCA	909
Db	321	SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla	340
QY	910	GTTCTGCTATTGACAAAACTAGTAAAAATACCGAGGTATACACATGCCCATGCTCAGAA	969

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|||||...|||||
341 ValArgAlaIleGluLeuThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCATTATACCTAGCTCTCGAGGTGGGACGATTCGATCTATGATTGGGCATCAAAATAT 1029
Db 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCAGCTGTAGAGAGCTTTTCCGCTGTCTCTAAA 1079
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414

RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Alignment Scores:
Pred. No.: 9,4e-181 Length: 423
Score: 1824.00 Matches: 354
Percent Similarity: 85.75% Conservative: 1
Best Local Similarity: 85.51% Mismatches: 5
Query Match: 94.41% Indels: 55
DB: Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-09-813-133A-4 (1-423)
QY 1 ATGAGCTTTTCAGCCTTCGAGTCTCTGATCCCATTTGTTCTCTCTGTCAGCAGCATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGTTCAGAGTGGCCAGTTCTAGTGTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGCCGCTAACAGCTGAC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGTCATCTGTGTCGACAATGTG 240
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTGTCGGCAGAGTGGAAAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACACAGATTTCACACACAGCAGTCCAGCCCGAGCTCCGCGATCGTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTCGATAGAAATTTATTAAGTGAAGCAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140

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QY 421 CCTGATGCTTACAAAAATCCACATTTGGATCCTCATTGTGAGAAAGTACCCACTCTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAGGTTTCTGAAAAGAACAAACAGCCAAAAATGCCATATGCATATGATGACTGTGGAAATC 540
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 541 CATCCAGAGAAATCGATCTCTCTGCTTTCTGCTTGTGGTTCATAGGCCAT----- 591
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 -----TAC 591
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----AATCGAATGTGGAGAAAG 609
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTTCTATGCGAACAAATCATTTGCATCGGAACAGACCTGAATAGCAACTTTGTC 669
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCCAAACACTGCTGTGAGGAGGTGCATCCAGTTCCCTCATGCTCGGAACCTACTGTGGA 729
Db 261 SerLysHisTrpCysGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCTGAGTCTGAGGAGGTGAGGAGTGAAGCAGTGGCTAGTTCTTCTGAGAAAGAAATATC 789
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
QY 790 AACGAGATTAAAGCATACATCAGCATGATTCATCTCCAGCATATAGTGTTCCTCATAT 849
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACACAGTAAAGCAAGCAACATGAGCAGTCTCTCTAGTAGCCAGTGAAGCA 909
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTGACAAACTAGTAAAAAATACACAGGTATACACATGGCCATGGCTCAGAA 969
Db 341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATACCTAGTCTCTGAGAGTGGGACGATTCGATCTATGATTTGGGCATCAAAATAT 1029
Db 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCAGCTGTAGAGAGCTTTTCCGCTGTCTCTAAA 1079
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414

RESULT 5
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

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; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-10-212-877-4

Alignment Scores:
Pred. No.: 9,4e-181 Length: 423
Score: 1824.00 Matches: 354
Percent Similarity: 85.75% Conservative: 1
Best Local Similarity: 85.51% Mismatches: 5
Query Match: 94.41% Indels: 55
DB: 14 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-10-212-877-4 (1-423)

QY 1 ATGAAGCTTTGAGCGCTTCAGCTCCTTGACCATGTTCTCTCTGAGCAGCATGTC 60
DB 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGCTTCAGAGTGGCCCAAGTCTTAGCTGCTCTCTAGAACCTCTAGGCAAGTCAA 120
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGAATCTTACTACAATAGATTGTTCTCTGCGAGCCGGTAACAGCTGAC 180
DB 41 ValLeuGlnAsnLeuThrThrThrThrGluIleValLeuTrpGlnProValThrAlaasp 60
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATCGACATGTG 240
DB 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATCCATGAGTGTCTTGTGGCAGACGTGGAAGAT 300
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaaspValGluasp 100
QY 301 CTTATTCAACAGCAGATTTCCACAGCACAGTCCAGCCCGCGCTCCGCTACTACT 360
DB 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCAATAAGAAATCTATTCTTGATAGATAATTAATCTAGAGGCAT 420
DB 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTACAAAATCCATGTCATCTGATCTTGCAGAGTACCCTCTATGTT 480
DB 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAGGTTTCTGAAAAAGAACAAACAGCCCAAAATGCCATATGGAATGACTGTGGAATC 540
DB 161 LysLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleaspCysGlyIle 180
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTGTTCTGTTGTTTCATAGGCCAT 591
DB 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 ----- 591
DB 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValaspPheTyrValMet 220
QY 592 -----AATCGAATGTGGAGAAAG 609
DB 221 ProValValAsnValaspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpAglLys 240
QY 610 AACGGTTCTTTCTATGCGAAACAATCAATTGATCGGAACAGACCTGGAATGCACTTTGTC 669
DB 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 280
QY 670 TCCMAACACTGGTGTGAGGAGGTGCATCCAGTCTCTCATGCTCGGAAACCTACTGTGA 729
DB 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCTCAGTTCAGAACAGAGTGAAGCGAGTGGCTAGTTCTTTGAGAAGAAATATC 789
DB 730 -----
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DB 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
QY 790 AACCAGATTAAAGCATATCATCATGATTCATCATATCCACAGCATATAGTGTTCCTCAT 849
DB 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACAGAGTAAAGCAAGACCATCAGGAACCTGTCTCTAGTAGCCAGTGAAGCA 909
DB 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTGACAAAACCTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGAA 969
DB 341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATACCTAGCTCTCGAGGTGGGACGATGGATCTATGATTTGGGCATCAAAAT 1029
DB 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
DB 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCACTGTAGAGAAGCTTTTCCCGCTGCTCTATAA 1079
DB 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414
```

RESULT 6

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US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
```

```

; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Alignment Scores:
Pred. No.: 1,898-179 Length: 428
Score: 1811.50 Matches: 354
Percent Similarity: 84.73% Conservative: 1
Best Local Similarity: 84.49% Mismatches: 5
Query Match: 93.76% Indels: 60
DB: 15 Gaps: 3

US-09-980-881a-1_copy_18_1097 (1-1080) x US-10-115-479-68 (1-428)

QY 1 ATGAGCTTTGAGCGCTTGCAGTCTCTGACCAATGTTCTCTCTGAGCAGCATGTC 60
DB 1 MetLysLeuCysSerLeuAlaValLeuValProLleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGGTTCCAGAGTGGCCAGTCTCTAGCTGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGATCTTACTACAAATATGAGATTTGTTCTCTGGCAGCGGTAAACAGCTGAC 180
DB 41 ValLeuGlnAsnLeuThrThrThrTyrGluLeuValLeuLeuProValThrAlaAsp 60
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACAATGTG 240
DB 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGGGGAATCCATGCAGTGTCTGCTGGCAGAGCTGGAAGAT 300
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTTCAACGACACAGTACGCCCCCGAGCTCCGCACTCGTACTAT 360
DB 101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCTACTACTAAATCAATCTATTCTTGGATAGAAATTTAATCACTGAGAGGCAT 420
DB 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTyrPheIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTACAAAATCCACATTCGATGCTCTCTTGGAGTACCCACTCTATGTT 480
DB 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAG-----GTTTCTCGAAAAGAACAAACAGCCCAAAATGCCATATGG 525
DB 161 LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrp 180
QY 526 ATTGACTGTGAATCCATGCCAGAGAATGGATCTCTCTGCTTTCTGCTTGTGGTTCATA 585
DB 181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 200
QY 586 GCCCAT----- 591
DB 201 GlyHisIleThrGlnPheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuVal 220
QY 592 -----AAT 594
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DB 221 AspPheTyrValMetProValValAsnValAspGlyTyrAspTyrSerTrpLysAsn 240
QY 595 CGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACCAATCATTCGATCGGAACGAGCTG 654
DB 241 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 260
QY 655 AATAGCAACTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCG 714
DB 261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 280
QY 715 GAAACCTACTGTGAGCTTTTATCTGAGTCAAGAACAGAGTGAAGGAGTGGCTAGTTTC 774
DB 281 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 300
QY 775 TTGAGAAATAATATCAACAGATTAAAGCATATACATCAGCATGCAATTCATCTCCAGCAT 834
DB 301 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 320
QY 835 ATAGTGTTCATATTCCTATACACGAAGTAAAGCAAAAGCAACCATGAGGAAGTCTCTCTA 894
DB 321 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 340
QY 895 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAAACCTAGTAAATAATACAGGTATACAT 954
DB 341 ValAlaSerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHis 360
QY 955 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCGAGTGGGAGCATGGATGATATGAT 1014
DB 361 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAsp 380
QY 1015 TTGGGCATCAATATTCGTT----- 1034
DB 381 LeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeu 400
QY 1035 -----TACATCAAAACCCACCTGTAGAGAACTTTTCCGCTGCTCTCTAAA 1079
DB 401 LeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaValSerLys 419

RESULT 7
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine B.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479

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; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-70

Alignment Scores:
Pred. No.: 1,896-179 Length: 428
Score: 1811.50 Matches: 354
Percent Similarity: 84.73% Conservative: 1
Best Local Similarity: 84.49% Mismatches: 5
Query Match: 93.76% Indels: 60
DB: 15 Gaps: 3

US-09-980-881a-1\_COPY\_18\_1097 (1-1080) x US-10-115-479-70 (1-428)
QY 1 ATGAAGCTTTCAGCCCTTCAGCTCTGTATACCATGTTCTCTCTGTGTGAGCAGATGTC 60
DB 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGCTTCAGAGTGGCCAGTCTTAGCTGCTCTTCCCTAGAACCTCTAGGCAAGTTCAA 120
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGAACTTACTACAAATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGAC 180
DB 41 ValLeuGlnAsnLeuThrThrThrTyrgluValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTGAAGAAAAAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACATGTG 240
DB 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTAATGTGACGGNAATCCATGAGTGTCTTCTGTGGCAGACGTGGAGAT 300
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTCACACGACAGTACAGCCCGGAGCTCCGATCGTACTAT 360
DB 101 LeuIleGlnGlnLileSerAsnAspThrValSerProArgAlaSerAlaSerTyTy 120
QY 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATTAAGTACGAGGCAT 420
DB 121 GluGlnTyHisSerLeuAsnGluIleTySerTrpIleGluPheIleThrGluAtgHis 140
QY 421 CCTGATATGCTTACAAAAATCCATTTGGATCCTCATTTGAGAGTACCCACTCTATGTT 480
DB 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTyVal 160
QY 481 TTAAG-----GTTCTTGGAAAGAACAAACAGCCAAATGCCATATGG 525

Db 161 LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrp 180
QY 526 ATTGACTGTGAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGTTGTTGTTCAATA 585
DB 181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 200
QY 586 GCCCAT----- 591
DB 201 GlyHisIleThrGlnPheTyrglyIleIleGlyGlnTyThrAsnLeuLeuArgLeuVal 220
QY 592 -----AAT 594
DB 221 AspPheTyValMetProValValAsnValAspGlyTyArgTySerTrpLysLysAsn 240
QY 595 CGAATGTGAGAAAGAACCGTTCTTTCTATCGAACAAATCATTTGCATCGGAACAGACCTG 654
DB 241 ArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAspLeu 260
QY 655 AATAGCAACTTTGCTCCAAACACATGTTGTGAGGAAGTGCATCCAGTTCCTCATGCTCG 714
DB 261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 280
QY 715 GAACTACTGTGGACTTTATCTCAGTCAGAACAGACAGATGCAAGTGAAGCAGTGGCTAGTTTC 774
DB 281 GluThrTyCysGlyLeuTyProGluSerGluProGluValLysAlaValAsnSerPhe 300
QY 775 TTGAGAAGAAATATCAACAGATTAAGCATACATCAGCATGCATTCATCTACTATCCAGCAT 834
DB 301 LeuArgArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGlnHis 320
QY 835 ATAGTGTTCATATTCCTATACAGAAAGTAAACAAAGACCATGAGGAATCTGCTCTA 894
DB 321 IleValPheProTySerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeu 340
QY 895 GTAGCCAGTGAAGCAGTTCGCTATTGACAAACTAGCTATAAAATACCAAGTATACACAT 954
DB 341 ValAlaSerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyThrHis 360
QY 955 GCCCATGGCTCAGAAACCTTATACCTAGCTCTGGAGTGGGAGCAGATTGGATCTATGAT 1014
DB 361 GlyHisGlySerGluThrLeuTyLeuAlaProGlyGlyGlyAspAspTrpIleTyArgP 380
QY 1015 TTGGGCATCAAAATATTCGTT----- 1034
DB 381 LeuGlyIleLysTySerPheThrIleGluLeuArgAspThrGlyThrTyGlyPheLeu 400
QY 1035 -----TACATCAACCCACCTGTAGAGAGCTTTTGGCGCTGCTCTCTAAA 1079
DB 401 LeuProGluArgTyIleLysProThrCysArgGluAlaPheAlaValSerLys 419

RESULT 8
US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-10-379-836-2
Alignment Scores: 1.26e-172 Length: 423
Pred. No.:

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Score: 1746.00 Matches: 338
Percent Similarity: 83.82% Conservative: 9
Best Local Similarity: 81.64% Mismatches: 13
Query Match: 90.37% Indels: 55
DB: 14 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-10-379-836-2 (1-423)

QY 1 ATGAAGCTTTGAGCGCTTGCAGTCTTGTACCATTGTTCTCTCTCTGTGAGCAGCATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGTTCCAGAGTGGCCAGTTCTAGCTCTCTCTCTAGAACCTCTAGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGAATCTTACTACAACTATGAGATTGTTCTCTGCGCAGCCGGTAACAGCTGAC 180
Db 41 ValLeuGlnAsnLeuThrThrThrTyrrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGTGACAAATGTG 240
Db 61 LeuIleGluLysLysGlnValHisPhePheValAsnSerSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGCGGAATTCATGCACTGTTCTGCTGGCAGAGTGGAAAGAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTCACACACAGCAGTCCCGAGCTCCGCGATCGTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrr 120
QY 361 GAACAGTATCACTCAATAAATATATTTCTTCGATAGATAATTTATTAACGTAGAGGCAT 420
Db 121 GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluLeuIleThrGluLysTyrr 140
QY 421 CCTGATATGCTTACAAAATCCACATTCGATCTCATTTGAGAGTACCCACTCTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerTyrrGluLysHisProLeuTyrrVal 160
QY 481 TTAAAGGTTTCTGGAAGAAACAAACAGCCAAAAATGCCATATGATGATTGCTGGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaMetTrpIleAspCysGlyIle 180
QY 541 CATGCCAGAAATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGlu 200
QY 591 ----- 591
Db 201 TyrTyrrGlyIleIleGlyGluTyrrThrAsnLeuLeuArgHisValAspPheTyrrValMet 220
QY 592 -----AATCGAATGTGGAAGAAAG 609
Db 221 ProValValAsnValAspGlyTyrrAspTyrrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTCTATGCGAAACAAATCATTCGATCGGAACAGACCTCGAATAGCAACTTTGTC 669
Db 241 AsnArgSerPheTyrrAlaAsnAsnArgCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCCAAACACTGTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 729
Db 261 SerLysHisTrpCysGluGluGlyAlaSerPheSerCysSerSerGluThrTyrrCysGly 280
QY 730 CTTTATCTCTAGTCAGAACCAAGTGAAGGAGTGGCTAGTTTCTTCTGAGAAGAAATATC 789
Db 281 LeuTyrrProGluSerGluProGluAlaLysAlaValAlaAsnPheLeuArgAsnIle 300
QY 790 AACCAAGTTAAAGCATACATACGATGCAATTCATATCTCCAGCATATATGTGTTCCATAT 849
Db 301 AsnHisIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPheProTyrr 320
QY 850 TCCTATACAGGAAGTAAAAAGCAAGACCATGAGGAAGTCTCTCTAGTAGCCAGTAGCA 909
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Db 321 SerTyrrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTGACAAAACCTAGTAAAAATACCAAGGTATACACATGCGCCATGGCTCAGAA 969
Db 341 ValArgAlaIleGlnLysThrSerLysAsnIleArgTyrrThrHisGlyArgGlySerGlu 360
QY 970 ACCTTATACCTAGTCTCTGAGGTGGGACGATGGAATGGAATGATTTGGGCAATCAATAT 1029
Db 361 ThrLeuTyrrLeuAlaProGlyGlyAlaAspAspTrpIleTyrrAspLeuGlyIleLysTyrr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyLysTyrrGlyPheLeuLeuProGluArgTyrr 400
QY 1038 ATCAAAACCCACCTGTAGAGAGCTTTTTCGCCGCTCTCTCTATAA 1079
Db 401 IleLysProThrCysLysAspAlaPheAlaValSerLys 414

RESULT 9
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-836-18

Alignment Scores: 2.97e-152 Length: 422
Score: 1550.50 Matches: 302
Percent Similarity: 78.99% Conservative: 25
Best Local Similarity: 72.95% Mismatches: 32
Query Match: 80.25% Indels: 56
DB: 14 Gaps: 3

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-10-379-836-18 (1-422)

QY 1 ATGAAGCTTTGACGCTTGCAGTCTTGTACCATTGTTCTCTCTCTGTGAGCAGCATGTC 60
Db 1 MetLysLeuHisGlyLeuGlyIleLeuValAlaIleIleLeuTyrr---GluGlnHisGly 19
QY 61 TTCGGTTCCAGAGTGGCCAGTTCTAGCTCTCTCTCTAGAACCTCTAGCAAGTTCAA 120
Db 20 PheAlaPheGlnSerGlyGlnValLeuSerAlaLeuProArgThrSerArgGlnValGln 39
QY 121 GTTCTACAGAATCTTACTACAACTATGAGATTGTTCTCTGCGCAGCCGGTAACAGCTGAC 180
Db 40 LeuLeuGlnAsnLeuThrThrThrTyrrGluValValLeuTrpGlnProValThrAlaGlu 59
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGTGAGCAAGTGAAGAT 240
Db 60 PheIleGluLysLysGluValHisPhePheValAsnAlaSerAspValAspSerVal 79
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGTTCTCTGCGCAGCCGGTGAAGAT 300
Db 80 LysAlaHisLeuAsnValSerArgIleProPheAsnValLeuMetAsnAsnValGluAsp 99
QY 301 CTTATTCAACAGCAGATTTTCCACACAGCAGTACGCCCCGAGCTCCGCAATCGTACTAT 360
Db 100 LeuIleGluGlnThrPheAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrr 119
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Db 260 SerLysHisTrpCysGluLysGlyAlaSerSerPheSerCysSerGluThrTyrCysGly 279
Qy 730 CTTTATCTGAGTCAGAACCAAGTGAAGCAGTGGCTAGTCTTCTTGAGAAATATC 789
Db 280 LeuTyrProGluSerGluProGluValLysAlaValAlaAspPheLeuArgAsnile 299
Qy 790 AACAGATTAAAGCATATCATGCGATGATTCATCTACTCCAGCATATAGTGTTCATAT 849
Db 300 AsnHisIleLysAlaTyrIleSerMetHisSerTyrSerGlnGlnIleLeuPheProTyr 319
Qy 850 TCCTATACACGAAGTAAAGCAAGAACACCATGAGGAGCTGCTCTAGTAGCCAGTGAAGCA 909
Db 320 SerTyrAsnArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 339
Qy 910 GTTCGTGCTATTGACAAAACCTAGTAAATAATACCAGGTATACACATGGCCATGGCTCAGAA 969
Db 340 ValArgAlaIleGluSerIleAsnLysAsnThrArgTyrThrHisGlySerGlySerGlu 359
Qy 970 ACCTTATACCTAGCTCCTGGAGGTGGGACGAGTGGATGATGATGATGATGATGATGAT 1029
Db 360 SerLeuTyrLeuAlaProGlyGlySerAspAspTrpIleTyrAspLeuGlyIleLysTyr 379
Qy 1030 TCGTTTACATC----- 1040
Db 380 SerPheThrIleGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluArgPhe 399
Qy 1041 ---AAACCCACCTGTAGAGAAGCTTTTCCCGCTGTCTCTAAA 1079
Db 400 IleLysProThrCysAlaGluAlaLeuAlaValSerLys 413

RESULT 11
US-10-115-479-64
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytke, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
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; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-64

Alignment Scores:
Pred. No.: 4.9e-141 Length: 322
Score: 1442.50 Matches: 292
Percent Similarity: 77.72% Conservative: 1
Best Local Similarity: 77.45% Mismatches: 3
Query Match: 74.66% Indels: 82
DB: 15 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-10-115-479-64 (1-322)

Qy 1 ATGAAGCTTTGCACGCTTGCAGTCCTTGTACCCATTGTTCTTCTGTGACGACGATGTC 60
Db 1 MetLysLeuCySerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Qy 61 TTGCGGTTCCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Qy 121 GTTCTACAGATCTTACTACAACTATGAGATTGTTCTTGGCAGCGGTAAACAGCTGAC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Qy 181 CTTATTGTGAAGAAAAACAAGTCCATTTTCTTAATGTCATCTGTGTCGCAACTGTG 240
Db 61 LeuIleValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
Qy 241 AAAGCCCATTTAAATGTGAGCGGAATTCACGAGTGTCTTGTGGCAGAGCTGGAAGAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Qy 301 CTTATTCAACAGCAGATTTTCCACGACACAGTACGCCCCCGAGCTCCGCACTGTAAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Qy 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGGTAGAATTTATTAACCTGAGGCGAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Qy 421 CCTGATATGCTTACAAAAATCCACATTTGGATTCCTCATTTGAGAAAGTACCCACTCTAT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Qy 481 TTAAGGTTTCTGAAAGAAACAAACACGCCAAAATATGTCATATGATGATGATGGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAsp----- 177
Qy 541 CATGCCAGAGAAATGGAATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCAATAATCGAATG 600
Db 177 ----- 177
Qy 601 TGGAGAAAGAACCGTTCTTTCTATCGGAACAATCATTTGTCATCGGAACAGACCTGTAATAGC 660
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Db 177 ----- 177

Qy 661 AACTTTGTCTCCAAACACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAAACC 720

Db 177 ----- 177

Qy 721 TACTGTGGACTTTATCTCTGAGTCAGAACACAGAAAGTGAAGCGAGTGGCTAGTTCTTTGAGA 780

Db 178 ---CysGlyLeuTyrProGluSerGluProGluValValAlaValAlaSerPheLeuArg 196

Qy 781 AGAATATCAACACAGATTAAAGCATACATCAGCATGCATTCATCCAGCATATAGTG 840

Db 197 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 216

Qy 841 TTTCCATATTCCTATACACGAACTAAAGCAAGACCATGAGGAAGTGTCTCTAGTAGCC 900

Db 217 PheProTyrSerTyrThrArgSerLysSerLysPheAspHisGluGluLeuSerLeuValAla 236

Qy 901 AGTGAAGCAGTTCGTGCTATTGACAAACATAGTAAATAATACACAGGTATACATGCGCAT 960

Db 237 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis 256

Qy 961 GGCTCAGAACCTTATACCTAGTCTCTGGAGGTGGGAGCATTTGGATCTATGATTTGGGC 1020

Db 257 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 276

Qy 1021 ATCAATATTCGGTT----- 1034

Db 277 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 296

Qy 1035 -----TACATCAAAACCCACTGTAGAGAAGCTTTTGGCGCTCTCTAAA 1079

Db 297 GluArgTyrIleLysProThrCysArgGluAlaPheAlaValSerLys 313

RESULT 12

US-10-115-479-66

Sequence 66, Application US/10115479

Publication No. US20040006205A1

GENERAL INFORMATION:

APPLICANT: Li, Li

APPLICANT: Gerlach, Valerie L.

APPLICANT: Liu, Xiaohong

APPLICANT: Miller, Charles E.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Zerhusen, Bryan D.

APPLICANT: Pena, Carol E.A.

APPLICANT: Shenoy, Suresh G.

APPLICANT: Zhong, Haihong

APPLICANT: Smithson, Glendda

APPLICANT: Casman, Stacie J.

APPLICANT: Boldog, Ferenc L.

APPLICANT: Voss, Edward

APPLICANT: Vernet, Corine

APPLICANT: MacDougall, John A.

APPLICANT: Rastelli, Luca

APPLICANT: Anderson, David W.

APPLICANT: Zhong, Mei

APPLICANT: Mezes, Peter S.

APPLICANT: Furtak, Katarzyna

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.

APPLICANT: Malyanker, Uriel M.

APPLICANT: Shinkets, Richard A.

APPLICANT: Taupier, Raymond J.

APPLICANT: Edinger, Shlomit R.

APPLICANT: Mazur, Ann

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE

FILE REFERENCE: 21402-322 B (Cura 622 PT)

CURRENT APPLICATION NUMBER: US/10/115,479

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 60/281,136

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: 60/281,863

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Db 181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheile 200
Qy 586 GCCCAT----- 591
Db 201 GlyHisIleThrGlnPheTyrglyIleileGlyGlnTyThrAsnLeuLeuArgLeuVal 220
Qy 592 -----AAT 594
Db 221 AspPheTyrValMetProValValAsnValAspGlyTyArgTySerTrpIlyslsAsn 240
Qy 595 CGAATGTGGAGAAAGACCGTTCTTCTATGCGAACAATCATGTCATCGGAACACACCTG 654
Db 241 ArgMetTrpArgAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 260
Qy 655 AATACCAACTTTGTCTCCAAACACCTGGTGTGAGGAGGTGCATCCAGTTCTCTCATGCTCG 714
Db 261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerCysSer 280
Qy 715 GAAACCTACTGTGGACTTTATCTCAGTCAGTCAGAACAGAGTGAAGGCAGTGGCTAGTTTC 774
Db 281 GluThrTyrcysGlyLeuTyProGlu----- 289
Qy 775 TTGAGAAGAAATATCAACAGATTAAAGCATATACATACATCAGATGCATTATCATCTCCAGCAT 834
Db 289 ----- 289
Qy 835 ATAGTGTTCATATTCCTATACACGAAGTAAAGCAAGACCATGAGGAACTGTCTCTA 894
Db 289 ----- 289
Qy 895 GTAGCCAGTGAAGCAGTTCGTCTATTGACAAACTAGTAAATAATACAGGTATACACAT 954
Db 289 ----- 289
Qy 955 GGCCATGGCTCAGAAACCTTATACCTAGCTCTGAGTGGGAGATTGGATCTATGAT 1014
Db 290 -----SerGluThrLeuTyLeuAlaProGlyGlyAspTrpIleTyraSp 306
Qy 1015 TTGGGCATCAATATTCGTT----- 1034
Db 307 LeuGlyIleLysTySerPheThrIleGluLeuArgAspThrGlyThrTyGlyPheLeu 326
Qy 1035 -----TACATCAAAACCCCTGTAGAGAGCTTTTGGCGCTCTCTTAAA 1079
Db 327 LeuProGluArgTyIleLysProThrCysArgGluAlaPheAlaAlaValSerLys 345

RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Alignment Scores:
Pred. No.: 3,326-78 Length: 211
Score: 839.00 Matches: 164
Percent Similarity: 82.59% Conservative: 2
Best Local Similarity: 81.59% Mismatches: 9

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Query Match: 43.43% Indels: 27
DB: 9 Gaps: 3
US-09-980-881A-1_COPY_18_1097 (1-1080) x US-09-925-302-467 (1-211)
Qy 553 TGGATCTCTCTGCTTTCTGCTGCTGCTTATA-----GGC 588
Db 3 TrpIleSer---MetLeuCysArgTrpLeuMetTrpMetValMetAsnTySerTrpIlys 21
Qy 589 CATAATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACAATCATGTCATCGGAACA 648
Db 22 LysAsnArgMetTrpArgLysAsnArgSerPheTyralaAsnAsnHisCysIleGlyThr 41
Qy 649 GACCTGAATACCAACTTTGTCTCCAAACACCTGGTGTGAGGAGGTGCATCCAGTTCTCTCA 708
Db 42 AspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSer 61
Qy 709 TGCTCGGAAACCTACTGTGGACTTTATCTCAGTCAGAACCCAGAGTGAAGGCAGTGGCT 768
Db 62 CysSerGluThrTyrcysGlyLeuTyProGluSerGluProGluValLysAlaValAla 81
Qy 769 AGTTCTTGTGAGAAATATCAACAGATTAAAGCATATACATCAGCATGCATTATCATCTCC 828
Db 82 SerPheLeuArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySer 101
Qy 829 CAGATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACGTG 888
Db 102 GlnHisIleValPheProTySerTyThrArgSerLysSerLysAspHisGluGluLeu 121
Qy 889 TCTCTAGTACGCTGAGCAGATTCTGCTGCTATTCACAAAACCTAGTAAATAATACAGGTAT 948
Db 122 SerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTy 141
Qy 949 ACACATGCCATGCTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGAGCATTTGGATC 1008
Db 142 ThrHisGlyHisGlySerGluThrLeuTyLeuAlaProGlyGlyGlyAspAspTrpIle 161
Qy 1009 TATGATTGGGCATCAATATTCGTT----- 1034
Db 162 TyrAspLeuGlyIleLysTySerPheThrIleGluLeuArgAspThrGlyThrTyGly 181
Qy 1035 -----TACATCAAAACCCCTGTAGAGAGCTTTTGGCGCTCTCTCT 1076
Db 182 PheLeuLeuProGluArgTyIleLysProThrCysArgGluAlaPheAlaAlaValSer 201
Qy 1077 AAA 1079
Db 202 Lys 202

RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Alignment Scores:
Pred. No.: 3,326-78 Length: 211

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Score: 839.00 Matches: 164
Percent Similarity: 82.5% Conservative: 2
Best Local Similarity: 81.5% Mismatches: 9
Query Match: 43.4% Indels: 27
DB: 10 Gaps: 3

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-09-925-302-467 (1-211)
QY 553 TCGATCTCTCGCTTCTGCTTGGTTCATA-----GGC 588
Db 3 TrpIleSer--MetLeuCysArgTrpLeuMetTrpMetValMetAsnTyrSerTrpLys 21
QY 589 CATAATCGAATGTGAGAAAGACGTTCTTTCTATGCGAACAACTATTGCATCGGAACA 648
Db 22 LysAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThr 41
QY 649 GACCTGAATAGCAATTTCTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCA 708
Db 42 AspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSer 61
QY 709 TGCTCGGAACCTACTGTGGACTTTATCTCTGAGTCAGAACCAAGAGTGAAGCAGTGGCT 768
Db 62 CysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAla 81
QY 769 AGTTCTTTCAGAGAATAATCAACAGATTAAAGCATACATCAGCATGCACTCATCTCC 828
Db 82 SerPheLeuArgAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSer 101
QY 829 CAGCATATAGTGTTCATATTCCTATACACGAAGTAAAGCAAGACCATCAGGAATG 888
Db 102 GlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeu 121
QY 889 TCTTAGTAGCAGAGTGAACAGTCTGCTGATTATGACAAACTAGTAAATAACCATCT 948
Db 122 SerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyr 141
QY 949 ACATGAGCCATGGCTCAGAAACCTTATACCTAGCTCTGGAGTGGGAGCAGTGGATC 1008
Db 142 ThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIle 161
QY 1009 TATGATTGGGCATCAATATTCGTT----- 1034
Db 162 TyrAspLeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGly 181
QY 1035 -----TACATCAAAACCCACTGTAGAGAGCTTTTCCCGCTGCTCT 1076
Db 182 PheLeuLeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaValSer 201
QY 1077 AAA 1079
Db 202 Lys 202

RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Spytex, Kimberly A
; APPLICANT: Leite, Mario
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Bialock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
```

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; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074, 978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268, 221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335, 109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312, 284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268, 496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276, 703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330, 293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322, 127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280, 899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310, 797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268, 646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 269
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-074-978A-269

Alignment Scores:
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Score: 646.00 Matches: 140
Percent Similarity: 53.40% Conservative: 64
Best Local Similarity: 36.65% Mismatches: 134
Query Match: 33.44% Indels: 44
DB: 15 Gaps: 7

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QY 67 ----TTCCAGAGTGGCCAGTTCTTCTCTAGAACCTCTAGGCAAGTTCAAGTT 123
Db 21 HisPheGluGlyGluLysValPheArgValAsnValGluAspGluAsnAspSerLeu 40
QY 124 CTACAGAATCTTACTACACATATGAGATTGTTCTTGGCAGCCGGTAAACAGTCACCTT 183
Db 41 LeuHisGluLeuAlaSerThrArgGlnIleAspPheTrpLysProAspSerValThrGln 60
QY 184 ATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGTCATGTCGACAAATGTGAAA 243
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Db 61 IleLysProHisSerThrValAspPheArgVallYsAlaGluAspIleLeuAlaValGlu 80
Qy 244 GCCATTAAATGTCAGCGGAATCCATGCGAGTCTTGTGGCAGACGTGGAAGATCTT 303
Db 81 AspPheLeuGluGlnAsnGluGlnThrGluValLeuIleAsnAsnLeuArgSerVal 100
Qy 304 ATTCACAGCAGATTTCACAGACACAGTCAGCCCGCGCTCCGCATCGTACTATGAA 363
Db 101 LeuGluAlaGlnPheAspSerArgVal-----ArgThrThrGlyHisSerThrGlu 117
Qy 364 CAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCATCCT 423
Db 118 LysTyrAsnAsnTrpGluThrIleGluAlaTrpThrLysGlnValThrSerGluAsnPro 137
Qy 424 GATATGCTTACAAAATCCATTTGGATCCCTCATTTGAGAAGTACCCACTCTATGTTTA 483
Db 138 AspLeuIleSerArgThrAlaIleGlyThrPheLeuGlyAsnAsnIleTyrLeuLeu 157
Qy 484 AAGGTTTCTGGAAGAAAGACCAACGCCAAATGCGATATGGATTGACTGTGGAATCCAT 543
Db 158 LysVal---GlyLysProGlyProAsnLysProAlaIlePheMetAspCysGlyPheHis 176
Qy 544 GCCAGAGATGATCTCTCTGCTTTCTGCTTGTGTTCTATA----- 585
Db 177 AlaArgGluTrpIleSerHisAlaPheCysGlnTrpPheValArgGluAlaValLeuThr 196
Qy 585 ----- 585
Db 197 TyrGlyTyrGluSerHisMetThrGluPheLeuAsnLysLeuAspPheTyrValLeuPro 216
Qy 586 -----GGCCAT-----AATCGAATGTGGAGAAAGAAC 612
Db 217 ValLeuAsnIleAspGlyTyrIleTyrThrTrpThrLysAsnArgMetTrpArgLysThr 236
Qy 613 CGTCTCTTCTATGCGAACAATCATTCGACAGACAGACCTCAATAGCAACTTTGTCTCC 672
Db 237 ArgSerThrAsnAlaGlyThrThrCysIleGlyThrAspProAsnArgAsnPhe---Asp 255
Qy 673 AAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTT 732
Db 256 AlaGlyTyrCysThrThrGlyAlaSerThrAspProCysAspGluThrTyrCysGlySer 275
Qy 733 TATCTGTAGTCAGACCAAGTGAAGCAGTGGCTAGTTCTTTCGAGAAGAAATATCAAC 792
Db 276 AlaAlaGluSerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnAsnLeuSer 295
Qy 793 CAGATTAAGCATACATCAGCATGCAATTCATACCTCCAGCATATAGTGTTCATATTC 852
Db 296 SerIleLysAlaTyrLeuThrIleHisSerTyrSerGlnMetIleLeuTyrProTyrSer 315
Qy 853 TATACAGCAAGTAAAGCAAGCAACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTT 912
Db 316 TyrAspTyrLysLeuProGluAsnAsnAlaGluLeuAsnAsnLeuAlaLysAlaVal 335
Qy 913 CGTGTATTGACAAACTAGTAAATAATACCAGGTATACACATGGCGTCGAGAAACC 972
Db 336 LysGluLeu---AlaThrLeuTyrGlyThrLysTyrThrTyrGlyProGlyAlaThrThr 354
Qy 973 TTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTATGATTTGGGCATCAAAATATTCG 1032
Db 355 IleTyrProAlaAlaGlySerAspAspTrpAlaTyrAspGlnGlyIleLysTyrSer 374
Qy 1033 TTATCA 1038
Db 375 PheThr 376
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 06:04:49 ; Search time 120 Seconds  
(without alignments)  
6397.100 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
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5: /cgn2\_6/prodata/1/ina/FACTUS COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfileseq1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1025.2	94.9	1625	4	US-09-813-133A-1
2	909	84.2	1272	2	US-08-869-057-1
3	909	84.2	1749	1	US-07-649-591B-2
4	909	84.2	1749	1	US-08-277-540-2
5	909	84.2	1749	1	US-08-430-787A-2
6	204	18.9	55827	4	US-09-813-133A-3
7	124	11.5	927	2	US-08-782-760-5
8	124	11.5	927	5	PCT-US96-00995-5
9	123.4	11.4	921	1	US-08-696-139-3
10	123.4	11.4	1215	1	US-08-696-139-1
11	109	10.1	1263	4	US-09-011-769A-38
12	107.6	10.0	1622	4	US-09-023-655-1020
13	107.4	9.9	999	2	US-08-860-882A-67
14	107.4	9.9	999	4	US-09-011-769A-50
15	107.4	9.9	1053	2	US-08-860-882A-64
16	107.4	9.9	1053	4	US-09-011-769A-46
17	107.4	9.9	1263	2	US-08-860-882A-56
18	107.4	9.9	1284	2	US-08-860-882A-71
19	107.4	9.9	1284	4	US-09-011-769A-55
20	104.2	9.6	1053	4	US-09-463-451-27
21	104.2	9.6	1053	4	US-09-463-451-28
22	104.2	9.6	1059	2	US-08-860-882A-74
23	104.2	9.6	1059	2	US-08-860-882A-77
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25	104.2	9.6	1059	4	US-09-011-769A-63
26	101	9.4	1870	3	US-09-171-945-112
27	101	9.4	2154	3	US-09-171-945-124

28	92.8	8.6	1311	4	US-09-675-305-9	Sequence 9, Appli
29	92.8	8.6	1311	4	US-10-200-344-9	Sequence 9, Appli
30	92.8	8.6	2128	4	US-09-675-305-13	Sequence 13, Appli
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32	88.6	8.2	1050	4	US-09-675-305-11	Sequence 11, Appli
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34	87.6	8.1	1200	4	US-09-710-099-7	Sequence 7, Appli
35	87.6	8.1	1200	4	US-10-200-910-7	Sequence 7, Appli
36	83.6	7.7	945	4	US-09-710-099-3	Sequence 3, Appli
37	83.6	7.7	945	4	US-09-710-099-11	Sequence 11, Appli
38	83.6	7.7	945	4	US-10-200-910-3	Sequence 3, Appli
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41	78.4	7.3	741	4	US-09-675-305-5	Sequence 5, Appli
42	78.4	7.3	741	4	US-10-200-344-5	Sequence 5, Appli
43	71.6	6.6	1251	3	US-08-640-906-3	Sequence 3, Appli
44	71.6	6.6	1251	3	US-09-395-936-3	Sequence 3, Appli
45	70.6	6.5	1251	3	US-08-640-906-1	Sequence 1, Appli

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US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Query Match 94.9%; Score 1025.2; DB 4; Length 1625;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1030; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	1	ATGAAGCTTTTGAGCGCTTGCAGTCCCTGTGACCATTTGTTCTTCTGTGAGCAGCATGTC	60
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QY	61	TTTCGGTTCCAGAGTGCCCAAGTTCTAGCTGCTCTTCTAGAACCTCTTAGGCAAGTTCAA	120
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QY	121	GTCTTACAGAACTTACTACAAATATGAGATTTGTTCTTCTGGCAGCGGTAAACAGTGAC	180
Db	137	GTCTTACAGAACTTACTACAAATATGAGATTTGTTCTTCTGGCAGCGGTAAACAGTGAC	196
QY	181	CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGTCATCTGATTCGACAATGTG	240
Db	197	CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGTCATCTGATTCGACAATGTG	256
QY	241	AAAGCCCATTTAAATGTCAGCGGAATTTCCATGCAGTCTTGTGTCAGACGTTGGAAGAT	300
Db	257	AAAGCCCATTTAAATGTCAGCGGAATTTCCATGCAGTCTTGTGTCAGACGTTGGAAGAT	316
QY	301	CTTATTCAACAGCAGATTTTCCAAACGACACAGTCAGCCCCCGAGCCTCCGTCATCTAT	360
Db	317	CTTATTCAACAGCAGATTTTCCAAACGACACAGTCAGCCCCCGAGCCTCCGTCATCTAT	376
QY	361	GAAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTAATCTGAGAGCAT	420

ALIGNMENTS





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Db 641 TTCTATGGGTAATAGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700
Qy 592 -----AATCGAATGTGGAGAAAG 609
Db 701 CCGGTGGTTAATGTGCGGTTATGACTACTCATGGAAGAAAGATCGAATGTGGAGAAAG 760
Qy 610 AACCGTCTTCTATGCGAAACATCATTTGCGATCGGAACAGACCTGAAATAGCACTTTGTC 669
Db 761 AACCGTCTTCTATGCGAAACATCATTTGCGATCGGAACAGACCTGAAATAGCACTTTGCT 820
Qy 670 TCCAAACACTGTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 729
Db 821 TCCAAACACTGTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 880
Qy 730 CTTTATCCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTTCCTTGGAGAAATATC 789
Db 881 CTTTATCCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTTCCTTGGAGAAATATC 940
Qy 790 AACAGATTAAGCATATACATCAGCATGATTCATCTACTCCAGCATATAGTGTTCATAT 849
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Qy 850 TCCTATACAGAGTAAAGCAAGCAACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 909
Db 1001 TCCTATACAGAGTAAAGCAAGCAACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1060
Qy 910 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 969
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Qy 970 ACCTTATACCTAGTCTCTGGAGGTGGGAGCGATTCGATCTATGATTTGGGCATCAATAT 1029
Db 1121 ACCTTATACCTAGTCTCTGGAGGTGGGAGCGATTCGATCTATGATTTGGGCATCAATAT 1180
Qy 1030 TCGTTTACA 1038
Db 1181 TCGTTTACA 1189

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RESULT 4

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US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Hasak, Janet E. 28,616
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-277-540-2

Query Match 84.2%; Score 909; DB 1; Length 1749;
Best Local Similarity 89.9%; Pred. No. 7.2e-281;
Matches 1033; Conservative 0; Mismatches 5; Indels 111; Gaps 1;

Qy 1 ATGAAGCTTTTCAGCCTTGCAGTCTTGTACCCCAATGTTCTCTTCTGTGACGACGATGTC 60
Db 41 ATGAAGCTTTTCAGCCTTGCAGTCTTGTACCCCAATGTTCTCTTCTGTGACGACGATGTC 100
Qy 61 TTCCGCTTTCCAGAGTGGCCAAAGTTCTAGTCTCTCTTCTAGAACTCTCTAGCAAGTTCAA 120
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Qy 121 GTTCTACAGAACTTTACTTACAAATATAGATTTGTTCTCTGCGAGCCGGTAAACAGTGCAC 180
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Db 221 CTTATTGGAAGAAAAAACAAGTCCATTTTCTGTAATGCTATCTGATGTCGACAAATGTG 280
Qy 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGTCCTGCTGGCAGACGTTGGAAGAT 300
Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGTCCTGCTGGCAGACGTTGGAAGAT 340
Qy 301 CTTATTCAACAGCAGATTTTCCAAACGACACAGTACGCCCCCGAGCTCCGCAATCGTACTAT 360
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Qy 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGAT 420
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Qy 421 CTTGATATGCTTACAAAAATCCACATTTGGATCTCTCAATTTGAGAAAGTACCCACTCTATGTT 480
Db 461 CTTGATATGCTTACAAAAATCCACATTTGGATCTCTCAATTTGAGAAAGTACCCACTCTATGTT 520
Qy 481 TTAAGAGTTTCTGGAAAGAAACAAACAGCCAAAAATGCCATATGGAATGACTGTGGAATC 540
Db 521 TTAAGAGTTTCTGGAAAGAAACAAACAGCCAAAAATGCCATATGGAATGACTGTGGAATC 580
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Db 581 CATGCCAGAGAAATGGAATCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 640
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Db 641 TTCTATGGGTAATAGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700
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QY      730 CTTTATFCTGAGTCAGAACAGAGTGAAGGAGTGGCTAGTCTTCTTGAGAGAAATATC 789
Db      881 CTTTATCCTGAGTCAGAACAGAGTGAAGGAGTGGCTAGTCTTCTTGAGAGAAATATC 940
QY      790 ACCAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 849
Db      941 ACCAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 1000
QY      850 TCCTATACAGAAAGTAAAGCAAGCAACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 909
Db      1001 TCCTATACAGAAAGTAAAGCAAGCAACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 1060
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Db      1061 GTTCGTGCTATTGAGAAAACCTAGTAAATAACAGGTATACACATGGCCATGGCTCAGAA 1120
QY      970 ACCTTATACCTAGCTCCTCGAGTGGGAGCATTTGGATCTATGATTTGGGCATCAAATAT 1029
Db      1121 ACCTTATACCTAGCTCCTCGAGTGGGAGCATTTGGATCTATGATTTGGGCATCAAATAT 1180
QY      1030 TCGTTTACA 1038
Db      1181 TCGTTTACA 1189

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## RESULT 5

US-08-430-787A-2

; Sequence 2, Application US/08430787A

; Patent No. 553674

; GENERAL INFORMATION:

; APPLICANT: Drayna, Dennis T., Eaton, Dan L.

; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/430,787A

; FILING DATE: 27-APR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/277,540

; FILING DATE: 19-JUL-1994

; APPLICATION NUMBER: 08/167727

; FILING DATE: 15-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/959944

; FILING DATE: 14-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/649591

; FILING DATE: 01-FEB-91

; ATTORNEY/AGENT INFORMATION:

; NAME: Haseak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 689D1C1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1749 bases

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-430-787A-2

Query Match      84.2%; Score 909; DB 1; Length 1749;
Best Local Similarity 89.9%; Pred. No. 7.2e-281;
Matches 1033; Conservative 0; Mismatches 5; Indels 111; Gaps 1;

QY      1 ATGAAGCTTTGCAGCCTTGCAGTCCCTCTACCCATTGTTCTCTCTGTGAGCAGCATGTC 60
Db      41 ATGAAGCTTTGCAGCCTTGCAGTCCCTCTACCCATTGTTCTCTCTGTGAGCAGCATGTC 100
QY      61 TTCCGGTTTCCAGAGTGGCCAAAGTCTTAGTCTGCTCTTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db      101 TTCCGGTTTCCAGAGTGGCCAAAGTCTTAGTCTGCTCTTCTCTAGAACCTCTAGGCAAGTTCAA 160
QY      121 GTTCTACAGAAATCTTATCTACCAATATGAGATTTGTTCTTCTGCGACCGGTAAACAGTGTAC 180
Db      161 GTTCTACAGAAATCTTATCTACCAATATGAGATTTGTTCTTCTGCGACCGGTAAACAGTGTAC 220
QY      181 CTTATTGTGAAGAAAAACAAAGTCCATTTTGTAAATGTCATCTGATGTCGACAAATGTG 240
Db      221 CTTATTGTGAAGAAAAACAAAGTCCATTTTGTAAATGTCATCTGATGTCGACAAATGTG 280
QY      241 AAAGGCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTCTGTCGACAGCTGGAAGAT 300
Db      281 AAAGGCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTCTGTCGACAGCTGGAAGAT 340
QY      301 CTTATTCAACAGCAGATTTCCAAACACACAGTACAGCCCCCGAGCCCTCCGCATCTGTAAT 360
Db      341 CTTATTCAACAGCAGATTTCCAAACACACAGTACAGCCCCCGAGCCCTCCGCATCTGTAAT 400
QY      361 GAACAGTATCACTCACTAAATGAAATCTTCTCGATAGAAATTTATTAATCTGAGAGGCAT 420
Db      401 GAACAGTATCACTCACTAAATGAAATCTTCTCGATAGAAATTTATTAATCTGAGAGGCAT 460
QY      421 CCGTATATGCTTTACAAAATCCACATTTGGATCCTCATTTTGAGAAAGTACCACCTCTATGTT 480
Db      461 CCGTATATGCTTTACAAAATCCACATTTGGATCCTCATTTTGAGAAAGTACCACCTCTATGTT 520
QY      481 TTTAAAGTTTCTGGAAAAGAAACAAACAGCAGCAAAATGCCATATGGAATTCAGCTGTGGAATC 540
Db      521 TTTAAAGTTTCTGGAAAAGAAACAAACAGCAGCAAAATGCCATATGGAATTCAGCTGTGGAATC 580
QY      541 CATGCCAGAAATGGATCTCTCTCTGTTTCTGCTGTGCTTCTATAGGCCAT 591
Db      581 CATGCCAGAAATGGATCTCTCTCTGTTTCTGCTGTGCTTCTATAGGCCATATAACTCAA 640
QY      592 ----- 591
Db      641 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700
QY      592 -----AATCGAATGTGGAGAAAG 609
Db      701 CCGGTGTTTAAATGTGGACGGTTATGACTACTCATGGAAAAAGAAATCGAATGTGGAGAAAG 760
QY      610 AACCGTTCTTCTATCGGAACATCAATTCATCGGACAGACCTGAAATAGCAACTTTGTC 669
Db      761 AACCGTTCTTCTATCGGAACATCAATTCATCGGACAGACCTGAAATAGCAACTTTGTC 820
QY      670 TCCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAAACCTACTGTGGA 729
Db      821 TCCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAAACCTACTGTGGA 880
QY      730 CTTTATCCTGAGTTCAGAACCCAGAGGAGTGGCTAGTGTCTTTTGAGAGAAATATC 789
Db      881 CTTTATCCTGAGTTCAGAACCCAGAGGAGTGGCTAGTGTCTTTTGAGAGAAATATC 940
QY      790 AACCAAGTTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 849
Db      941 AACCAAGTTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 1000

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QY 850 TCCTATACAGAGTAAAGCAAGCAACCATGAGGAAGTCTCTCTAGTAGCCAGTGAAGCA 909  
Db 1001 TCCTATACAGAGTAAAGCAAGCAACCATGAGGAAGTCTCTCTAGTAGCCAGTGAAGCA 1060  
QY 910 GTTCGTGCTATTGACAAAGTAAAGTAAATACCAAGTATACATCGGCGCTCGAGAA 969  
Db 1061 GTTCGTGCTATTGACAAAGTAAAGTAAATACCAAGTATACATCGGCGCTCGAGAA 1120  
QY 970 ACCTTATACCTAGCTCCTGGAGTGGGAGCGATTCGATCTATGATTTGGGCATCAAAATAT 1029  
Db 1121 ACCTTATACCTAGCTCCTGGAGTGGGAGCGATTCGATCTATGATTTGGGCATCAAAATAT 1180  
QY 1030 TCGTTTACA 1038  
Db 1181 TCGTTTACA 1189  
RESULT 6  
US-09-813-133A-3  
; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 55827  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-3

Query Match 18.9%; Score 204; DB 4; Length 55827;  
Best Local Similarity 100.0%; Pred. No. 5.6e-54;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 685 GAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGAGGACTTTATCTCTGAGTCA 744  
Db 48643 GAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGAGGACTTTATCTCTGAGTCA 48702  
QY 745 GAACAGAGTGAAGGCGAGTGGCTAGTTCTTTGAGAAGAAATATCAACAGATTAAGCA 804  
Db 48703 GAACAGAGTGAAGGCGAGTGGCTAGTTCTTTGAGAAGAAATATCAACAGATTAAGCA 48762  
QY 805 TACATCAGATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGGAAGT 864  
Db 48763 TACATCAGATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGGAAGT 48822  
QY 865 AAAAGCAAGACCATGAGGAAGT 888  
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 7  
US-08-782-760-5  
; Sequence 5, Application US/08782760  
; Patent No. 5948688  
; GENERAL INFORMATION:  
; APPLICANT: Hartman, Jacob  
; APPLICANT: Fulga, Netta  
; APPLICANT: Mendelovitch, Simona  
; APPLICANT: Gorecki, Marian  
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
; TITLE OF INVENTION: CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/782,760  
FILING DATE: 13-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/378,233  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0336/43847  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 927 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..927  
US-08-782-760-5

Query Match 11.5%; Score 124; DB 2; Length 927;  
Best Local Similarity 57.9%; Pred. No. 2.1e-29;  
Matches 278; Conservative 0; Mismatches 195; Indels 7; Gaps 3;  
QY 596 GAATGTGAGAAAGAACCGTTCTTTCTATGGAACAATCATTTGATCGGAACAGACCTGA 655  
Db 362 GAATGTGAGAAAGAACCGCTCTACTATGGCTGGAAGTCTCTGTTGGGTGAGACCCA 421  
QY 656 ATAGCAACTTTGTCTCTCAAAACATCTGGTGTGAGGAAGGTGCATCCAGTTCTCATGCTCGG 715  
Db 422 ACAGGAATTTTAATGC---TGGCTGGTGTGGAAGTGGGAGCTTCTCGGAGTCCCTGCTCTG 478  
QY 716 AAACCTACTGTGGACTTTATCTCTGATGAGAACAGAGTGAAGGAGTGGCTAGTTCT 775  
Db 479 AAACCTACTGTGGAGCAAGCCCGAGCTGTGAAAGAGACAAAGGCCCTGCGAGATTTCA 538  
QY 776 TGAGAAGAAATATCAACCCAGATTAAGCATACATCAGCATCATTCATCTACTCCAGCATA 835  
Db 539 TCCGCAACACCTCTCCACCATCAAGGCTACCTGACCATCCATCCATCTACTCTACAGATGA 598  
QY 836 TAGTGTTTTCCATATTTCCATATACAGGAAGTAAAGCAAGCAAGCATGAGGAAGTGTCTCTAG 895  
Db 599 TGCTCTACCTTTACTCTCTATGACTACAACTGCCTGAGAACTATCAGGAATTTGAATGCC 658  
QY 896 TAGCCAGTGAAGCAGTTCTGCTCTATTGAAAAAATAGTAAAAATACCAAGTATACACATG 955  
Db 659 TGGTGAAGGTGCGGCAAGGAGCTTGCC---ACTCTGATGAGCAAGCAAGTACACATATG 715  
QY 956 GCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGTGGGAGCATTTGGATCTATGAT 1015  
Db 716 GCCCAGGAGCTACACATCTATCTGCTGTGGGGATCTGACGACTGGTCTTATGATC 775  
QY 1016 TGGGCATCAAAATATTCGTTTACATCAAAACCACTGTGAGAAAGCTTTTGGCGTGTCTC 1075  
Db 776 AGGGAATCAAAATATTCCTTTACCTTTGA-ACCTCGGGATACAGGCTTCTTTGGCTTTCTC 834

RESULT 8  
PCT-US96-00995-5  
; Sequence 5, Application PC/TUS9600995  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
; TITLE OF INVENTION: CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00995  
; FILING DATE: 25-JAN-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 927 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..927  
PCT-US96-00995-5

Query Match 11.5%; Score 124; DB 5; Length 927;  
Best Local Similarity 57.9%; Pred. No. 2.1e-29;  
Matches 278; Conservative 0; Mismatches 195; Indels 7; Gaps 3;  
QY 596 GAATGTGGAGAAAGACCGTTCTTTCTATCGGACAAATCATTCGCATCGGAACAGACCTGA 655  
DB 362 GAATGTGGAGAAAGACCGTTCTTTCTATCGGACAAATCATTCGCATCGGAACAGACCTGA 421  
QY 656 ATAGCAACTTTGCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGG 715  
DB 422 ACAGGAATTTTATGCG---TGGCTGGTGTGAAAGTGGAGGCTTCGAGAGTCCCTGCTG 478  
QY 716 AAACCTACTGTGGAGCTTTATCTTCAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTTTCT 775  
DB 479 AAACCTACTGTGGAGCTTTATCTTCAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTTTCT 538  
QY 776 TGAGAGAAATATCAACAGATTAAGCATATACATCAGCATGCAATTCATATCTCCAGCAT 835  
DB 539 TCGGCAACACCTCTCCACCATCAAGGCTTACCTGACCATCCACTCATATCTACAGATGA 598  
QY 836 TAGTGTTCATATTTCTATATACAGAGTAAAGCAAGACCATGAGGAACTGCTCTAG 895  
DB 599 TGCTCTACCTTTACTCTATGACTACAACTGGCTGGAACATGAGGAATGGAATGCC 658  
QY 896 TAGCCAGTGAAGCAGTTTCGTGCTATTGACAAAACTAGTAAAAATACAGGTATACATG 955  
DB 659 TGGTGAAGGTGGCGCAAGAGGCTTGCC---ACTCTGATGCGCAACCAAGTACACATATG 715

QY 956 GCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTTGGATCTATGATT 1015  
DB 716 GCCCAGGAGCTACCAACATCTATCTGCTGCTGGGATCTGACGACTGGTCTTATGATC 775  
QY 1016 TGGGCATCAATATTCGTTTACATCAACACCACTGTAGAGAACCTTTTGGCGGTGCTC 1075  
DB 776 AGGAATCAATATTCCTTTTACCTTTGA-ACTCCGGGATACAGGCTTCTTTGGGCTTTCTC 834

RESULT 9  
US-08-696-139-3  
; Sequence 3, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hersenberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 921 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..921  
US-08-696-139-3

Query Match 11.4%; Score 123.4; DB 1; Length 921;  
Best Local Similarity 56.3%; Pred. No. 3.3e-29;  
Matches 273; Conservative 0; Mismatches 206; Indels 6; Gaps 2;  
QY 555 GATCTCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATCGAATGTGAGAAAGACCG 614  
DB 321 GCTCAATATTGATGCTACATCTACACCTGGACCAAGAACCCGAATGTGAGAAAGACCG 380  
QY 615 TTCTTTCTATGGAACAATCATTCGATCGGAACAGACCTGATGCAACTTTGTCTCCAA 674  
DB 381 CTCTACCAATGCTGGAACTACCTGCAATGCGACACCCCAACAGAAATTTTGTGCTGG 440

```

QY 675. AACTGCTGTGAGGAGTGCATCCAGTTCTCTCATGCTCGGAAACCTACTGTGGACTTTA 734
Db 441 G---TGGTGCAAACTGGAGGCTCTACAGACCCCTGCGATGAGACTTACTGTGGATCTGC 497
QY 735 TCCTCAGTCAGAACCAAGAGTGAAGGCTAGTGTCTTCTTGAGAGAAATATCAACCA 794
Db 498 TGCAGAGTCTGAAAAGAGACCAAGGCTGTGATTTATACCAACACCTCTCTCTC 557
QY 795 GATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTGTTTCCATATTCCTA 854
Db 558 CATCAAGCATACCTGACGATCCACTCATCTACAGATGATCTCTACCTCTTATTCCTA 617
QY 855 TACAGAAATTAAGCAAGACCATGAGCACTGTCTCTAGTAGCCAGTGAAGCATGTCG 914
Db 618 TGATTACAAACTCCCGAGAACATGCTGAGTTGAATAACCTGGCTAAGGCTGCGGTGAA 677
QY 915 TGCTATTGACAAACTAGTAAATAATACCAAGGTATACATGCGCATGCTCAGAAACCTT 974
Db 678 AGAAGTTG---CTACACTGTATGGCACCACAGTACACATACGCCCCAGGAGTACACAAAT 734
QY 975 ATACCTAGCTCTCTGAGGTGGGAGCATTTGGATCTATGATTTGGGCATCAAAATATTCGTT 1034
Db 735 CTATCTCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAAATATTCCTT 794
QY 1035 TACAT 1039
Db 795 CACCT 799

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RESULT 10

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US-08-696-139-1
; Sequence 1, Application US/08696139
; Patent No. 5672496
; GENERAL INFORMATION:
; APPLICANT: Fayerman, Jeffrey T.
; APPLICANT: Greenen, David P.
; APPLICANT: Hersberger, Charles L.
; APPLICANT: Larson, Jeffrey L.
; APPLICANT: Sterner, Jane L.
; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,139
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,258
; FILING DATE: 16-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1215 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1215
US-08-696-139-1

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Query Match 11.4%; Score 123.4; DB 1; Length 1215;
Best Local Similarity 55.3%; Pred. No. 3.9e-29;
Matches 273; Conservative 0; Mismatches 206; Indels 6; Gaps 2;

QY 555 GATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATAATCGATGTGGAGAAAGACCG 614
Db 615 GCTCAATATTGATGGCTTACATCTACACCTGGCAAGAACCGAATGTGGAGAAAGACCG 674
QY 615 TTCTTTCTATGCGAAACAAATCATTCATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 674
Db 675 CTCTACCAATGCTGGAATCTACCTGCAATGGCACAGACCCCAACAGAAATTTGATGCTGG 734
QY 675 ACATGTGTGAGGAAGGTGCACTCCAGTTCTCTATGCTCGGAAACCTACTGTGAGACTTTA 734
Db 735 G---TGGTGCAAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTTACTGTGATCTGC 791
QY 735 TCCTGAGTCAGAACCAAGTGAAGGCGAGTGGCTAGTTCTTTGAGAGAAATATCAACCA 794
Db 792 TGCAGAGTCTGAAAAGAGAGACCAAGGCCCTGGCTGATTTATACGCAACACCTCTCTC 851
QY 795 GATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATATTCCTA 854
Db 852 CATCAAGCATACCTGACGATCCACTCATCTACAGATGATCTCTACCTTATTCCTA 911
QY 855 TACACGAAGTAAAGCAAGACCAATGAGGAACCTCTCTAGTAGCCAGTGAAGCATGTCG 914
Db 912 TGATTACAAACTCCCGAGAACATGCTGAGTTGAATAAACCCTGAAGGCTGCGGTGAA 971
QY 915 TGCTATTGACAAACTAGTAAATAATACCAAGTATACATGCGCCATGCTCAGAAACCTT 974
Db 972 AGAAGTTG---CTACACTGTATGGCACCACAGTACACATACGCCCCAGGAGTACACAAAT 1028
QY 975 ATACCTAGCTCTCTGAGGTGGGAGCATTTGGATCTATGATTTGGGCATCAAAATATTCGTT 1034
Db 1029 CTATCTCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAAATATTCCTT 1088
QY 1035 TACAT 1039
Db 1089 CACCT 1093

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RESULT 11

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US-09-011-769A-38
; Sequence 38, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-011-769A-38  
Query Match 10.1%; Score 109; DB 4; Length 1263;  
Best Local Similarity 54.4%; Pred. No. 1.6e-24;  
Matches 264; Conservative 0; Mismatches 215; Indels 6; Gaps 2;  
QY 555 GATCTCTCTGCTTTCTGCTGTGGTTCTAGGCCATAATCGAATGGAGAAAGAACCG 614  
DB 645 GCTCAATATTGATGGCTATCATCTACCTGGACCAAGCCGATTTTGGAGAAAGACTCG 704  
QY 615 TTCTTTCTATGCGAACAAATCATTCGATCGGAACAGACCTGAATAGCAACTTTGTCTCAA 674  
DB 705 CTCACCCCTACTGGATCTAGCTGCATTTGCGACAGACCCCAACAGAAATTTTGATGC--- 761  
QY 675 ACATCGGTGAGGAAGGTGCATCCAGTTCTCTCATCTCGGAACCTACTGTGGACTTTA 734  
DB 762 TGGTTGGTGTGAAATTTGGAGCCTCTCGAAACCCCTGTGATGAAACTTTACTGTGGACCTGC 821  
QY 735 TCTGTAGTCGAGACCAAGAGTGAAGCAGTCAGTGGCTAGTTCTTGAGAGAAATATCAACCA 794  
DB 822 CGCAGAGTCGAAAGAAAGAAACCAAGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTC 881  
QY 795 GATTAAAGCATATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCCTATTTCTTA 854  
DB 882 CATCAAGGCATATCTGCAATCCACTCGTACTCCCAATGATGATCTACCCCTTACTCATA 941  
QY 855 TACAGGAAGTAAAGCAAGAACCATAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTTCG 914  
DB 942 TGCTTACAACTCGGTGAGAACCAATGCTGAGTTGAAATGCCCTGGCTAAAGACTACTGTGAA 1001  
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DB 1002 AGAACTTGCC---TACTGCACGCGCAAGTATACATATGGCCGCGGAGCTACACAAAT 1058  
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QY 1035 TACAT 1039  
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RESULT 12  
US-09-023-655-1020  
; Sequence 1020, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1020:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1622 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g179933  
; US-09-023-655-1020  
Query Match 10.0%; Score 107.6; DB 4; Length 1622;  
Best Local Similarity 55.6%; Pred. No. 5.4e-24;  
Matches 250; Conservative 0; Mismatches 194; Indels 6; Gaps 2;  
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DB 686 AGAACCGCATGTGGAGAAAAAATCGTTCCAAGAACCAAACTCCAATATGATCGGCACATG 745  
QY 650 ACTGTAATAGCAACTTGTCTCCAAACACTGCTGTGGAGAGGTGCATCCAGTTCTCTCAT 709  
DB 746 ACCTCAACAGGAATTTAATGTTCA---TGGAACTCCATTCTTAACACCAATGACCCAT 802  
QY 710 GCTCGAAACCTACTGTGGACTTTTATCTCTGAGTCAGAACCAAGAGTGAAGCGAGTGGCTA 769  
DB 803 GTGCAGATTAACCTATCGGGCTCTGCACAGAGTCCGAGAAAGAGACGAAAGCTGTCACTA 862  
QY 770 GTTCTTGTGAGAAATAATCAACAGATTAAGAGATATACATCAGCATGCAATTCATATCCC 829  
DB 863 ATTTCAATTAGAAGCCACCTGAAATCAAGGTTTACATCACCTTCCATTCTCTACTCCC 922  
QY 830 AGCATATAGTGTTCATATTCCTATACACAGTAAGTAAAGCAAGCAACCACTAGGAACTGT 889  
DB 923 AGATGCTATTGTTTCCCTATGATATACATCAAACTGCCCACTTAACCATGAGACTTGG 982  
QY 890 CTCCTAGTAGCAGTGAAGCAGTTTCGTGCTATTTCACAAAACTAGTAAAAATACCAGGTATA 949  
DB 983 CCAAGTTGCAA---AGATTGGCACTGATGTTCTATCACTCGATATGAACCGCTACA 1039  
QY 950 CACATGGCCATGGCTCAGAAACCTTATACCTAGTCTCTCGAGGTGGGAGCGATTGATCT 1009









Thu Oct 28 07:16:08 2004

us-09-980-881a-1\_copy\_18\_1097.rnpb

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 09:01:10 ; Search time 569 Seconds

(without alignments)  
9732.531 Million cell updates/sec

Title: US-09-980-881a-1\_COPY\_18\_1097

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1025.2	94.9	1625	9	US-09-813-133A-1
2	1025.2	94.9	1625	14	Sequence 1, Appli
3	909	84.2	1728	9	Sequence 2396, Ap
4	880.8	81.6	1344	16	US-10-115-479-69
5	880.8	81.6	1743	16	US-10-115-479-67
6	854.6	79.1	1272	15	US-10-379-836-1
7	636	58.9	1037	16	US-10-115-479-63
8	593.4	54.9	1132	16	US-10-115-479-65
9	441	40.8	1400	9	US-09-925-302-24
10	441	40.8	1400	10	US-09-925-302-24
11	331.2	30.7	416	9	US-09-960-352-14595
12	282.4	26.1	397	9	US-09-960-352-8425
					Sequence 1, Appli
					Sequence 2396, Ap
					Sequence 69, Appl
					Sequence 67, Appl
					Sequence 1, Appli
					Sequence 63, Appl
					Sequence 65, Appl
					Sequence 24, Appl
					Sequence 24, Appl
					Sequence 14595, A
					Sequence 8425, Ap

13	204	18.9	55827	9	US-09-813-133A-3
14	204	18.9	55827	14	US-10-212-877-3
15	131	12.1	1547	13	US-10-027-632-265133
16	131	12.1	1547	13	US-10-027-632-265134
17	131	12.1	1547	13	US-10-027-632-265135
18	131	12.1	1547	13	US-10-027-632-265136
19	131	12.1	1547	13	US-10-027-632-265133
20	131	12.1	1547	15	US-10-027-632-265134
21	131	12.1	1547	15	US-10-027-632-265135
22	131	12.1	1547	15	US-10-027-632-265136
23	129.6	12.0	431	9	US-09-917-800A-468
24	107.6	10.0	1254	14	US-10-229-546-3
25	107.6	10.0	1622	14	US-10-229-546-1
26	107.6	10.0	1622	15	US-10-429-802-21
27	107.6	10.0	1622	16	US-10-430-503-12
28	107.6	10.0	1622	16	US-10-262-511-71
29	107.6	10.0	1622	16	US-10-641-643-1020
30	107.6	10.0	1633	15	US-10-341-434-187
31	107.6	10.0	1740	14	US-10-116-802-95
32	104.8	9.7	473	16	US-10-242-535A-42160
33	104.8	9.7	473	16	US-10-085-783A-42160
34	101	9.4	1870	9	US-09-910-059-112
35	101	9.4	1870	17	US-10-688-710-3
36	101	9.4	2154	9	US-09-910-059-124
37	94.6	8.8	1332	9	US-09-954-456-1141
38	92.8	8.6	1302	17	US-10-477-515-1
39	92.8	8.6	1311	13	US-10-200-344-9
40	92.8	8.6	1907	18	US-10-757-262-127
41	92.8	8.6	1993	15	US-10-274-639-33
42	92.8	8.6	1993	16	US-10-333-574-33
43	92.8	8.6	2128	13	US-10-200-344-13
44	91.6	8.5	936	15	US-10-106-698-1866
45	88.6	8.2	517	14	US-10-198-846-12472

## ALIGNMENTS

## RESULT 1

US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication NO. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Query Match 94.9%; Score 1025.2; DB 9; Length 1625;  
Best Local Similarity 99.2%; Pred. No. 1.8e-297;  
Matches 1030; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	1	ATGAAGCTTTGCAGCCTTCAGTCCTTGACCATGTTCTCTTCTGTGAGCAGCATGTC	60
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QY	61	TTGCGCTTCCAGAGTGGCCAAAGTTCTAGTGTCTTTCTAGAACCTTCTAGGCAAGTTCAA	120
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QY	121	GTTCACAGAACTTCTACTACACATATGAGATGTTCTCTGGCAGCGGTAACAGCTGAC	180
Db	137	GTTCACAGAACTTCTACTACACATATGAGATGTTCTCTGGCAGCGGTAACAGCTGAC	196

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QY 181 CTTATTGTGAAGAAAAAACAAGTCATCTTTTGTGAAATGTCATGTCGACAAATGTG 240
Db 197 CTTATTGTGAAGAAAAAACAAGTCATCTTTTGTGAAATGTCATGTCGACAAATGTG 256
QY 241 AAAGCCCAATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGCGGACAGAGTGAAGAT 300
Db 257 AAAGCCCAATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGCGGACAGAGTGAAGAT 316
QY 301 CTTATTCAACAGCAGATTTCAACACACACAGTCAGCCCGGAGCCTCCGCAATCGTACTAT 360
Db 317 CTTATTCAACAGCAGATTTCAACACACACAGTCAGCCCGGAGCCTCCGCAATCGTACTAT 376
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATTAACATGAGAGGAT 420
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QY 421 CCTGATATGCTTACAAAAATCCAGATTTGGATCTCTATTGAGAGTACCCACTCTATGTT 480
Db 437 CCTGATATGCTTACAAAAATCCAGATTTGGATCTCTATTGAGAGTACCCACTCTATGTT 496
QY 481 TTAAGGTTTCTGGAAGAAAGCAACACAGCAGCAATGCAATGATGATGATGATGATGATG 540
Db 497 TTAAGGTTTCTGGAAGAAAGCAACACAGCAGCAATGCAATGATGATGATGATGATGATG 556
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTATAGGCCATAATCGAATG 600
Db 557 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTATAGGCCATAATCGAATG 616
QY 601 TGGAGAAAGAACCGTTCTTCTATCGGAACCAATCAATTCGATCGGACAGACTGATAGC 660
Db 617 TGGAGAAAGAACCGTTCTTCTATCGGAACCAATCAATTCGATCGGACAGACTGATAGC 676
QY 661 AACTTTGTCTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACC 720
Db 677 AACTTTGTCTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACC 736
QY 721 TACTGTGAGATTTATCTGAGTCAAGACAGAACGAGGAGTGGCTAGTTTCTTTGAGA 780
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QY 781 AGAATATCAACAGATTTAAAGCATAATCAGCATGCAATTCATCTCCAGCATATAGTG 840
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Db 1037 ATCAATATTTCTGTTTACA 1054

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RESULT 2

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US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877

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; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

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Query Match 94.9%; Score 1025.2; DB 14; Length 1625;
Best Local Similarity 99.2%; Pred. No. 1.8e-29;
Matches 1030; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 61 TTCCGCTTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTTAGGCAAGTTCAA 120
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QY 121 GTTCTACAGATCTTACTACACATATGAGATTTGTTCTCTGGCAGCCGTTAAACAGCTGAC 180
Db 137 GTTCTACAGATCTTACTACACATATGAGATTTGTTCTCTGGCAGCCGTTAAACAGCTGAC 196
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTAAATGATCTGATGTCGACAAATGTG 240
Db 197 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTAAATGATCTGATGTCGACAAATGTG 256
QY 241 AAAGCCCAATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGCGACAGCTGGAAGAT 300
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QY 301 CTTATTCAACAGCAGATTTCCACAGCAGACAGTCCGAGCCCGAGCCTCCGCAATCGTACTAT 360
Db 317 CTTATTCAACAGCAGATTTCCACAGCAGACAGTCCGAGCCCGAGCCTCCGCAATCGTACTAT 376
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QY 481 TTAAGGTTTCTGGAAGAAAGCAACACAGCAGCAATGCAATTCATCTCCAGCATATAGTG 540
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QY 601 TGGAGAAAGAACCGTTCTTCTATGCGAAACATCATTTGTCATCGGAAACAGACTGATAGC 660
Db 617 TGGAGAAAGAACCGTTCTTCTATGCGAAACATCATTTGTCATCGGAAACAGACTGATAGC 676
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Db 677 AACTTTGTCTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACC 736
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Db 737 TACTGTGAGATTTATCTGAGTCAAGACAGAACGAGGAGTGGCTAGTTTCTTTGAGA 796
QY 781 AGAATATCAACAGATTTAAAGCATAATCAGCATGCAATTCATCTCCAGCATATAGTG 840
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Db 857 TTTCATATTCCTATACAGAAAGTAAAGCAAGAACCATGAGGAAGTGTCTCTAGTAGCC 916  
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 Db 977 GCGTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTGGATCTTATGATTGGGC 1036  
 QY 1021 ATCAAAATATTCGTTTACA 1038  
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RESULT 3

US-09-880-107-2396  
 ; Sequence 2396, Application US/09880107  
 ; Patent No. US20020142981A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horne, Darci T.  
 ; APPLICANT: Vockley, Joseph G.  
 ; APPLICANT: Scherf, Uwe  
 ; APPLICANT: Gene Logic, Inc.  
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
 ; FILE REFERENCE: 44921-5028-WO  
 ; CURRENT APPLICATION NUMBER: US/09/880,107  
 ; PRIOR FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/211,379  
 ; PRIOR FILING DATE: 2000-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/237,054  
 ; PRIOR FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 3950  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2396  
 ; LENGTH: 1728  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
 US-09-880-107-2396

Query Match 84.2%; Score 909; DB 9; Length 1728;  
 Best Local Similarity 89.9%; Pred. No. 1.8e-262;  
 Matches 1033; Conservative 0; Mismatches 5; Indels 111; Gaps 1;

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 Db 200 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTCGACAATGTG 259  
 QY 241 AAAGCCCATTTAAATGTAGCGGAAATTCATGAGTGTCTGTGCGAGACGTGGGAAGAT 300  
 Db 260 AAAGCCCATTTAAATGTAGCGGAAATTCATGAGTGTCTGTGCGAGACGTGGGAAGAT 319  
 QY 301 CTTATTCAACAGCAGATTTCCACAGCACAGTCAGCCCGAGCCTCCGATCGTACTAT 360  
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QY 421 CCTGATATGCTTACAAAAATCCATTTGGATCTCTCAATTTGAGAAAGTACCCACTCTATGTT 480  
 Db 440 CCTGATATGCTTACAAAAATCCATTTGGATCTCTCAATTTGAGAAAGTACCCACTCTATGTT 499  
 QY 481 TTAAGGTTTCTGAAAAAGAAACAAACAGCCAAAAATGCGCATATGATGATGCTGGAATC 540  
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 QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTTGCTGTTGCTCATAGGCCAT----- 591  
 Db 560 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTTGCTGTTGCTCATAGGCCATATAAATCAA 619  
 QY 592 ----- 591  
 Db 620 TTCTATGGGTAATAGGGCAATATACCAATCTCTCTGAGGCTTGTGGAATTTCTATGTTATG 679  
 QY 592 -----ATCGAATGTGGAGAAAG 609  
 Db 680 CCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAGAAAGATCGAATGTGGAGAAAG 739  
 QY 610 AACCGTTCTTTCTATGCGAAACAAATTCGATCGGAACAGACCTCGAATAGCAACTTTGTC 669  
 Db 740 AACCGTTCTTTCTATGCGAAACAAATTCGATCGGAACAGACCTCGAATAGCAACTTTGTC 799  
 QY 670 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTTACTGTGGA 729  
 Db 800 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTTACTGTGGA 859  
 QY 730 CTTTATCTCTGAGTCAGAACCCAGAGTGAAGGAGTGGTGTGTTCTTGAGAAAGAAATATC 789  
 Db 860 CTTTATCTCTGAGTCAGAACCCAGAGTGAAGGAGTGGTGTGTTCTTGAGAAAGAAATATC 919  
 QY 790 AACGAGATTAAAGCATATCATGAGCATGCTATCATCTCCAGCATATAGTGTTCATAT 849  
 Db 920 AACGAGATTAAAGCATATCATGAGCATGCTATCATCTCCAGCATATAGTGTTCATAT 979  
 QY 850 TCCTATACAGAAAGTAAAGCAAGCAATCAGGAACTGTCTCTAGTAGCCAGTGAAGCA 909  
 Db 980 TCCTATACAGAAAGTAAAGCAAGCAATCAGGAACTGTCTCTAGTAGCCAGTGAAGCA 1039  
 QY 910 GTTCTGCTATTGACAAAACCTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGAA 969  
 Db 1040 GTTCTGCTATTGAGAAAACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGAA 1099  
 QY 970 ACCTTATACCTAGTCTCTGAGGTGGGACGATGATGATCTATGATTTGGGCAATCAATAT 1029  
 Db 1100 ACCTTATACCTAGTCTCTGAGGTGGGACGATGATGATCTATGATTTGGGCAATCAATAT 1159  
 QY 1030 TCGTTTACA 1038  
 Db 1160 TCGTTTACA 1168

RESULT 4

US-10-115-479-69  
 ; Sequence 69, Application US/10115479  
 ; Publication No. US20040006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine



APPLICANT: Zhong, Haibong  
APPLICANT: Smithson, Glenda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIORITY APPLICATION NUMBER: 60/281,136  
PRIORITY FILING DATE: 2001-04-03  
PRIORITY APPLICATION NUMBER: 60/281,863  
PRIORITY FILING DATE: 2001-04-05  
PRIORITY APPLICATION NUMBER: 60/281,906  
PRIORITY FILING DATE: 2001-04-05  
PRIORITY APPLICATION NUMBER: 60/282,934  
PRIORITY FILING DATE: 2001-04-10  
PRIORITY APPLICATION NUMBER: 60/283,657  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/283,678  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/283,687  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/283,710  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/284,234  
PRIORITY FILING DATE: 2001-04-17  
PRIORITY APPLICATION NUMBER: 60/285,325  
PRIORITY FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 67  
LENGTH: 1743  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (20)..(1304)

US-10-115-479-67  
Query Match 81.68; Score 880.8; DB 16; Length 1743;  
Best Local Similarity 88.66; Pred. No. 5.6e-254;  
Matches 1031; Conservative 0; Mismatches 7; Indels 126; Gaps 2;

QY 1 ATGAAGCTTTGCGAGCTTGCAGTCTTGTACCCATTTCTCTTCTGTGAGCAGCATGTC 60  
DB 20 ATGAAGCTTTGCGAGCTTGCAGTCTTGTACCCATTTCTCTTCTGTGAGCAGCATGTC 79  
QY 61 TTCGCGTTCCAGAGTGCGCAAGTTCTAGCTGCTTCTCTAGAACCTCTAGGCAAGTTCAA 120  
DB 80 TTCGCGTTTCAGAGTGCGCAAGTTCTAGCTGCTTCTCTAGAACCTCTAGGCAAGTTCAA 139  
QY 121 GTTCTACAGATCTTACTACACATATCAGATTGCTCTCTGGCAGCGGTAAACAGCTGAC 180  
DB 140 GTTCTACAGATCTTACTACACATATCAGATTGCTCTCTGGCAGCGGTAAACAGCTGAC 199  
QY 181 CTTATTGTGAAGAAAAACAGTCCATTTTTTGTAAATGATCTGTATGCGACAATGTG 240  
DB 200 CTTATTGTGAAGAAAAACAGTCCATTTTTTGTAAATGATCTGTATGCGACAATGTG 259

241 AAAGCCCAATTTAAATGTGAGCGGAATTCATGCAAGTGTCTTCTGTGGCAGACGTGGAAGAT 300  
DB 260 AAAGCCCAATTTAAATGTGAGCGGAATTCATGCAAGTGTCTTCTGTGGCAGACGTGGAAGAT 319  
QY 301 CTTATTCAACAGCAGATTTTCAAACGACACAGTCAGCCCCCGAGCCCTCGCATCTGACTAT 360  
DB 320 CTTATTCAACAGCAGATTTTCAAACGACACAGTCAGCCCCCGAGCCCTCGCATCTGACTAT 379  
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAATTTATTAACAGAGGCAT 420  
DB 380 GAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAATTTATTAACAGAGGCAT 439  
QY 421 CTTGATATGCTTTACAAAAATCCACATTTGGATCTCTCATTTTGAGAAATGACCATCTATGTT 480  
DB 440 CTTGATATGCTTTACAAAAATCCACATTTGGATCTCTCATTTGAGAAATGACCATCTATGTT 499  
QY 481 TTAA-----AGSTTTCTGAAAGAACAAACAGCCCAAAATGCCATATGG 525  
DB 500 TTAAAGGGTTTCTTTGAGCAGGTTTCTGAAAGAACAAAGCAGCCAAATGCCATATGG 559  
QY 526 ATTGACTGTGGAATCCATGCCAGAGAAATGGATCTCTCTGCTTTCTGCTTTGTTGTTTCA 585  
DB 560 ATTGACTGTGGAATCCATGCCAGAGAAATGGATCTCTCTGCTTTCTGCTTTGTTGTTTCA 619  
QY 586 GGCCAT----- 591  
DB 620 GGCCATATACTCAATTTCTATGGGATAATAGGGCAATATACCAATCTCTCGAGGCTTGTG 679  
QY 592 -----AAT 594  
DB 680 GATTTCTATGTTATGCCAGTGGTTAATGTGGATGTTATGACTACTCATCGSAAAAAGAA 739  
QY 595 CGAATGTGAGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCAATCGGAACAGACCTG 854  
DB 740 CGAATGTGAGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCAATCGGAACAGACCTG 799  
QY 655 AATAGCAACTTTTGTCTCCAAACACATGTTGTGAGGAGGTGCATCCAGTTTCTCATGCTCG 714  
DB 800 AATAGCAACTTTTGTCTCCAAACACATGTTGTGAGGAGGTGCATCCAGTTTCTCATGCTCG 859  
QY 715 GAAACCTACTGTGGACTTTATCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGTTTC 774  
DB 860 GAAACCTACTGTGGACTTTATCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGTTTC 919  
QY 775 TTGAGAGAAATATCAACAGATTTAAAGCATATCATCAGCATGCAATTCATCTACTCCAGCAT 834  
DB 920 TTGAGAGAAATATCAACAGATTTAAAGCATATCATCAGCATGCAATTCATCTACTCCAGCAT 979  
QY 835 ATAGTGTTCCTATATTCCTATACAGAAAGTAAAGCAAAAGACCATGAGGAATGTCTCTTA 894  
DB 980 ATAGTGTTCCTATATTCCTATACAGAAAGTAAAGCAAAAGACCATGAGGAATGTCTCTTA 1039  
QY 895 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAATAGTAGTAAATAATACCAGGTATACACAT 954  
DB 1040 GTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAAATAGTAAAAAATACCAGGTATACACAT 1099  
QY 955 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCAGTTCGATCTATGAT 1014  
DB 1100 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCAGTTCGATCTATGAT 1159  
QY 1015 TTGGGCATCAATATTTCTGTTTACA 1038  
DB 1160 TTGGGCATCAATATTTCTGTTTACA 1183

RESULT 6

US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON

```

; TITLE OF INVENTION: TAPI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
US-10-379-836-1

Query Match          79.1%; Score 854.6; DB 15; Length 1272;
Best Local Similarity 86.9%; Pred. No. 3.6e-246;
Matches 999; Conservative 0; Mismatches 39; Indels 111; Gaps 1;

QY 1 ATGAAGCTTTGAGCGCTTGCAGTCTTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 60
DB 1 ATGAAGCTTTGAGCTTTCAGCTTTCGAGTCTTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 60
QY 61 TTCGGCTTCCAGAGTGGCCAAAGTTCTAGTGTCTTCTCTAGAACCTCTAGGCAAGTTCAA 120
DB 61 TTCGGCTTCCAGAGTGGCCAAAGTTCTAGTGTCTTCTCTAGAACCTCTAGGCAAGTTCAA 120
QY 121 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGACCGGTAAACAGCTGAC 180
DB 121 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGACCGGTAAACAGCTGAC 180
QY 181 CTTATTGTGAAGAAAAAACAAGTCCCAATTTTTTGTAAATGTCATCTGTGCGACAATGTG 240
DB 181 CTTATTGTGAAGAAAAAACAAGTCCCAATTTTTTGTAAATGTCATCTGTGCGACAATGTG 240
QY 241 AAAGCCCAATTAATGTGAGCGGAATTCATGTCAGTGTCTTGTGCGAGAGCTGGAAGAT 300
DB 241 AAAGCCCAATTAATGTGAGCGGAATTCATGTCAGTGTCTTGTGCGAGAGCTGGAAGAT 300
QY 301 CTTATTCAACAGCAGATTTCCAAACACACAGTCAGCCCCCGAGCTCCGCTCGTACTAT 360
DB 301 CTTATTCAACAGCAGATTTCCAAACACACAGTCAGCCCCCGAGCTCCGCTCGTACTAT 360
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGCAT 420
DB 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGCAT 420
QY 421 CCTGATATGCTTTACAAAATCCACATTTGATGCTCTTGTGAGAGTACCCACTCTATGTT 480
DB 421 CCTGATATGCTTTACAAAATCCACATTTGATGCTCTTGTGAGAGTACCCACTCTATGTT 480
QY 481 TTAAGAGTTTCTGGAAGAGAACAAACAGCAGCAAAATGCCATGATGATGCTGGAATC 540
DB 481 TTAAGAGTTTCTGGAAGAGAACAAACAGCAGCAAAATGCCATGATGATGCTGGAATC 540
QY 541 CATGCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
DB 541 CATGCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
QY 592 ----- 591
DB 601 TACTACGGGATAATAGGGGAATATACCAATCTTCTGAGGCATGTGGATTTCTATGTTATG 660
QY 592 ----- AATCGAATGTGGAAG 609
DB 661 CCAGTGGTTAATGCGATGGTTATGACTACTCATGCGAAAGAAATCGAATGTGGAAG 720
QY 610 AACCGTTCTTCTATCGGAACAAATCAATTCATCGGAACAGACCTGAAATAGCAATTTGTC 669
DB 721 AACCGTTCTTCTATCGGAACAAATCGTTGATCGGAACAGACCTGAAACAGGAACCTTTCG 780

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QY 670 TCCAAACACTGGTGTGAGGAGGTGCATCCAGTTTCTCATGCTCGGAAACCTACTGTGGA 729
DB 781 TCCAAACACTGGTGTGAGGAGGTGCATCCAGTTTCTCATGCTCGGAAACCTACTGTGGA 840
QY 730 CTTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTTCTTCTGAGAGAAATATC 789
DB 841 CTTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTTCTTCTGAGAGAAATATC 900
QY 790 AACAGATTAAAGCATACATCAGCATGATTCATATCTCCAGCATATAGTGTTCATAT 849
DB 901 AACAGATTAAAGCATACATCAGCATGATTCATATCTCCAGCATATCGTGTTCATAT 960
QY 850 TCCTATACAGAGTAAAGCAAGACCAAGCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 909
DB 961 TCCTATATCTGAAGCAAAAGCAAGACCAAGCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 1020
QY 910 GTTCGTGCTATTGACAAAACCTAGTAAATAACACAGGTATACATATGGCCATGGCTCAGAA 969
DB 1021 GTTCGTGCTATTGACAAAACCTAGTAAATAACACAGGTATACATATGGCCATGGCTCAGAA 1080
QY 970 ACCTTATACCTAGTCTCTGAGAGTGGGAGCGAATTTGATGATTTGGGCGATCAATAT 1029
DB 1081 ACCTTATACCTAGTCTCTGAGAGTGGGAGCGAATTTGATGATTTGGGCGATCAATAT 1140
QY 1030 TCGTTTACA 1038
DB 1141 TCGTTTACA 1149

RESULT 7
US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10

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PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining prior application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 63  
LENGTH: 1037  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (41)..(1007)  
US-10-115-479-63

Query Match 58.9%; Score 636; DB 16; Length 1037;  
Best Local Similarity 81.0%; Pred. No. 2.2e-180;  
Matches 841; Conservative 0; Mismatches 5; Indels 192; Gaps 1;

QY 1 ATGAAGCTTTGAGCCTTCGAGTCCTTGACCAATGTTCTCTCTGTGAGCAGCATGTC 60  
DB 41 ATGAAGCTTTGAGCCTTCGAGTCCTTGACCAATGTTCTCTCTGTGAGCAGCATGTC 100  
QY 61 TTGCGGTTCCAGAGTGGCAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 120  
DB 101 TTGCGGTTCCAGAGTGGCAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 160  
QY 121 GTTCTACAGAATCTTACTACAAATGAGATTGTTCTCTGCGAGCGGTAAACAGCTGAC 180  
DB 161 GTTCTACAGAACTTACTACAAATGAGATTGTTCTCTGCGAGCGGTAAACAGCTGAC 220  
QY 181 CTTATTGTGAAGAAAAAAGTCCATTTTTTTTGTAAATGTCATCTGATCGACATGTG 240  
DB 221 CTTATTGTGAAGAAAAAAGTCCATTTTTTTTGTAAATGTCATCTGATCGACATGTG 280  
QY 241 AAGGCCATTTAAATCTGAGCGGAATCCATGCGAGTCTTGTGTCGACAGCTGGGAAGAT 300  
DB 281 AAGGCCATTTAAATCTGAGCGGAATCCATGCGAGTCTTGTGTCGACAGCTGGGAAGAT 340  
QY 301 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGTCCGAGCCCGGAGCCTCCGATCTACTAT 360  
DB 341 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGTCCGAGCCCGGAGCCTCCGATCTACTAT 400  
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAATTTTAACTGAGAGGCAT 420  
DB 401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAATTTTAACTGAGAGGCAT 460  
QY 421 CCTGATATGCTTACAAAATCCACATTTGATCTCTCTTTGAGAGTACCACCTCTATGTT 480  
DB 461 CCTGATATGCTTACAAAATCCACATTTGATCTCTCTTTGAGAGTACCACCTCTATGTT 520  
QY 481 TTAAGGTTCTTGAAAAAGAAACAAACAGCCAAAAATGCCATATGGATTGAGTGGAAATC 540  
DB 521 TTAAGGTTCTTGAAAAAGAAACAAACAGCCAAAAATGCCATATGGATTGAGTGGAAATC 569  
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATGAATG 600  
DB 570 ----- 569  
QY 601 TGGAGAAAGAACCGTTCTTTCTATGCGAACATCATTTGCAATCGGACAGACCTGAATAGC 660  
DB 570 ----- 569  
QY 661 AACTTTGTCTCCAAACACTGGTGTGAGGAAGTGTCATCCAGTTCTCTCATCTCGGAAACC 720

570 ----- 569  
QY 721 TACTGTGAGCTTTATCTCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTTCTTTGAGA 780  
DB 570 -ACTGTGAGCTTTATCTCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTTCTTTGAGA 628  
QY 781 AGAAATATCAACAGATTTAAAGCATATCATCAGCATGCAATTCATCTCCAGCATATAGTG 840  
DB 629 AGAAATATCAACAGATTTAAAGCATATCATCAGCATGCAATTCATCTCCAGCATATAGTG 688  
QY 841 TTTCCATATTTCTTATACAGGAAGTAAAGCAAGCAACCATGAGGAAGTCTCTCTAGTAGCC 900  
DB 689 TTTCCATATTTCTTATACAGGAAGTAAAGCAAGCAACCATGAGGAAGTCTCTCTAGTAGCC 748  
QY 901 AGTGAAGCAGTTCTGCTATTGACAAAATAGTAAAAATACCAAGGTATACACATGSCCAT 960  
DB 749 AGTGAAGCAGTTCTGCTATTGAGAAAATTTAGTAAAAATACCAAGGTATACACATGSCCAT 808  
QY 961 GGCTCAGAAACCTTTATACCTAGTCTCTGGAGTGGGAGCGATTGGATCTATGATTTGGGC 1020  
DB 809 GGCTCAGAAACCTTTATACCTAGTCTCTGGAGTGGGAGCGATTGGATCTATGATTTGGGC 868  
QY 1021 ATCAAAATATTCGTTTACA 1038  
DB 869 ATCAAAATATTCGTTTACA 886

RESULT 8  
US-10-115-479-65  
Sequence 65, Application US/10115479  
Publication No. US20040006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Hailong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Purnak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shimkete, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)...(1103)
US-10-115-479-65

Query Match 54.9%; Score 593.4; DB 16; Length 1132;
Best Local Similarity 84.9%; Pred. No. 1.5e-167;
Matches 743; Conservative 0; Mismatches 6; Indels 126; Gaps 2;

Qy 1 ATGAGCTTTCAGCCTTCAGTCCCTGATCCCATTTCTCTGAGCAGCATGTC 60
Db 41 ATGAGCTTTCAGCCTTCAGTCCCTGATCCCATTTCTCTGAGCAGCATGTC 100
Qy 61 TTCGGTTCAGAGTGGCCAGTCTAGTCTGCTCTCTAGAACCTCTAGCAAGTTCAA 120
Db 101 TTCGGTTCAGAGTGGCCAGTCTAGTCTGCTCTCTAGAACCTCTAGCAAGTTCAA 160
Qy 121 GTTCTACAGAACTTTACTACAAATATAGATTTGTTCTCTGGCAGCCGGTAACAGCTGAC 180
Db 161 GTTCTACAGAACTTTACTACAAATATAGATTTGTTCTCTGGCAGCCGGTAACAGCTGAC 220
Qy 181 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGATCTGATGTCGACAAATGTG 240
Db 221 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGATCTGATGTCGACAAATGTG 280
Qy 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCGAGTCTTCTGCGCAGAGCTGGAAGAT 300
Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGCGAGTCTTCTGCGCAGAGCTGGAAGAT 340
Qy 301 CTTATTCAACAGCAGATTTCCAAACAGACAGTCAAGCCCCGAGCTCCGCAATCGTACTAT 360
Db 341 CTTATTCAACAGCAGATTTCCAAACAGACAGTCAAGCCCCGAGCTCCGCAATCGTACTAT 400
Qy 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATTAACCTGAGAGGAT 420
Db 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATTAACCTGAGAGGAT 460
Qy 421 CCGATATGCTTTACAAAAATCCAAATGGATCTCTCAATTTGAGAGTACCCACTCTATGTT 480
Db 461 CCGATATGCTTTACAAAAATCCAAATGGATCTCTCAATTTGAGAGTACCCACTCTATGTT 520
Qy 481 TTAA-----AGTTTCTGAAAGAAACAAACAGCCAAAAATGCCATATGG 525
Db 521 TTAAAGGGTTTCTTGGAGCAGGTTCTGAAAGAAACAAACAGCCAAAAATGCCATATGG 580
Qy 526 ATTGACTCTGGAATCCATGCCAGAGATGATCTCTCTGCTTTCTGCTTCTGCTGTTTCA 585
Db 581 ATTGACTCTGGAATCCATGCCAGAGATGATGATCTCTCTGCTTTCTGCTTCTGCTGTTTCA 640
Qy 586 GGCAT----- 591
Db 641 GGCATATACTCAATTTCTATGGGATTAATAGGGCAATATACCAATCTCTGAGGCTTGTG 700
Qy 592 -----AAT 594
Db 701 GATTTCTATGTTATGCCGGTGGTTAAATGTGGATGTTATGACTACTCATGGAAGAAAT 760

595 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACATCATTTGATCGGAACAGACGCTG 654
Db 761 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACATCATTTGATCGGAACAGACGCTG 820
Qy 655 AATAGCAACTTTTGTCTCCAAACACTGCTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCG 714
Db 821 AATAGGAACCTTTGCTCTCCAAACACTGCTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCG 880
Qy 715 GAAACCTACTGTGAGACTTTTATCTGAGTCAAGACC 749
Db 881 GAAACCTACTGTGAGACTTTTATCTGAGTCAAGAAC 915

RESULT 9
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL04
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Query Match 40.8%; Score 441; DB 9; Length 1400;
Best Local Similarity 98.9%; Pred. No. 1.3e-121;
Matches 444; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 590 ATATCGAATGTGAGAAAGAACCGTTCTTTCTATGCGAAACATCATTTGATCGGAACAG 649
Db 177 AGAATCGAATGTGAGAAAGAACCGTTCTTTCTATGCGAAACATCATTTGATCGGAACAG 236
Qy 650 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCAT 709
Db 237 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCAT 296
Qy 710 GCTCGAAACCTACTGTGAGACTTTTATCTGAGTCAGAACCCAGAGTGAAGCAGTGGCTA 769
Db 297 GCTCGAAACCTACTGTGAGACTTTTATCTGAGTCAGAACCCAGAGTGAAGCAGTGGCTA 356
Qy 770 GTTCTTTGAGAGAAATATCAACAGATTAAGCATACATCAGCATCATTCATCTACTCCC 829
Db 357 GTTCTTTGAGAGAAATATCAACAGATTAAGCATACATCAGCATCATTCATCTACTCCC 416
Qy 830 AGCATATAGTGTTCCTATATACAGAACTAAAGCAAGCAAGCATGAGGAACCTGT 889
Db 417 AGCATATAGTGTTCCTATATACAGAACTAAAGCAAGCAAGCATGAGGAACCTGT 476
Qy 890 CTCTAGTAGCAGTGAAGCAGTTCGTCGTAATTGACAAAACTAGTAAAAATACCAAGGTATA 949
Db 477 CTCTAGTAGCAGTGAAGCAGTTCGTCGTAATTGACAAAACTAGTAAAAATACCAAGGTATA 536
Qy 950 CACATGCCATGGCTCAGAAACCTTATACCTAGCTCTCGAGGTGGGAGCGATTGGATCT 1009
Db 537 CACATGCCATGGCTCAGAAACCTTATACCTAGCTCTCGAGGTGGGAGCGATTGGATCT 596
Qy 1010 ATGATTTGGGCATCAAAATATTTCGTTTACA 1038



Db 597 ATGATTGGGCATCAATATTGGTTTACA 625

RESULT 10

US-09-925-302-24

; Sequence 24, Application US/09925302

; Publication No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 1400

; TYPE: DNA

; ORGANISM: Homo sapiens

; NAME/KEY: misc feature

; LOCATION: (25)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-302-24

Query Match 40.8%; Score 441; DB 10; Length 1400;

Best Local Similarity 98.9%; Pred. No. 1.3e-121;

Matches 444; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 590 ATAATCGAATGTGGAGAAAGAACCGTTCTTATCGGAACAATCATTTGCATCGGAACAG 649

Db 177 AGAATCGAATGTGGAGAAAGAACCGTTCTTATCGGAACAATCATTTGCATCGGAACAG 236

QY 650 ACCTGAATAGCACTTTGCTCCAAACACCTGGTGTGAGGAAGTGCATCCAGTTCTCAT 709

Db 237 ACCTGAATAGCACTTTGCTTCCAAACACCTGGTGTGAGGAAGTGCATCCAGTTCTCAT 296

QY 710 GCTCGGAACCTACTGTGGACTTTATCCTGAGTCAGAACACAGAGTGAAGCGCAGTGGCTA 769

Db 297 GCTCGGAACCTACTGTGGACTTTATCCTGAGTCAGAACACAGAGTGAAGCGCAGTGGCTA 356

QY 770 GTTCTTTGAGAGAAATATCAACAGATTAAAGCATATCAGCATGTCATCTCC 829

Db 357 GTTCTTTGAGAGAAATATCAACAGATTAAAGCATATCAGCATGTCATCTCC 416

QY 830 AGCATATAGTTTCCATATTCCTATACACGAGTAAAGCAAGCCATGAGGAAGTGT 889

Db 417 AGCATATAGTTTCCATATTCCTATACACGAGTAAAGCAAGCCATGAGGAAGTGT 476

QY 890 CTCTAGTAGCCAGTGAAGCAGTGTCTGCTATTGACAAAACTAGTAAAAATACCAGGTATA 949

Db 477 CTCTAGTAGCCAGTGAAGCAGTGTCTGCTATTGAAAACTAGTAAAAATACCAGGTATA 536

QY 950 CACATGCCATGGCTCAGAAACCTTTACTAGTCTCTGAGGTGGGAGCATTTGATCT 1009

Db 537 CACATGCCATGGCTCAGAAACCTTTACTAGTCTCTGAGGTGGGAGCATTTGATCT 596

QY 1010 ATGATTTGGGCATCAATATTGGTTTACA 1038

Db 597 ATGATTTGGGCATCAATATTGGTTTACA 625

RESULT 11

US-09-960-352-14595

; Sequence 14595, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 14595

; LENGTH: 416

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 62-LIB34-032-Q1-E1-H10

US-09-960-352-14595

Query Match 30.7%; Score 331.2; DB 9; Length 416;

Best Local Similarity 87.3%; Pred. No. 7.9e-89;

Matches 363; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 150 GATTCTTCTCGGCAGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTT 209

Db 1 GATTCTTCTCGGCAGCCGGTAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTT 60

QY 210 TTTTGTAAATGCATCTGATGTCGA CAATGTGAAAGCCCATTTAAATGTGAGCGGAATTC 269

Db 61 TTTTGTAAATGCATCTGATGTAAGCAATGTGAAAGCCCATTTAAATGTGAGCGGAATTC 120

QY 270 ATGCAGTGTCTTGTGGCAGACGTGGAAGATCTTATTCAACAGCAGATTTCCAACGACAC 329

Db 121 ATTCAGGGTCTGTGGTGGAAATGTGGAAGATCTTATTCGGCAGCAGACTTCCANTGACAC 180

QY 330 AGTCAGCCCCGAGCCTCCGCACTGTAATGAACAGTATCACTCACTAAATGAAATCTA 389

Db 181 CATCAGCCCCCGGCATCTCTCTACTATGAACAGTATCACTCACTAAATGAGATCTA 240

QY 390 TTCTTGGATAGAAATTTAATCTGAGAGGCATCTGATATGCTTACAAAAATCCACATGG 449

Db 241 TTCTTGGATAGAAATTTAATCTGAGAGGCATCTGATATGCTTACAAAAATCCACATGG 300

QY 450 ATCTCTATTTGAGAAGTACCCACTCTATGTTTAAAGTTTCTGGAAGAAACAAACAGC 509

Db 301 ATCTCTATGAGAAGTACCCACTCTATGTTTAAAGTTTCTGGAAGAAACAAAGGGC 360

QY 510 CAAAATGCCATATGGAATGACTGTGGAATCCATGCCAGAGATGGATCTCTCTG 565

Db 361 CAAAATGCCATATGGAATGACTGTGGAATCCATGCCAGAGATGGATCTCTCTG 416

RESULT 12

US-09-960-352-8425

; Sequence 8425, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 8425

; LENGTH: 397

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 36-LIB34-005-Q1-E1-A12

US-09-960-352-8425

Query Match 26.1%; Score 282.4; DB 9; Length 397;

Best Local Similarity 83.9%; Pred. No. 3.8e-74;

Matches 319; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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QY 1 ATGAAGCTTTGAGAGCTTGCAGCTTGCAGTCTCTGTATACCATGTTCTTCTGTGAGAGCATGTC 60
Db 18 ATGAAGCTTTATAGCTTGGAGTCTCTTGTGCGACCGTCTGTTCTGTGGGAGCATGCC 77
QY 61 TTCGGTTTCCAGAGTGGCCAAAGTTCTAGCTCTCTTCTAGAACTCTAGCAAGTTCAA 120
Db 78 TTCGGCTTTTCAGAGGGGCGAGTTTATCTGCTCTCTTCTAGAACCTCCAGGCAAGTTCAA 137
QY 121 GTTCTACAGAATCTTACTACAACATATGAGATGTTCTCTGCGAGCCGGTAACAGCTGAC 180
Db 138 ATTCTGCAAGATGTTACTACAACATACAAAGATGTTCTCTGCGAGCCAGTAGCAGTGAA 197
QY 181 CTTATTGTGAAGAAAAACAAGTCAATTTTTTTTGTAAATGATCATGTGTCGACAAATGTG 240
Db 198 TATATTGTGAAGGGATAGCAAGTCCATTTTTTTTGTGAATGCAATCATGTGTAAGCAATGTG 257
QY 241 AAAGCCCAATTTAAATGTGAGCGGAATTCATCCAGTGTCTTCTGCGCAGAGCTGGAAGAT 300
Db 258 AAAGCCCAATTTAAATGTGAGCGAGAAATTCATTCAGGGTCTGCTGGTGAAGAAATGTGGAAGAT 317
QY 301 CTTATTCAACAGCAGATTTCCAACGACACAGTCAAGCCCGAGCCTCCGCGATCTGTAAT 360
Db 318 CTTATCCGGCAGCAGACTTCCAATGACACCATCAGCCCCCGGCGATCTCTCTCTACTAT 377
QY 361 GAACAGTATCACTCACTAAA 380
Db 378 GAACAGTATCACTCACTAAA 397

RESULT 13
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: US 09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Query Match 18.9%; Score 204; DB 9; Length 55827;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 744
Db 48643 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 48702
QY 745 GAACAGAAAGTGAAGCGAGTGGCTAGTTCTTGAAGAAGAAATATCAACAGATTAAAGCA 804
Db 48703 GAACAGAAAGTGAAGCGAGTGGCTAGTTCTTGAAGAAGAAATATCAACAGATTAAAGCA 48762
QY 805 TACATCAGATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATACACGAAAGT 864
Db 48763 TACATCAGATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATACACGAAAGT 48822
QY 865 AAAAGCAAGACCATGAGGAAGT 888
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 14
US-10-212-877-3
; Sequence 3, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: US 10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 09/813,133
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-3

Query Match 18.9%; Score 204; DB 14; Length 55827;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 744
Db 48643 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 48702
QY 745 GAACAGAAAGTGAAGCGAGTGGCTAGTTCTTGAAGAAGAAATATCAACAGATTAAAGCA 804
Db 48703 GAACAGAAAGTGAAGCGAGTGGCTAGTTCTTGAAGAAGAAATATCAACAGATTAAAGCA 48762
QY 805 TACATCAGATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATACACGAAAGT 864
Db 48763 TACATCAGATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATACACGAAAGT 48822
QY 865 AAAAGCAAGACCATGAGGAAGT 888
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846
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; NAME/KEY: misc feature
; LOCATION: (1)_(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265133

Query Match      12.1%; Score 131; DB 13; Length 1547;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 GAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCA 744
Db 1417 GAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCCTGAGTCA 1476
QY 745 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAGATTAAAGCA 804
Db 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAGATTAAAGCA 1536
QY 805 TACATCAGCAT 815
Db 1537 TACATCAGCAT 1547
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Search completed: October 27, 2004, 10:39:53  
Job time : 576 secs





QY 61 LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
DB 61 LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
QY 121 EOYSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
DB 121 EOYSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
QY 181 HAREWISPAFLWFIH 197  
DB 181 HAREWISPAFLWFIH 197

## RESULT 2

US-08-277-540-3  
; Sequence 3, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-277-540-3

Query Match 54.7%; Score 197; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 8.9e-186;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60  
DB 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60  
QY 61 LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
DB 61 LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
DB 121 EOYSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
QY 181 HAREWISPAFLWFIH 197  
DB 181 HAREWISPAFLWFIH 197

## RESULT 3

US-08-430-787A-3  
; Sequence 3, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-430-787A-3

Query Match 54.7%; Score 197; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 8.9e-186;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60  
DB 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60  
QY 61 LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
DB 61 LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
QY 121 EOYSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180

Db 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQKEQTAKNAIWIDCGI 180  
QY 181 HAREWISPAFLWFIQH 197  
Db 181 HAREWISPAFLWFIQH 197

RESULT 4  
US-08-869-057-2  
; Sequence 2, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, MariKO  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94904-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Plasma  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 23..401  
US-08-869-057-2

Query Match 54.7%; Score 197; DB 2; Length 423;  
Best Local Similarity 100.0%; Pred. No. 8.9e-186; Mismatches 0; Indels 0; Gaps 0;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCSLAVLPVILVFCEQHVFAFGQGVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60  
Db 1 MKLCSLAVLPVILVFCEQHVFAFGQGVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60  
QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQKEQTAKNAIWIDCGI 180  
Db 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQKEQTAKNAIWIDCGI 180  
QY 181 HAREWISPAFLWFIQH 197  
Db 181 HAREWISPAFLWFIQH 197

RESULT 5  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813.133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match 46.7%; Score 168; DB 4; Length 386;  
Best Local Similarity 100.0%; Pred. No. 3.2e-157; Mismatches 0; Indels 0; Gaps 0;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MKLCSLAVLPVILVFCEQHVFAFGQGVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60  
QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQKEQ 168  
Db 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQKEQ 168

RESULT 6  
US-09-813-133A-4  
; Sequence 4, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813.133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-4

Query Match 46.7%; Score 168; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 3.5e-157; Mismatches 0; Indels 0; Gaps 0;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MKLCSLAVLPVILVFCEQHVFAFGQGVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60  
QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQKEQ 168  
Db 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQKEQ 168





ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-1

Query Match 8.6%; Score 31; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 4.3e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 FOSGQVLAALPRTSRQVQLNLTYYEIVL 31

RESULT 10  
US-07-649-591B-7  
Sequence 7, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:  
APPLICANT: Dennis Drayna and Daniel Eaton  
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-649-591B-7

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Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 DCGIHAREWISPAFC 191  
Db 172 DCGIHAREWISPAFC 186

RESULT 11  
US-08-277-540-7  
Sequence 7, Application US/08277540  
Patent No. 5474901  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,540  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-277-540-7

Query Match 4.2%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 DCGIHAREWISPAFC 191  
Db 172 DCGIHAREWISPAFC 186

RESULT 12  
US-08-430-787A-7  
Sequence 7, Application US/08430787A  
Patent No. 5593674  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

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; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-430-787A-7

Query Match 4.2%; Score 15; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 DCGIHAREWISAPFC 191
Db 172 DCGIHAREWISAPFC 186

RESULT 13
US-09-675-305-6
; Sequence 6, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-6

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Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 WIDCGIHAREWI 186
Db 190 WIDCGIHAREWI 201

RESULT 15
US-09-675-305-12
; Sequence 12, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 350
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-12

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 WIDCGIHAREWI 186
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Db           |||||||  
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Job time : 21.4492 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:41:12 ; Search time 47.2881 Seconds  
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2464.743 Million cell updates/sec

Title: US-09-980-881A-2  
Perfect score: 360  
Sequence: 1 MKLCSLAVLPVILFCEQHV.....IKYFSTSNPPVEKLPLSLK 360

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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20: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	197	54.7	423	14	US-10-379-836-17
2	168	46.7	322	15	US-10-115-479-64
3	168	46.7	386	9	US-09-813-133A-2
4	168	46.7	386	14	US-10-212-877-2
5	168	46.7	423	9	US-09-813-133A-4
6	168	46.7	423	14	US-10-212-877-4
7	162	45.0	354	15	US-10-115-479-66
8	162	45.0	428	15	US-10-115-479-68
9	162	45.0	428	15	US-10-115-479-70
10	84	23.3	211	9	US-09-925-302-467
11	84	23.3	211	10	US-09-925-302-467
12	62	17.2	423	14	US-10-379-836-2
13	27	7.5	422	14	US-10-379-836-18

14	26	7.2	422	14	US-10-379-836-16	Sequence 16, Appl
15	12	3.3	210	16	US-10-363-829-401	Sequence 401, Appl
16	12	3.3	247	13	US-10-200-344-6	Sequence 6, Appl
17	12	3.3	315	9	US-09-888-615-60	Sequence 60, Appl
18	12	3.3	350	13	US-10-200-344-12	Sequence 12, Appl
19	12	3.3	434	16	US-10-477-515-2	Sequence 2, Appl
20	12	3.3	437	13	US-10-200-344-10	Sequence 10, Appl
21	12	3.3	437	14	US-10-274-639-12	Sequence 12, Appl
22	12	3.3	437	15	US-10-333-574-12	Sequence 12, Appl
23	12	3.3	437	17	US-10-757-262-128	Sequence 128, Appl
24	11	3.1	118	15	US-10-074-978A-274	Sequence 274, Appl
25	11	3.1	231	15	US-10-074-978A-48	Sequence 48, Appl
26	11	3.1	231	15	US-10-074-978A-50	Sequence 50, Appl
27	11	3.1	231	15	US-10-074-978A-52	Sequence 52, Appl
28	11	3.1	349	15	US-10-074-978A-46	Sequence 46, Appl
29	11	3.1	402	14	US-10-379-836-20	Sequence 20, Appl
30	11	3.1	416	15	US-10-074-978A-266	Sequence 266, Appl
31	11	3.1	417	15	US-10-074-978A-267	Sequence 267, Appl
32	11	3.1	417	15	US-10-074-978A-268	Sequence 268, Appl
33	11	3.1	417	16	US-10-477-515-3	Sequence 3, Appl
34	11	3.1	613	9	US-09-910-059-113	Sequence 113, Appl
35	11	3.1	613	16	US-10-608-710-4	Sequence 4, Appl
36	11	3.1	716	9	US-09-910-059-125	Sequence 125, Appl
37	10	2.8	231	15	US-10-074-978A-54	Sequence 54, Appl
38	10	2.8	310	16	US-10-470-390A-20	Sequence 20, Appl
39	10	2.8	374	9	US-09-888-615-61	Sequence 61, Appl
40	10	2.8	416	15	US-10-074-978A-270	Sequence 270, Appl
41	10	2.8	444	14	US-10-176-306-74	Sequence 74, Appl
42	9	2.5	286	16	US-10-408-765A-1959	Sequence 1959, Ap
43	9	2.5	323	14	US-10-369-493-6610	Sequence 6610, Ap
44	9	2.5	323	14	US-10-369-493-6611	Sequence 6611, Ap
45	9	2.5	417	14	US-10-229-546-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-379-836-17  
; Sequence 17, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; TITLE OF INVENTION: TAFI  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 17  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-379-836-17

Query Match	54.7%	Score 197;	DB 14;	Length 423;
Best Local Similarity	100.0%	Pred. No. 2.6e-182;		
Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKLCSLAVLPVILFCEQHVAFQSQGVLAALPRTSRQVQLQNLATTYEVILWQPVAD 60		
Db	1	MKLCSLAVLPVILFCEQHVAFQSQGVLAALPRTSRQVQLQNLATTYEVILWQPVAD 60		
Qy	61	LIVKKQVHFFVNASDVNVKAHLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASY 120		
Db	61	LIVKKQVHFFVNASDVNVKAHLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASY 120		
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Qy	181	HAREWISPAFCLWFIGH	197
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RESULT 2  
 US-10-115-479-64  
 ; Sequence 64, Application US/10115479  
 ; Publication No. US20040006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerkhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Camman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.  
 ; APPLICANT: Furtak, Katarzyna  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Maiyanker, Uriel M.  
 ; APPLICANT: Shimkets, Richard A.  
 ; APPLICANT: Taupier, Raymond J.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Mazur, Ann  
 ; TITLE OF INVENTION: THERAPEUTIC POL  
 ; FILE REFERENCE: 21402-322 B (Cura 6  
 ; CURRENT APPLICATION NUMBER: US/10/1  
 ; CURRENT FILING DATE: 2002-11-18  
 ; CURRENT APPLICATION NUMBER: 60/281,13  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,86  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,90  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/282,93  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/283,65  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,67  
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 ; PRIOR APPLICATION NUMBER: 60/285,32  
 ; PRIOR FILING DATE: 2001-04-19  
 ; Remaining of Prior Application data re  
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 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-115-479-64

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RESULT 3
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Publication No. US2002013719A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match 46.7%; Score 168; DB 9; Length 386;
Best Local Similarity 100.0%; Pred. No. 3.3e-154; Indels 0; Gaps 0;
Matches 168; Conservative 0; Mismatches 0;

Qy 1 MKLCSLAVLPVILFCEQHVFAFQSGOVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60
Db 1 MKLCSLAVLPVILFCEQHVFAFQSGOVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60
Qy 61 LIVKKQVHFFVNASDVNDNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
Db 61 LIVKKQVHFFVNASDVNDNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
Qy 121 EQVHSLNEIYSWTFETERHPDMLTKIHGSSPEKYPYLKVSQKEQ 168
Db 121 EQVHSLNEIYSWTFETERHPDMLTKIHGSSPEKYPYLKVSQKEQ 168

RESULT 4
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-877-2

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```
Query Match          46.7%; Score 168; DB 14; Length 386;
Best Local Similarity 100.0%; Pred. No. 3.3e-154;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60
DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60

QY 61 LIVKKQVHFFVNASDVNDVNKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYVLKVSQKEQ 168
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYVLKVSQKEQ 168

RESULT 5
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Query Match          46.7%; Score 168; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.6e-154;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60
DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60

QY 61 LIVKKQVHFFVNASDVNDVNKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYVLKVSQKEQ 168
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYVLKVSQKEQ 168

RESULT 6
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
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; ORGANISM: Human
US-10-212-877-4

Query Match          46.7%; Score 168; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.6e-154;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60
DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60

QY 61 LIVKKQVHFFVNASDVNDVNKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYVLKVSQKEQ 168
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYVLKVSQKEQ 168

RESULT 7
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
```

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; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-66

Query Match      45.0%; Score 162; DB 15; Length 354;
Best Local Similarity 100.0%; Pred. No. 2e-148;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLCSLAVLPVILFCEQHVFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTD 60
Db 1 MKLCSLAVLPVILFCEQHVFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTD 60

Qy 61 LIVKKQVHFFVNASDVNDNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
Db 61 LIVKKQVHFFVNASDVNDNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKPYLYVLK 162
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKPYLYVLK 162

RESULT 8
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
```

```
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Query Match      45.0%; Score 162; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.4e-148;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLCSLAVLPVILFCEQHVFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTD 60
Db 1 MKLCSLAVLPVILFCEQHVFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTD 60

Qy 61 LIVKKQVHFFVNASDVNDNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
Db 61 LIVKKQVHFFVNASDVNDNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKPYLYVLK 162
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKPYLYVLK 162

RESULT 9
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
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; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-70

```

```

RESULT 10
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

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Qy      284  SYTRSKSDHEELSLVASEAVRAI 307
      |||||
Db      109  SYTRSKSDHEELSLVASEAVRAI 132
      |||||

RESULT 11
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

```

```

RESULT 12
US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-10-379-836-2

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	Qy	Db	Qy	Db
1	1	1	61	61
2	1	1	62	62
3	1	1	63	63
4	1	1	64	64
5	1	1	65	65
6	1	1	66	66
7	1	1	67	67
8	1	1	68	68
9	1	1	69	69
10	1	1	70	70
11	1	1	71	71
12	1	1	72	72
13	1	1	73	73
14	1	1	74	74
15	1	1	75	75
16	1	1	76	76
17	1	1	77	77
18	1	1	78	78
19	1	1	79	79
20	1	1	80	80
21	1	1	81	81
22	1	1	82	82
23	1	1	83	83
24	1	1	84	84
25	1	1	85	85
26	1	1	86	86
27	1	1	87	87
28	1	1	88	88
29	1	1	89	89
30	1	1	90	90
31	1	1	91	91
32	1	1	92	92
33	1	1	93	93
34	1	1	94	94
35	1	1	95	95
36	1	1	96	96
37	1	1	97	97
38	1	1	98	98
39	1	1	99	99
40	1	1	100	100

```

RESULT 13
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-836-18

Query Match      7.5%; Score 27; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 NDTVSPRASVYEQYHSLNIYSWIE 134
Db 107 NDTVSPRASVYEQYHSLNIYSWIE 133

RESULT 14
US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-379-836-16

Query Match      7.2%; Score 26; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 KNAIWIDCGIHAREWISPAFLWIFG 196
Db 170 KNAIWIDCGIHAREWISPAFLWIFG 195

RESULT 15
US-10-363-829-401
; Sequence 401, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;

```

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; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Iman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 401
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LG:366783.1.orf1:2000SEP08
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 102
; OTHER INFORMATION: unknown or other
US-10-363-829-401

Query Match      3.3%; Score 12; DB 16; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 WIDCGIHAREWI 186
Db 48 WIDCGIHAREWI 59

Search completed: October 27, 2004, 01:56:32
Job time : 48.2881 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 27, 2004, 01:56:38 ; Search time 94.5763 Seconds  
(without alignments)  
2705.583 Million cell updates/sec

Title: US-09-980-881A-2  
Perfect score: 360  
Sequence: 1 MKLCLAVLPVILVFCQHV.....IKYFTSNPPVKKLLPLSLK 360

Scoring table:  
OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues  
Word size: 1

Total number of hits satisfying chosen parameters: 1643622

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool\_p/US0980881/runat\_26102004\_084212\_7599/app\_query.fasta\_1.1429  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=oli.rni -MINMATCH=0.1 -LOOPCL=0  
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-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	197	54.7	1272	US-08-869-057-1	Sequence 1, Appli
2	197	54.7	1749	US-07-649-591B-2	Sequence 2, Appli
3	197	54.7	1749	US-08-277-540-2	Sequence 2, Appli
4	197	54.7	1749	US-08-430-787A-2	Sequence 2, Appli
5	168	46.7	1625	US-09-813-133A-1	Sequence 1, Appli
6	68	18.9	55827	US-09-813-133A-3	Sequence 3, Appli
7	12	3.3	741	US-09-875-305-5	Sequence 5, Appli
8	12	3.3	741	US-10-200-344-5	Sequence 5, Appli
9	12	3.3	1050	US-09-675-305-11	Sequence 11, Appl
10	12	3.3	1050	US-10-200-344-11	Sequence 11, Appl
11	12	3.3	1311	US-09-675-305-9	Sequence 9, Appli
12	12	3.3	1311	US-10-200-344-9	Sequence 9, Appli

13	12	3.3	2128	4	US-09-675-305-13	Sequence 13, Appl
14	12	3.3	2128	4	US-10-200-344-13	Sequence 13, Appl
15	11	3.1	258	4	US-09-270-767-25119	Sequence 25119, A
16	11	3.1	359	4	US-09-513-999C-3571	Sequence 3571, Ap
17	11	3.1	927	2	US-08-782-760-5	Sequence 5, Appli
18	11	3.1	927	5	FCT-US96-00995-5	Sequence 5, Appli
19	11	3.1	999	2	US-08-860-882A-67	Sequence 67, Appl
20	11	3.1	999	4	US-09-011-769A-50	Sequence 50, Appl
21	11	3.1	1053	2	US-08-860-882A-64	Sequence 64, Appl
22	11	3.1	1053	4	US-09-011-769A-46	Sequence 46, Appl
23	11	3.1	1053	4	US-09-463-451-27	Sequence 27, Appl
24	11	3.1	1053	4	US-09-463-451-28	Sequence 28, Appl
25	11	3.1	1059	2	US-08-860-882A-74	Sequence 74, Appl
26	11	3.1	1059	2	US-08-860-882A-77	Sequence 77, Appl
27	11	3.1	1059	4	US-09-011-769A-59	Sequence 59, Appl
28	11	3.1	1059	4	US-09-011-769A-63	Sequence 63, Appl
29	11	3.1	1150	4	US-09-270-767-9829	Sequence 9829, Ap
30	11	3.1	1263	2	US-08-860-882A-56	Sequence 56, Appl
31	11	3.1	1263	4	US-09-011-769A-38	Sequence 38, Appl
32	11	3.1	1284	2	US-08-860-882A-71	Sequence 71, Appl
33	11	3.1	1284	4	US-09-011-769A-55	Sequence 55, Appl
34	11	3.1	1870	3	US-09-171-945-112	Sequence 112, App
35	11	3.1	2154	3	US-09-171-945-124	Sequence 124, App
36	9	2.5	486	4	US-09-248-796A-870	Sequence 870, App
37	9	2.5	1622	4	US-09-023-655-1020	Sequence 1020, Ap
38	8	2.2	873	4	US-09-583-110-2322	Sequence 2322, Ap
39	8	2.2	882	4	US-09-252-991A-11174	Sequence 11174, A
40	8	2.2	918	4	US-09-252-991A-11018	Sequence 11018, A
41	8	2.2	1113	4	US-09-252-991A-11239	Sequence 11239, A
42	8	2.2	1325	3	US-09-412-102-3	Sequence 3, Appli
43	8	2.2	1325	3	US-09-217-787-3	Sequence 3, Appli
44	8	2.2	1347	3	US-09-412-102-1	Sequence 1, Appli
45	8	2.2	1347	3	US-09-217-787-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs

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;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; PUBLICATION INFORMATION:
;; AUTHORS: Eaton, Dan L.
;; AUTHORS: Malloy, Beth E.
;; AUTHORS: Tsai, Siao P
;; AUTHORS: Henzel, William
;; AUTHORS: Drayna, Dennis
;; TITLE: Isolation, Molecular Cloning, and Partial
;; TITLE: Characterization of a No. 5985562el Carboxypeptidase B
;; TITLE: from Human Plasma
;; JOURNAL: J. Biol. Chem.
;; VOLUME: 266
;; ISSUE: 32
;; PAGES: 21833-21838
;; DATE: No. 5985562 15-1991
US-08-869-057-1

Alignment Scores:
Pred. No.: 3.08e-197 Length: 1272
Score: 197.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.72% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-2 (1-360) x US-08-869-057-1 (1-1272)

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Db 1 ATGAGCTTTTCAGACCTTGACCTTGATGCCATTTGTTCTCTTGAGCAGCATGTC 60

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
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Qy 41 ValLeuGlnAenLeuThrThrThrTyrGluLeuValLeuThrGlnProValThrAlaAsp 60
Db 121 GTTCTACAGATCTTACTACAACTATGAGATTGTTCTCTGGCAGCGGTAACAGCTGAC 180

Qy 61 LeuLeuValLysLysGlnValHisPhePheValAenAlaSerAspValAspVal 80
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Qy 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100
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Qy 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheLeuThrGluArgHis 140
Db 361 GAACAGTATCACTCACTAAATGAATATTTCTTGGATAGAAATTTATAACTGAGAGGAT 420

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Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIleTrpIleAspCysGlyIle 180
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Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197
Db 541 CATGCCAGAGAATGGATCTCTCTGCTTTCTGCTTGTGTTGTTTCATAGGCCAT 591

RESULT 2
US-07-649-591B-2
; Sequence 2, Application US/07649591B
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;; Patent No. 5206161
;; GENERAL INFORMATION:
;; APPLICANT: Dennis Drayna and Daniel Eaton
;; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: patin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/649,591B
;; FILING DATE: 19910201
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hasak, Janet E.
;; REGISTRATION NUMBER: 28,616
;; REFERENCE/DOCKET NUMBER: 689
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/266-1896
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1749 bases
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: hybridization probe
;; LOCATION: 133 to 178
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; FEATURE:
;; NAME/KEY: potential clip site
;; LOCATION: 380 to 382
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; NAME/KEY: signal sequence
;; LOCATION: 41 to 106
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
US-07-649-591B-2

Alignment Scores:
Pred. No.: 4.22e-197 Length: 1749
Score: 197.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.72% Indels: 0
DB: 1 Gaps: 0

US-09-980-881A-2 (1-360) x US-07-649-591B-2 (1-1749)

Qy 1 MetLysLeuCySerLeuAlaValLeuValProLeuValLeuPheCysGluGlnHisVal 20
Db 41 ATGAGCTTTTCAGACCTTGACCTTGATGCCATTTGTTCTCTTGAGCAGCATGTC 100

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 101 TTCCGGTTTCAGAGTGCCAGTCTAGCTGCTCTCTAGAACCTCTAGCAAGTTCAA 160
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Db 221 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGCATCTGATCGACAAATGTG 280
QY 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100
Db 281 AAAGCCCATTTAAATGTGAGCGAATTCATGCAGTGTCTTGTGGCAGACGTGGAAGAT 340
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Db 341 CTTATTCAACAGAGATTTTCCACAGACACAGTCAGCCCCGAGGCTCCGCATCTACTAT 400
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Db 461 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTATTGAGAAGTACCCTCTATGTT 520
QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheIleAspCysGlyIle 180
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QY 181 HisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheIleGlyHis 197
Db 581 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGGTTTCATAGGCCAT 631
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## RESULT 3

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US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-277-540-2
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Alignment Scores:
Pred. No.: 4,22e-197 Length: 1749
Score: 197.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.72% Indels: 0
DB: 1 Gaps: 0
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US-09-980-881A-2 (1-360) x US-08-277-540-2 (1-1749)

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Db 41 ATGAAGCTTTTCAGGCTTTCAGCTCTTGTACCCATTGTTCTTCTGTGAGCAGCATGTC 100
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 101 TTTCGGGTTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 160
QY 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Db 161 GTTCTACAGAACTTCTTACTACAACTATGAGATTTCTTCTGGCAGCCGGTAAACAGCTGAC 220
QY 61 LeuileValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
Db 221 CTTATTGTGAGAAAAACAAGTCCATTTTTTTGTAATGCATCTGATCGACAAATGTG 280
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 281 AAAGCCCATTTAAATGTGAGCGAATTCATGCAGTGTCTTCTGGCAGACGTGGAAGAT 340
QY 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 341 CTTATTCAACAGAGATTTTCCAAACAGACACAGTCAGCCCCGAGGCTCCGCATCTACTAT 400
QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTyrPheGluPheIleThrGluArgHis 140
Db 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 461 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCATTTTGAAGAAGTACCCTCTATGTT 520
QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheIleAspCysGlyIle 180
Db 521 TTAAGGTTTCTGGAAAAAGAACACAGCCAAATGCCATATGGATGACTGTGGAAATC 580
QY 181 HisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheIleGlyHis 197
Db 581 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGGTTTCATAGGCCAT 631
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## RESULT 4

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US-08-430-787A-2
; Sequence 2, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-430-787A-2

Alignment Scores:  
Pred. No.: 4,228-197 Length: 1749  
Score: 197.00 Matches: 197  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 54.72% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-2 (1-360) x US-08-430-787A-2 (1-1749)

Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAGCTTTGGAGCTTGCAGCTTCTGTACCATTTGTTCTTCTGTGAGCAGCATGTC 100

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTCGGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 160

Qy 41 ValLeuGlnAsnLeuThrThrThrGluIleValLeuThrGlnProValThrAlaAsp 60  
Db 161 GTTCTACAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220

Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
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Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 461 CCTGATATGCTTACAAAAATCCACATTTGGATCCCTCATTTGAGAAATACCCCACTCTATGTT 520

Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
Db 521 TTAAGGTTTCTGGAAGAACACACAGCCAAAATGCCATATGATGACTGTGGAAATC 580

Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197  
Db 581 CATGCCAGAGAATGATCTCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCAT 631

RESULT 5  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 1,14e-166 Length: 1625  
Score: 168.00 Matches: 304  
Percent Similarity: 98.06% Conservative: 0  
Best Local Similarity: 98.06% Mismatches: 3  
Query Match: 46.67% Indels: 6  
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 17 ATGAGCTTTTCAGCCTTGCAGCTTCTGTACCATTTGTTCTTCTGTGAGCAGCATGTC 76

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 77 TTCGGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 136

Qy 41 ValLeuGlnAsnLeuThrThrThrGluIleValLeuThrGlnProValThrAlaAsp 60  
Db 137 GTTCTACAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 196

Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Db 197 CTTATTGTGAGAAAACAAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACAAATGTG 256

Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCCATTTAAATGTGAGCGGAATTCATGCTGCTGGCAGATGTTGGAAGAT 316

Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTCAACAGCAGATTTCACACACACAGTACGCCCCCGAGCTCCGCACTCGTACTAT 376

Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 377 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCAT 436

Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160

437	Db	CCTGATATGCTTACAAAAATCCACATTGGATCTCTATTGGAGAAGATACCCACTCTATGTT	496
161	Qy	LeuLysValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyIle	180
497	Db	TTTAAAGGTTTCTGGAAGAAGAACAGC-AGCCAAAAATGCCATATGGATTGACTGTGCAAT	555
180	Qy	eHisIalaArgLutTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMe	200
556	Db	CCATGCCAGAGAATGGATCTCTCTGCTTTCTTGTTGTGTTCATAGGCCATTAATCGAAT	615
200	Qy	tTrpArgLysAsnArgSerPheTrpAlaAsnAsnHisCysIleGlyThrAspLeuAsnSe	220
616	Db	GTGGAGAAGAACCGTTCTTTCTATGGAAACAATCAATTGCATCGGAACAGACCTGGAATAG	675
220	Qy	r-AsnPheVal-SerLysHisTrpCysGluGluClyAlaSerSerSerSerCysSerGlu	239
676	Db	-GAACCTTTGC-TTCCAAACACTGGGTGTAGAAAGTGCATCCAGTTCCCTCATGCTCGGAA	733
240	Qy	ThrTyrCysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeu	259
734	Db	ACCTACTGTGGACTTTATCCTCTGAGTCAGAACCAAGAGTGGAAGGCAGTGGCTAGTTCTTG	793
260	Qy	ArgArgAsnIleAsnGlnIleLysAlaTyrlleSerMethHisSerTySerGlnHisIle	279
794	Db	AGAAGAAATATCAACACAGATTAAAGCATACATCAGCATGCATTATCATCTCCAGCATATA	853
280	Qy	ValPheProTySerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuVal	299
854	Db	GTGTTTCCATATCTCTATACAGAAAGTAAAGCAAGACCATGAGGAACTGTCTCTAGTA	913
300	Qy	AlaSerGluAlaValArgAlaIle	307
914	Db	GCAGTGAAGCAGTTCGTGCTATT	937

```

RESULT 6
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Alignment Scores:
Pred. No.: 4,15e-60 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.89% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-813-133A-3 (1-55827)

Qy 229 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 248
|||||
Db 48643 GAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 48702
|||||

Qy 249 GluProGluValIysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleIysAla 268
|||||
Db 48703 GAACCAAGAAGTGAAGCGAGTGGCTAGTTCTTTCGAGAGGAANAATATCAACCAAGATTAAAGCA 48762
|||||

Qy 269 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 288
|||||

```

Db	48763	TACATCAGCATGCATTCATCACTCCAGCATATAGTGTTCATATTCTCTAT
Qy	289	LysSerIysAepHisGluGLuLeu 296
Db	48823	AAAAGCAAGACCATGAGGAAGTG 48846
RESULT 7		
US-09-675-305-5		
; Sequence 5, Application US/09675305		
; Patent No. 6441153		
; GENERAL INFORMATION:		
; APPLICANT: Donoho, Gregory		
; APPLICANT: Turner, C. Alexander Jr.		
; APPLICANT: Nehls, Michael		
; APPLICANT: Friedrich, Glenn		
; APPLICANT: Zambrowicz, Brian		
; APPLICANT: Sands, Arthur T.		
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and		
; TITLE OF INVENTION: Polynucleotides Encoding the Same		
; FILE REFERENCE: LEX-0047-USA		
; CURRENT APPLICATION NUMBER: US/09/675,305		
; CURRENT FILING DATE: 2000-09-29		
; PRIOR APPLICATION NUMBER: US 60/156,685		
; PRIOR FILING DATE: 1999-09-29		
; NUMBER OF SEQ ID NOS: 13		
; SOFTWARE: FastSeq for Windows Version 4.0		
; SEQ ID NO 5		
; LENGTH: 741		
; TYPE: DNA		
; ORGANISM: homo sapiens		
US-09-675-305-5		

```

RESULT 8
US-10-200-344-5
; Sequence 5, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. 6780640el Human Carboxypeptidases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 741
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-5

```

```
Alignment Scores:
Pred. No.: 0.00382 Length: 741
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-10-200-344-5 (1-741)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 9
US-09-675-305-11
; Sequence 11, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: Lex-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-11

Alignment Scores:
Pred. No.: 0.00539 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-11 (1-1050)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 10
US-10-200-344-11
; Sequence 11, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: Lex-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-11

Alignment Scores:
Pred. No.: 0.00539 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-10-200-344-11 (1-1050)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 11
US-09-675-305-9
; Sequence 9, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: Lex-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-9

Alignment Scores:
Pred. No.: 0.00672 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-9 (1-1311)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 12
US-10-200-344-9
; Sequence 9, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
```



; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/10/200,344  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1311  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-200-344-9

Alignment Scores:  
Pred. No.: 1311  
Score: 0.00672  
Length: 1311  
Matches: 12  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 3.33%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-980-881A-2 (1-360) x US-10-200-344-9 (1-1311)

Qy 175 TptileAspCysGlyIleHisAlaArgGluTrpIle 186  
Db 568 TGGATAGACTGTGGTATTTCATCGAAGAATGGATT 603

RESULT 13  
US-09-675-305-13  
; Sequence 13, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6441133el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 2128  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-675-305-13

Alignment Scores:  
Pred. No.: 2128  
Score: 0.0109  
Length: 2128  
Matches: 12  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 3.33%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-13 (1-2128)

Qy 175 TptileAspCysGlyIleHisAlaArgGluTrpIle 186  
Db 933 TGGATAGACTGTGGTATTTCATCGAAGAATGGATT 968

RESULT 14  
US-10-200-344-13  
; Sequence 13, Application US/10200344  
; Patent No. 6780640  
; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/10/200,344  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 2128  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-200-344-13

Alignment Scores:  
Pred. No.: 2128  
Score: 0.0109  
Length: 2128  
Matches: 12  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 3.33%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-980-881A-2 (1-360) x US-10-200-344-13 (1-2128)

Qy 175 TptileAspCysGlyIleHisAlaArgGluTrpIle 186  
Db 933 TGGATAGACTGTGGTATTTCATCGAAGAATGGATT 968

RESULT 15  
US-09-270-767-25119  
; Sequence 25119, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25119  
; LENGTH: 258  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-25119

Alignment Scores:  
Pred. No.: 258  
Score: 0.0151  
Length: 258  
Matches: 11  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 3.06%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-980-881A-2 (1-360) x US-09-270-767-25119 (1-258)

Qy 179 GlyIleHisAlaArgGluTrpIleSerProAla 189  
Db 127 GGCATCCAGCCCGCGAATGGATCAGCCCCGCG 159

Search completed: October 27, 2004, 06:08:53  
Job time : 122.576 secs



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-MAXLEN=2000000000 -USER=US0980881@cgn\_1\_1034 @runat\_26102004\_084213\_7638  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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18: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	168	46.7	1037	16	US-10-115-479-63
3	168	46.7	1625	9	US-09-813-133A-1
4	168	46.7	1625	14	US-10-212-877-1
5	162	45.0	1132	16	US-10-115-479-65
6	162	45.0	1344	16	US-10-115-479-69
7	162	45.0	1743	16	US-10-115-479-67
8	84	23.3	1400	9	US-09-925-302-24
9	84	23.3	1400	10	US-09-925-302-24
10	68	18.9	55827	9	US-09-813-133A-3
11	68	18.9	55827	14	US-10-212-877-3
12	62	17.2	1272	15	US-10-379-836-1
13	43	11.9	1547	13	US-10-027-632-265133
14	43	11.9	1547	13	US-10-027-632-265134
15	43	11.9	1547	13	US-10-027-632-265135
16	43	11.9	1547	13	US-10-027-632-265136
17	43	11.9	1547	15	US-10-027-632-265133
18	43	11.9	1547	15	US-10-027-632-265134
19	43	11.9	1547	15	US-10-027-632-265135
20	43	11.9	1547	15	US-10-027-632-265136
21	19	5.3	60	10	US-09-908-975-8511
22	17	4.7	416	9	US-09-960-352-14595
23	16	4.4	65	10	US-09-908-975-26009
24	14	3.9	431	9	US-09-917-800A-468
25	13	3.6	65	10	US-09-908-975-25938
26	12	3.3	741	13	US-10-200-344-5
27	12	3.3	948	9	US-09-888-615-1
28	12	3.3	1050	13	US-10-200-344-11
29	12	3.3	1187	14	US-10-198-846-13457
30	12	3.3	1295	17	US-10-363-829-148
31	12	3.3	1302	17	US-10-477-515-1
32	12	3.3	1311	13	US-10-200-344-9
33	12	3.3	1907	18	US-10-757-262-127
34	12	3.3	1993	15	US-10-274-639-33
35	12	3.3	1993	16	US-10-333-574-33
36	12	3.3	2128	13	US-10-200-344-13
37	11	3.1	230	14	US-10-060-036-3042
38	11	3.1	230	14	US-10-060-036-3068
39	11	3.1	230	14	US-10-060-036-3096
40	11	3.1	230	14	US-10-060-036-3131
41	11	3.1	230	14	US-10-060-036-3150
42	11	3.1	230	14	US-10-060-036-3153
43	11	3.1	230	14	US-10-060-036-3164
44	11	3.1	230	14	US-10-060-036-3168
45	11	3.1	230	14	US-10-060-036-3175

ALIGNMENTS

RESULT 1  
US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Barci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396
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Alignment Scores:
Pred. No.:      6,21e-195      Length:      1728
Score:          197.00         Matches:      197
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:    0
Query Match:     54.72%        Indels:        0
DB:              9            Gaps:          0
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US-09-980-881A-2 (1-360) x US-09-880-107-2396 (1-1728)

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Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 20 ATGAAGCTTTGAGGCTTGAGCTCTTGACCATTTGTTCTTCTGTGAGCAGCATGTC 79
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 80 TTCGGGTTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 139
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Db 140 GTTCTACAGAATCTTACTACACATATGAGATTGTTCTGCGACCGGTAAACAGCTGAC 199
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
Db 200 CTTATTGTGAGAAAAACAGTCCATTTTGTAAATGATCTGATGTCGACATGTG 259
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuAlaAspValGluAsp 100
Db 260 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGTTCTGCGCAGCGTGAAGAT 319
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 320 CTTATTCAACAGCAGATTTCACACACACAGTCAAGCGCCGAGCTCCGCATCGTACT 379
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 380 GAACAGTATCACTCAATAAGTAATCTATTCTGGATAGAAATTTATTAACAGAGGAT 439
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 440 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCAATTTGAGAGTAGCCACTCTATGTT 499
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 500 TTAAAGGTTTCTGGAAAGAAACAAACAGCCAAAAATGCCAATATGATGACTGTGGAATC 559
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197
Db 560 CATGCCAGAGATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCAT 610
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## RESULT 2

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US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
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```
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
```

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; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera E.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
```

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; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD.
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 69/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
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; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1007)
US-10-115-479-63
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Alignment Scores:
Pred. No.:      6,29e-165      Length:      1037
Score:          168.00         Matches:      168
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:    0
Query Match:     46.67%        Indels:        0
DB:              16            Gaps:          0
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US-09-980-881A-2 (1-360) x US-10-115-479-63 (1-1037)

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Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 41 ATGAAGCTTTGAGGCTTGAGCTCTTGACCATTTGTTCTTCTGTGAGCAGCATGTC 100
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 101 TTCGGGTTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 160
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Db 161 GTTCTACAGAATCTTACTACAAACATATGAGATTGTTCTTCTGCGACCGGTAAACAGCTGAC 220
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
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Db 221 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATCGACATGTG 280  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 281 AAAAGCCCATTTAAATGTGAGCGGAATTCATCGAGTGTCTTGTGCGAGCGTGAAGAT 340  
Qy 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 341 CTTATTCAACAGCAGATTTCCAAACAGACAGTCAGCCCCGAGCCCTCGCATCTGACTAT 400  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 401 GAACAGTATCACTCACTAAATGAATATCTTCTGGATAGAATTTATAAATCAGAGGCAT 460  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 461 CCTGATATGCTTACAAAAATCCACATCGGATCTCTATTGAGAAGTACCCACTCTATGTT 520  
Qy 161 LeuLysValSerGlyLysGluGln 168  
Db 521 TTAAGGTTTCTGGAAAAAGAACAA 544

RESULT 3  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 9.6e-165 Length: 1625  
Score: 168.00 Matches: 304  
Percent Similarity: 98.06% Conservative: 0  
Best Local Similarity: 98.06% Mismatches: 3  
Query Match: 46.67% Indels: 6  
DB: 9 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 17 ATGAGCTTTGAGCCTTGAGTCCCTGTGATCCCATTTCTCTCTGTGAGCAGCATGTC 76  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 77 TTCGCGTTTCAGAGTGCGCAAGTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAC 136  
Qy 41 ValLeuGlnAsnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThr 60  
Db 137 GTTCTACAGAAATCTTACTACAAATATGAGATGTTCTCTGGCAGCGGTAACAGCTGAC 196  
Qy 61 LeuileValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80  
Db 197 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATCGACAATGTG 256  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCCATTTAAATGTGAGCGGAATTCATCGAGTGTCTTGTGCGAGATGTGAAGAT 316

Qy 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTCAACAGCAGATTTCCAAACAGACACAGTCCAGCCCCGAGCCTCGCATCTACTAT 376  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 377 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATAAATCAGAGGCAT 436  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 437 CTTGATATGCTTACAAAAATCCACATTCGATCTCTCATTTGAGAAAGTACCCACTCTATGTT 496  
Qy 161 LeuLysValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
Db 497 TTAAGGTTTCTGGAAAAAGAACAAAGC-AGCCAAAAATGCCATATGGATTGACTGTGGAAT 555  
Qy 180 eHiAlaArgGlnTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMe 200  
Db 556 CCATGCCAGAGAAATGGATCTCTCTGCTCTTCTGTTTGGTTTCATAGGCCATATTCGAAT 615  
Qy 200 tTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSe 220  
Db 616 GTGGAGAAAGAACCGTCTCTTCTATGCGAACATATTCATCGAACACAGACCTGAATAG 675  
Qy 220 r-AsnPheVal-SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGlu 239  
Db 676 -GAACTTTGCG-TTCCAAACACTGGTGTGAGGAAGTGCATCGCATCGAACACAGACCTGAATAG 733  
Qy 240 ThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaLaserPheLeu 259  
Db 734 ACCTACTGTGACTTTATCTCTGAGTCAGAACAGAAAGTGAAGGCGAGTGGTAGTTCTTGTG 793  
Qy 260 ArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIle 279  
Db 794 AGAAGAAATATCAACAGATTAAGCATACATACATGATGATCTATCTCCAGCATATA 853  
Qy 280 ValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuVal 299  
Db 854 GTGTTTCCATATTTCTATACAGAAAGTAAAGCAAGACCATGAGGAACCTGTCTCTAGTA 913  
Qy 300 AlaSerGluAlaValArgAlaIle 307  
Db 914 GCCAGTGAAGCAGTTCGTGCTATT 937

RESULT 4  
US-10-212-877-1  
; Sequence 1, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-877-1  
Alignment Scores:  
Pred. No.: 9.6e-165 Length: 1625  
Score: 168.00 Matches: 304  
Percent Similarity: 98.06% Conservative: 0  
Best Local Similarity: 98.06% Mismatches: 3  
Query Match: 46.67% Indels: 6  
DB: 14 Gaps: 0

US-09-980-881A-2 (1-360) x US-10-212-877-1 (1-1625)

QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 17 ATGAAGCTTTGCAGCCTTGCAGTCCTGTGACCAATGTTCTCTCTGTGAGCAGCATGTC 76  
QY 21 PheAlaPheGlnSerGlyGlnValValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 77 TTTCGGGTTTCAGAGTGGCAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 136  
QY 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60  
Db 137 GTTCTACAGAACTCTTACTACAAATATGAGATTGTTCTCTGCAGCCCGGTACAGCTGAC 196  
QY 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAlaAspVal 80  
Db 197 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAATGTG 256  
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTCTGCGCAGATGTGGAAGAT 316  
QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCCTCCGCATCGTACTAT 376  
QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 377 GAACAGTATCACTCAATAAGAAATCTATTCTTGATAGAAATTTATAACTGAGAGCAT 436  
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 437 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTATTGAGAAGTACCCTCTATGTT 496  
QY 161 LeuLysValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyI 180  
Db 497 TTAAGGTTTCTGGAAAAAGAACAGC-AGCCAAAAATGCCATATGGATTGACTGTGGAAT 555  
QY 180 eHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMe 200  
Db 556 CCATGCCAGAGAATGGATCT 615  
QY 200 tTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSe 220  
Db 616 GTGGAGAAGAACCGTTCTTCTATCGCAACAATCATTCGATCGGAACAGACCTGGAATAG 675  
QY 220 r-AsnPheVal-SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGlu 239  
Db 676 -GAACCTTTGC-TTCCAAACACTGGGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAA 733  
QY 240 ThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeu 259  
Db 734 ACCTACTGTGGACTTTATCTGAGTCAGACAGCCAGAGTGAAGCAGTGGCTAGTTCTTG 793  
QY 260 ArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIle 279  
Db 794 AGAAGAAATATCAACAGATTAAAGCATATACATCAGCATGCATTCATCTCCAGCATATA 853  
QY 280 ValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuVal 299  
Db 854 GTGTTTCATATTTCTTATACAGAGTAAAGACCAAGACCATGAGGAACCTGTCTCTAGTA 913  
QY 300 AlaSerGluAlaValArgAlaIle 307  
Db 914 GCCAGTGAAGCAGTTCGTGCTATT 937

RESULT 5

US-10-115-479-65  
; Sequence 65, Application US/10115479  
; Publication NO. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li

; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol B.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera E.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; FILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; TITLE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 65  
; LENGTH: 1132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (41)..(1103)  
US-10-115-479-65

Alignment Scores:  
Pred. No.: 1,22e-158 Length: 1132  
Score: 162.00 Matches: 162  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 45.00% Indels: 0  
DB: 16 Gaps: 0

US-09-980-881A-2 (1-360) x US-10-115-479-65 (1-1132)

QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
|||||

Db 41 ATGAGCTTTGAGCCTTGAGCTGCTGTGACCAATGTTCTCTCTGTGAGCAGCATGTC 100  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTGCGCTTTTCAGAGTGGCCAAAGTCTAGCTGCTCTTCCCTAGAACCTCTAGGCAAGTTCAA 160  
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAsp 60  
Db 161 GTTCTACAGANCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGAC 220  
Qy 61 LeuLeuValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Db 221 CTTATTGTGAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTCATGTCGACAAATG 280  
Qy 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGGCAGCGTGGAGAT 340  
Qy 101 LeuLeuGlnGlnGlnSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 341 CTTATTCAACAGACAGATTTCACACGACACAGTCAGCCCGAGCTCCGCACTGTAAT 400  
Qy 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheLeuThrGluArgHis 140  
Db 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATACTGAGAGCAT 460  
Qy 141 ProAspMetLeuThrLysLysLeuHisLysGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 461 CCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAGAAGTACCACCTATGTT 520  
Qy 161 LeuLys 162  
Db 521 TTAAG 526

RESULT 6

US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Szytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Raetelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863

; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 69  
; LENGTH: 1344  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (31)..(1315)  
US-10-115-479-69  
Alignment Scores:  
Pred. No.: 1,43e-158 Length: 1344  
Score: 162.00 Matches: 162  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 45.00% Indels: 0  
DB: 16 Gaps: 0  
US-09-980-881A-2 (1-360) x US-10-115-479-69 (1-1344)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 31 ATGAGCTTTGAGCCTTGAGCTGCTTGTGACCAATGTTCTCTCTGTGAGCAGCATGTC 90  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 91 TTGCGCTTTTCAGAGTGGCCAAAGTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 150  
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAsp 60  
Db 151 GTTCTACAGANCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGAC 210  
Qy 61 LeuLeuValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Db 211 CTTATTGTGAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTCATGTCGACAAATG 270  
Qy 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 271 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGGCAGCGTGGAGAT 330  
Qy 101 LeuLeuGlnGlnGlnSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 331 CTTATTCAACAGACAGATTTCACACGACACAGTCAGCCCGAGCTCCGCACTGTAAT 390  
Qy 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheLeuThrGluArgHis 140  
Db 391 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATACTGAGAGCAT 450  
Qy 141 ProAspMetLeuThrLysLysLeuHisLysGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 451 CCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAGAAGTACCACCTCTATGTT 510  
Qy 161 LeuLys 162  
Db 511 TTAAG 516





DB: 9 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

QY 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243

DB 257 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCATGCTCGGAACCTACTGTGGA 316

QY 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263

DB 317 CTTTATCTCTGAGTCAGAACAGAGTGAAGGAGTGGCTAGTTCTTCTGAGAGAAATATC 376

QY 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283

DB 377 AACCCAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 436

QY 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303

DB 437 TCCATATACACGAAGTAAAGCAAGACCATGAGGAAGTGTCTCTAGTAGCCAGTGAAGCA 496

QY 304 ValArgAlaIleAsp-LysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323

DB 497 GTTCGTGCTATTGA-GAAAACACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGA 555

QY 323 uThrLeuTyrLeuAlaProGlyGlyGlyAspTyrPileTyrAspLeuGlyIleLysTyr 343

DB 556 AACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTGGGCATCAATA 615

QY 343 rSerPheThr 346

DB 616 TTCGTTTACA 625

RESULT 9

US-09-925-302-24

; Sequence 24, Application US/09925302

; Publication No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 1400

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (25)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-302-24

Alignment Scores:

Pred. No.: 2,75e-77 Length: 1400

Score: 84.00 Matches: 122

Percent Similarity: 98.39% Conservative: 0

Best Local Similarity: 98.39% Mismatches: 1

Query Match: 23.33% Indels: 2

DB: 10 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

QY 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243

DB 257 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCGGAACCTACTGTGGA 316

QY 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263

DB 317 CTTTATCTCTGAGTCAGAACAGTGAAGGAGTGGCTAGTTCTTCTGAGAGAAATATC 376

QY 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283

DB 377 AACCCAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 436

QY 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303

DB 437 TCCATATACACGAAGTAAAGCAAGACCATGAGGAAGTGTCTCTAGTAGCCAGTGAAGCA 496

QY 304 ValArgAlaIleAsp-LysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323

DB 497 GTTCGTGCTATTGA-GAAAACACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGA 555

QY 323 uThrLeuTyrLeuAlaProGlyGlyGlyAspTyrPileTyrAspLeuGlyIleLysTyr 343

DB 556 AACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTGGGCATCAATA 615

QY 343 rSerPheThr 346

DB 616 TTCGTTTACA 625

RESULT 10

US-09-813-133A-3

; Sequence 3, Application US/09813133A

; Publication No. US20020137179A1

; GENERAL INFORMATION:

; APPLICANT: GAN, weiniu et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001173

; CURRENT APPLICATION NUMBER: US/09/813,133A

; CURRENT FILING DATE: 2001-08-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 55827

; TYPE: DNA

; ORGANISM: Human

US-09-813-133A-3

Alignment Scores:

Pred. No.: 4.15e-59 Length: 55827

Score: 68.00 Matches: 68

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 18.89% Indels: 0

DB: 9 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-813-133A-3 (1-55827)

QY 229 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 248

DB 48643 GAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTACTGTGGACTTTATCTCGAGTCA 48702

QY 249 GluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 268

DB 48703 GAACCCAGAAAGTGAAGGAGTGGCTAGTTCTTCTGAGAGAAATATCAACCCAGATTAAAGCA 48762

QY 269 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 288

DB 48763 TACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATATACACGAAGT 48822

QY 289 LysSerLysAspHisGluLeu 296

DB 48823 AAAAGCAAAGACCATGAGGAAGTCA 48846

RESULT 11

US-10-212-877-3

; Sequence 3, Application US/10212877

; Publication No. US20030017574A1



Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 11.94%  
DB: 13  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-980-881A-2 (1-360) x US-10-027-632-265133 (1-1547)

QY 229 GluGluGlyAlaSerSerSerSerSerSerGluThrTyrCysGlyLeuTyrProGluSer 248  
DB 1417 GAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCTCGAGTCA 1476  
QY 249 GluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 268  
DB 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAGATTAAAGCA 1536

QY 269 TyrIleSer 271  
DB 1537 TACATCAGC 1545

## RESULT 14

US-10-027-632-265134  
; Sequence 265134, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 265134  
; LENGTH: 1547  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1547)  
; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-265134

Alignment Scores:  
Pred. No.: 1.58e-34 Length: 1547  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 11.94%  
DB: 13  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-980-881A-2 (1-360) x US-10-027-632-265134 (1-1547)

QY 229 GluGluGlyAlaSerSerSerSerSerSerGluThrTyrCysGlyLeuTyrProGluSer 248  
DB 1417 GAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCTCGAGTCA 1476  
QY 249 GluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 268  
DB 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAGATTAAAGCA 1536

QY 269 TyrIleSer 271  
DB 1537 TACATCAGC 1545

## RESULT 15

US-10-027-632-265135  
; Sequence 265135, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 265135  
; LENGTH: 1547  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1547)  
; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-265135

Alignment Scores:  
Pred. No.: 1.58e-34 Length: 1547  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 11.94%  
DB: 13  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-980-881A-2 (1-360) x US-10-027-632-265135 (1-1547)

QY 229 GluGluGlyAlaSerSerSerSerSerSerGluThrTyrCysGlyLeuTyrProGluSer 248  
DB 1417 GAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCTCGAGTCA 1476

QY 249 GluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 268  
DB 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAGATTAAAGCA 1536

QY 269 TyrIleSer 271  
DB 1537 TACATCAGC 1545

Search completed: October 27, 2004, 09:20:28  
Job time : 531.085 secs





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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CEA binding
; OTHER INFORMATION: polypeptide
US-09-541-345-44

Query Match          2.2%; Score 42.5; DB 4; Length 16;
Best Local Similarity 43.8%; Pred. No. 5.6e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 174 IWDCGHHAREWISPA 189
DB 1 IW-DCNLFKNQWFCFA 15
||| : : |||

RESULT 3
US-08-467-023-211
; Sequence 211, Application US/08467023
; Patent No. 6090386
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; APPLICANT: Pollock, Joanne;
; APPLICANT: Bond, Julian F.;
; APPLICANT: Garman, Richard D.;
; APPLICANT: Kuo, Mei-Chang;
; APPLICANT: Yeung, Siu-mei H.;
; APPLICANT: Brauer, Andrew;
; APPLICANT: Exley, Mark A.;
; APPLICANT: Powers, Steven P.
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; TITLE OF INVENTION: Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
; STREET: 610 Lincoln St
; CITY: Waltham
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,023
; FILING DATE: June 6, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,225
; FILING DATE: December 6, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: 025.6 US2 (IMI-028CPD2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-467-023-211

Query Match          2.1%; Score 39.5; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 166 KEOTAKNAIWID 177
||| : : |||
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DB 2 KERTATN-IWID 12

RESULT 4
US-08-596-387B-6
; Sequence 6, Application US/08596387B
; Patent No. 5869270
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,387B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09816
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-596-387B-6

Query Match          2.0%; Score 39; DB 2; Length 13;
Best Local Similarity 58.3%; Pred. No. 9.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLIA 96
DB 1 NLCNIPCSALLS 12
||| : : |||

RESULT 5
US-09-067-615-6
; Sequence 6, Application US/09067615
; Patent No. 6309645
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
```

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;
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,387
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; US-09-067-615-6

Query Match 2.0%; Score 39; DB 3; Length 13;
Best Local Similarity 58.3%; Pred. No. 9.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLLA 96
Db 1 NLCNIPCSALLS 12

RESULT 6
PCT-US95-09816A-6
; Sequence 6, Application PC/TUS9509816A
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; APPLICANT: Rhode, Peter R.
; APPLICANT: Widanz, Jon A.
; APPLICANT: Grammer, Susan
; APPLICANT: Edwards, Ana C.
; APPLICANT: Chavallaz, Pierre-Andre
; APPLICANT: Jiao, Jin-An
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09816A
; FILING DATE: 31-JUL-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; PCT-US95-09816A-6

Query Match 2.0%; Score 39; DB 5; Length 13;
Best Local Similarity 58.3%; Pred. No. 9.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLLA 96
Db 1 NLCNIPCSALLS 12

RESULT 7
US-08-428-733A-55
; Sequence 55, Application US/08428733A
; Patent No. 5763284
; GENERAL INFORMATION:
; APPLICANT: Tal, Rony
; APPLICANT: Wong, Hing C.
; APPLICANT: Caspit, Clayton
; APPLICANT: Chavallaz, Pierre-Andre
; APPLICANT: Wittman, Vaughan
; TITLE OF INVENTION: Methods for Peptide Synthesis and
; TITLE OF INVENTION: Purification
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DADE INTERNATIONAL, INC.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: US
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,733A
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,178
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: DA-4623 CIP
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-428-733A-55

Query Match 2.0%; Score 39; DB 1; Length 17;  
Best Local Similarity 58.3%; Pred. No. 1.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 85 NVSGIPCSVLLA 96  
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Db 5 NLCNIPCSALLS 16

RESULT 8  
US-08-634-332A-2  
Sequence 2, Application US/08634332A  
Patent No. 6531578  
GENERAL INFORMATION:  
APPLICANT: ROBERT WEBBER  
TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING MONOCLONAL ANTIBODY REACTIVE TO HUMAN INOS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIELEN, PETERSON & LAMPE  
STREET: 1990 N CALIFORNIA BOULEVARD, SUITE 720  
CITY: WALNUT CREEK  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94596  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,332A  
FILING DATE: 12-Apr-1996  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NONE  
FILING DATE: NONE  
ATTORNEY/AGENT INFORMATION:  
NAME: THEODORE J. BIELEN, JR.  
REGISTRATION NUMBER: 27,420  
REFERENCE/DOCKET NUMBER: 12280  
TELEPHONE: (925) 937-1515  
TELEFAX: (925) 937-1529  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
NAME/KEY: MOUSE INOS (25-42)  
LOCATION:  
IDENTIFICATION METHOD: AMINO ACID ANALYSIS  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 2;  
US-08-634-332A-2

Query Match 2.0%; Score 39; DB 4; Length 18;  
Best Local Similarity 43.8%; Pred. No. 1.6e+03;  
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 85 NVSGIPCSVLLADVED 100  
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Db 3 NVKKTCAVLSPTIQD 18

RESULT 9  
US-09-822-624-20  
Sequence 20, Application US/09822624  
Patent No. 6440714  
GENERAL INFORMATION:  
APPLICANT: Abell, Creed W.  
APPLICANT: Kwan, Sua-Wah  
APPLICANT: Zhou, Binhua  
APPLICANT: Wo, Bo  
TITLE OF INVENTION: Tyr393 and Tyr398 Mutants of Monoamine Oxidase B  
FILE REFERENCE: D6237PCT  
CURRENT APPLICATION NUMBER: US/09/822,624  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 2000-03-30  
PRIOR FILING DATE: US 60/193,178  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 20  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence flanking the covalent FAD  
OTHER INFORMATION: binding residue of human monooxidase B (MAO B)  
US-09-822-624-20

Query Match 2.0%; Score 38.5; DB 4; Length 17;  
Best Local Similarity 53.3%; Pred. No. 1.7e+03;  
Matches 8; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 227 WCEGASSSCSETY 241  
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Db 1 WCEE-QYSGGYTTY 14

RESULT 10  
US-08-685-589A-198  
Sequence 198, Application US/08685589A  
Patent No. 5916872  
GENERAL INFORMATION:  
APPLICANT: Chang, Conway  
APPLICANT: Gu, Leo  
APPLICANT: Chen, Jie  
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD  
NUMBER OF SEQUENCES: 222  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,589A  
FILING DATE: 24-JUL-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-026-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090



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; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 198:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /product= "Cyclic"
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; US-08-685-589A-198
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; Query Match 2.0%; Score 38; DB 2; Length 14;
; Best Local Similarity 60.0%; Pred. No. 1.4e+03;
; Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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; QY 237 CSETYCGLYP 246
; DB 3 CSRRYCVCP 12
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; RESULT 11
; US-09-340-620A-47
; Sequence 47, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
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; US-09-340-620A-47
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; Query Match 2.0%; Score 38; DB 4; Length 16;
; Best Local Similarity 52.6%; Pred. No. 1.7e+03;
; Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;
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; QY 241 YCGLYPESEPKVAVASEL 259
; DB 1 YC--YPERDPE--EVFAFL 15
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; RESULT 12
; US-08-685-589A-140
; Sequence 140, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
;
; Query Match 2.0%; Score 38; DB 2; Length 17;
; Best Local Similarity 41.2%; Pred. No. 1.9e+03;
; Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
;
; QY 178 CGIHAREWISPAFLWLF 194
; DB 1 CLRYCKRRRCVRFCLWF 17
;
; RESULT 13
; US-08-182-967-25
; Sequence 25, Application US/08182967
; Patent No. 6413516
; GENERAL INFORMATION:
; APPLICANT: Chang, Jennie C.C.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,967
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
;
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /product= "Cyclic"
;
; US-08-685-589A-140
;
; Query Match 2.0%; Score 38; DB 2; Length 17;
; Best Local Similarity 41.2%; Pred. No. 1.9e+03;
; Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
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; QY 178 CGIHAREWISPAFLWLF 194
; DB 1 CLRYCKRRRCVRFCLWF 17
;
; RESULT 13
; US-08-182-967-25
; Sequence 25, Application US/08182967
; Patent No. 6413516
; GENERAL INFORMATION:
; APPLICANT: Chang, Jennie C.C.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,967
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/462,471  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,867  
FILING DATE: 14-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/644,611  
FILING DATE: 22-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/530,229  
FILING DATE: 30-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/382,085  
FILING DATE: 18-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/382,086  
FILING DATE: 18-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/326,314  
FILING DATE: 21-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IM 9830  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-03748-10

Query Match 2.0%; Score 38; DB 4; Length 17;  
Best Local Similarity 42.9%; Pred. No. 1.9e+03;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 110 TVSPRASASYEQY 123  
Db 4 SINTRASGRHYEQF 17

RESULT 14  
PCT-US93-03748-10  
Sequence 10, Application PC/TUS9303748  
GENERAL INFORMATION:  
APPLICANT: Howard, Russell J.  
APPLICANT: Leung, Lawrence L.K.  
TITLE OF INVENTION: Modulation of Thrombospondin-CD36 Interactions  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: One Giralda Farms  
CITY: Madison  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07940  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.5  
SOFTWARE: Microsoft Word 4.00B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/03748  
FILING DATE: 19930428  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/876,287  
FILING DATE: 30-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dulak, Norman C.

REGISTRATION NUMBER: 31,608  
REFERENCE/DOCKET NUMBER: DX0270K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-822-7375  
TELEFAX: 201-822-7039  
TELEX: 219165  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-03748-10

Query Match 2.0%; Score 38; DB 5; Length 18;  
Best Local Similarity 43.8%; Pred. No. 2.1e+03;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 34 RTSRQVQVLNLTYY 49  
Db 3 KPSEKIQLNLRNY 18

RESULT 15  
US-08-382-013A-59  
Sequence 59, Application US/08382013A  
Patent No. 5631222  
GENERAL INFORMATION:  
APPLICANT: Shibata, Kenji  
APPLICANT: Suzawa, Toshiyuki  
APPLICANT: Yamasaki, Motoo  
APPLICANT: Tanaka, Takeo  
APPLICANT: Tsukuda, Ei-ji  
APPLICANT: Yamada, Ko-ji  
APPLICANT: Ohno, Tetsuji  
TITLE OF INVENTION: Endothelin-Antagonizing Peptide  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/382,013A  
FILING DATE: 10-FEB-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 155031/93  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lippert, Neil T.  
REGISTRATION NUMBER: 25888  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8200  
TELEFAX: 212-354-8113  
TELEX: 233188  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-382-013A-59

Query Match 2.0%; Score 38; DB 1; Length 19;

Best Local Similarity 62.5%; Pred. No. 2.3e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 330 GGGDDWIY 337  
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Db 4 GWGNDWY 11

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Job time : 20.6864 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model  
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Title: US-09-980-881A-2  
Perfect score: 1911  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues  
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Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	46	2.4	11	15	US-10-410-764-87
4	42.5	2.2	16	10	US-09-825-517A-44
5	41	2.1	13	15	US-10-469-304-55
6	41	2.1	18	16	US-10-742-379-90
7	40	2.1	14	15	US-10-436-715-431
8	39	2.0	13	9	US-09-848-164-6
9	39	2.0	13	9	US-09-957-674-5
10	39	2.0	13	9	US-09-900-379-6
11	38.5	2.0	17	9	US-09-822-624-20
12	38	2.0	13	14	US-10-126-845-91
13	38	2.0	16	9	US-09-728-721-47
14	38	2.0	16	9	US-09-728-721-47

14	38	2.0	16	14	US-10-295-981-47	Sequence 47, Appl
15	38	2.0	18	14	US-10-125-869A-23	Sequence 23, Appl
16	38	2.0	18	15	US-10-462-262-247	Sequence 247, App
17	38	2.0	18	16	US-10-364-645A-54	Sequence 54, Appl
18	38	2.0	19	8	US-08-817-832B-25	Sequence 25, Appl
19	38	2.0	19	15	US-10-440-435-25	Sequence 25, Appl
20	37.5	2.0	14	14	US-10-126-845-7	Sequence 7, Appl
21	37.5	2.0	14	14	US-10-126-845-65	Sequence 65, Appl
22	37.5	2.0	14	14	US-10-116-275-95	Sequence 95, Appl
23	37.5	2.0	14	16	US-10-764-235-7	Sequence 7, Appl
24	37.5	2.0	14	16	US-10-764-235-58	Sequence 58, Appl
25	37.5	2.0	15	14	US-10-034-374-32	Sequence 32, Appl
26	37.5	2.0	17	15	US-10-624-153-66	Sequence 66, Appl
27	37.5	2.0	18	16	US-10-712-447-22	Sequence 22, Appl
28	37	1.9	13	15	US-10-469-304-56	Sequence 56, Appl
29	37	1.9	14	9	US-09-740-211-15	Sequence 15, Appl
30	37	1.9	14	13	US-10-007-968-15	Sequence 15, Appl
31	37	1.9	14	14	US-10-233-400-15	Sequence 15, Appl
32	37	1.9	15	14	US-10-371-540-30	Sequence 30, Appl
33	37	1.9	15	16	US-10-327-598-74	Sequence 74, Appl
34	37	1.9	16	14	US-10-225-567A-1864	Sequence 1864, Ap
35	37	1.9	16	14	US-10-083-768-15	Sequence 15, Appl
36	37	1.9	16	15	US-10-609-217-75	Sequence 75, Appl
37	37	1.9	16	15	US-10-632-588-75	Sequence 75, Appl
38	37	1.9	16	15	US-10-651-723-75	Sequence 75, Appl
39	37	1.9	16	15	US-10-645-761-75	Sequence 75, Appl
40	37	1.9	16	15	US-10-666-696-75	Sequence 75, Appl
41	37	1.9	16	15	US-10-653-048-75	Sequence 75, Appl
42	37	1.9	18	14	US-10-105-232-194	Sequence 194, App
43	37	1.9	18	14	US-10-189-437-181	Sequence 181, App
44	37	1.9	19	9	US-09-864-761-41546	Sequence 41546, A
45	37	1.9	19	10	US-09-931-325A-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-10-343-509-10  
; Sequence 10, Application US/10343509  
; Publication No. US20040101865A1  
; GENERAL INFORMATION:  
; APPLICANT: BASF  
; TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof  
; FILE REFERENCE: 0050/51654  
; CURRENT APPLICATION NUMBER: US/10/343,509  
; CURRENT FILING DATE: 2003-01-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Euglena gracilis  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (11)  
; OTHER INFORMATION: Xaa = (Phe/Tyr)  
US-10-343-509-10

Query Match 2.5%; Score 48; DB 16; Length 11;  
Best Local Similarity 70.0%; Pred. No. 5.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 331 GGGDWIYDLG 340  
Db 1 GGGDWAYDIG 10

RESULT 2  
US-09-799-760-5  
; Sequence 5, Application US/09799760  
; Patent No. US20010021771A1  
; GENERAL INFORMATION:

```
; APPLICANT: Prusiner, Stanley
; APPLICANT: Tremblay, Patrick
; APPLICANT: Moore, Richard
; APPLICANT: Westaway, David
; APPLICANT: Hood, Leroy E.
; APPLICANT: Lee, Inyoul
; TITLE OF INVENTION: PrP-like Gene
; FILE REFERENCE: 6510-130CON
; CURRENT APPLICATION NUMBER: US/09/799,760
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/309,317
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide
US-09-799-760-5

Query Match      2.5%; Score 47; DB 9; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      211 NHCIGTDLNMFVSKHC 228
Db      1 NHCFGAGNRYVYAANYC 18

RESULT 3
US-10-410-764-87
; Sequence 87, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Welch, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; FILE REFERENCE: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520MNM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zinc carboxypeptidase zinc-binding region 2
US-10-410-764-87

Query Match      2.4%; Score 46; DB 15; Length 11;
Best Local Similarity 63.6%; Pred. No. 8.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      273 HSYSQHIVFPY 283
Db      1 HSYSQMLMPY 11

RESULT 4
US-09-825-517A-44
; Sequence 44, Application US/09825517A
; Publication No. US20030203415A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
; FILE REFERENCE: DYX-016.1 (3421, 1005-001)
; CURRENT APPLICATION NUMBER: US/09/825,517A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/541,345
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEA binding polypeptide
US-09-825-517A-44

Query Match      2.2%; Score 42.5; DB 10; Length 16;
Best Local Similarity 43.8%; Pred. No. 3.4e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy      174 IWIDCGIHAREWISPA 189
Db      1 IW-DCNLFKNQWFCFA 15

RESULT 5
US-10-469-304-55
; Sequence 55, Application US/10469304
; Publication No. US200400091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
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US-10-469-304-55

Query Match 2.1%; Score 41; DB 15; Length 13;  
Best Local Similarity 42.1%; Pred. No. 3.5e+03;  
Matches 8; Conservative 2; Mismatches 1; Indels 1;

QY 53 LMQPVTADLVKKQVHFF 71  
||| |  
Db 2 LMQP-----KRECHFF 12

RESULT 6

US-10-742-379-90  
; Sequence 90, Application US/10742379  
; Publication No. US20040181033A1  
; GENERAL INFORMATION:  
; APPLICANT: Han, HQ  
; APPLICANT: Min, Hsueh  
; APPLICANT: Boone, Thomas Charles  
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN  
; FILE REFERENCE: A-828 (US)  
; CURRENT APPLICATION NUMBER: US/10/742,379  
; CURRENT FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: US 60/435,923  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 634  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 90  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Myostatin Binding Peptide  
US-10-742-379-90

Query Match 2.1%; Score 41; DB 15; Length 18;  
Best Local Similarity 83.3%; Pred. No. 5.6e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 226 HWCEEG 231  
||| |  
Db 2 HWCEQG 7

RESULT 7

US-10-436-715-431  
; Sequence 431, Application US/10436715  
; Publication No. US20040018976A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,  
; FILE REFERENCE: D0262 NP  
; CURRENT APPLICATION NUMBER: US/10/436,715  
; CURRENT FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: U.S. 60/380,335  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 431  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-436-715-431

Query Match 2.1%; Score 40; DB 15; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.9e+03;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 44 NLTTTYBIVLWQ 55  
:|:|:|:|:  
Db 3 DLNTGYDVLWK 14

RESULT 8

US-09-848-164-6  
; Sequence 6, Application US/09848164  
; Patent No. US20020034513A1  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; Jiao, Jin-An  
; Burkhardt, Martin  
; Wong, Hing  
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dade International, Inc.  
; STREET: 1717 Deerfield Road  
; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/848,164  
; FILING DATE: 03-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/067,615  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/382,454  
; FILING DATE: 01-FEB-1995  
; APPLICATION NUMBER: US 08/283,302  
; FILING DATE: 29-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pearson, Louise S.  
; REGISTRATION NUMBER: 32,369  
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708) 267-5300  
; TELEFAX: (708) 267-5376  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-848-164-6

Query Match 2.0%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLLA 96  
|:|:|:|:|:  
Db 1 NLCNIPCSALLS 12

RESULT 9

US-09-957-674-5  
; Sequence 5, Application US/09957674  
; Patent No. US20020120948A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Methods for Expressing Gene Products  
; FILE REFERENCE: 18396/2072  
; CURRENT APPLICATION NUMBER: US/09/957,674  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB990736  
; PRIOR FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/01225

; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 5  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Chicken  
US-09-957-674-5

Query Match 2.0%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 85 NVSGIPCSVLLA 96  
| : ||||| :  
Db 1 NLCNIPCSALLS 12

RESULT 10  
US-09-900-379-6  
; Sequence 6, Application US/09900379  
; Publication No. US20020198144A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; Rhode, Peter R.  
; Widanz, Jon A.  
; Grammer, Susan  
; Edwards, Ana C.  
; Chavallaz, Pierre-Andre  
; Jiao, Jin-An  
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
; NUMBER OF SEQUENCES: 123  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dade International, Inc.  
; STREET: 1717 Deerfield Road  
; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/900,379  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/776,084  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/US95/09816  
; FILING DATE: 31-JUL-1995  
; APPLICATION NUMBER: US 08/382,454  
; FILING DATE: 01-FEB-1995  
; APPLICATION NUMBER: US 08/283,302  
; FILING DATE: 29-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pearson, Louise S.  
; REGISTRATION NUMBER: 32,369  
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
; TELEPHONE: (708) 267-5300  
; TELEFAX: (708) 267-5376  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-900-379-6

Query Match 2.0%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 85 NVSGIPCSVLLA 96  
| : ||||| :  
Db 1 NLCNIPCSALLS 12

RESULT 11  
US-09-822-624-20  
; Sequence 20, Application US/09822624  
; Publication No. US2002004233A1  
; GENERAL INFORMATION:  
; APPLICANT: Abell, Creed W.  
; APPLICANT: Kwan, Sua-Wah  
; APPLICANT: Zhou, Binhua  
; APPLICANT: Wo, Bo  
; TITLE OF INVENTION: Tyr393 and Tyr398 Mutants of Monoamine Oxidase B  
; FILE REFERENCE: D6237PCT  
; CURRENT APPLICATION NUMBER: US/09/822,624  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 2000-03-30  
; PRIOR FILING DATE: US 60/193,178  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 20  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence flanking the covalent FAD  
; OTHER INFORMATION: Binding residue of human monooxidase B (MAO B)  
US-09-822-624-20

Query Match 2.0%; Score 38.5; DB 9; Length 17;  
Best Local Similarity 53.3%; Pred. No. 9.1e+03;  
Matches 8; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 227 WCEEGASSSSCSEY 241  
| |||| | : ||  
Db 1 WCEE-QYSGGCYTTY 14

RESULT 12  
US-10-126-845-91  
; Sequence 91, Application US/10126845  
; Publication No. US20030181367A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Lambkin, Imelda J.  
; APPLICANT: Pinilla, Clemencia  
; APPLICANT: Houghten, Richard  
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM  
; FILE REFERENCE: E1067/20058  
; CURRENT APPLICATION NUMBER: US/10/126,845  
; CURRENT FILING DATE: 2002-10-15  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 91  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: D form peptide  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(13)  
; OTHER INFORMATION: D form retroinversion peptide  
US-10-126-845-91

Query Match 2.0%; Score 38; DB 14; Length 13;  
Best Local Similarity 46.2%; Pred. No. 6.9e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;



QY 241 YCGLYPESEPEVKAVASFL 259  
Db 1 YC--YPERDPE--EVFAFL 15

RESULT 15  
US-10-125-869A-23  
; Sequence 23, Application US/10125869A  
; Publication No. US20030199671A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac Jesus  
; APPLICANT: Wu, Qi-Long  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Stochl, Mark  
; APPLICANT: Ranschoff, Thomas C.  
; APPLICANT: Potter, M. Daniel (deceased)  
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION  
; TITLE OF INVENTION: POLYPEPTIDES  
; FILE REFERENCE: 3421.1006-001  
; CURRENT APPLICATION NUMBER: US/10/125,869A  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/284,534  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc region binding polypeptide  
US-10-125-869A-23

Query Match 2.0%; Score 38; DB 14; Length 18;  
Best Local Similarity 35.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 178 CGIHAREWISPAFCLWFIGH 197  
Db 1 CRACSRDW--PGALVWCAGH 18

Search completed: October 27, 2004, 01:43:16  
Job time : 46.3814 secs

QY 4 CSLAVLVPIVLPC 16  
Db 1 CPAALLVPLLVAC 13

RESULT 13  
US-09-728-721-47  
; Sequence 47, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-728-721-47

Query Match 2.0%; Score 38; DB 9; Length 16;  
Best Local Similarity 52.6%; Pred. No. 9.3e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;

QY 241 YCGLYPESEPEVKAVASFL 259  
Db 1 YC--YPERDPE--EVFAFL 15

RESULT 14  
US-10-295-981-47  
; Sequence 47, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/10/295,981  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-981-47

Query Match 2.0%; Score 38; DB 14; Length 16;  
Best Local Similarity 52.6%; Pred. No. 9.3e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;



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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Maximum Match 100%  
Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1849.5	96.8	1625	4	US-09-813-133A-1
2	1832	95.9	1272	2	US-08-869-057-1
3	1832	95.9	1749	1	US-07-649-591B-2
4	1832	95.9	1749	1	US-08-277-540-2
5	1832	95.9	1749	1	US-08-430-787A-2
6	640.5	33.5	1215	1	US-08-696-139-1
7	639	33.4	1263	2	US-08-860-882A-56
8	639	33.4	1263	4	US-09-011-769A-38
9	631.5	33.0	1284	2	US-08-860-882A-71
10	631.5	33.0	1284	4	US-09-011-769A-55
11	623	32.6	2154	3	US-09-171-945-124
12	619.5	32.4	1622	4	US-09-023-655-1020

13	611.5	32.0	1311	4	US-09-675-305-9	Sequence 9, Appli
14	611.5	32.0	1311	4	US-10-200-344-9	Sequence 9, Appli
15	604	31.6	927	2	US-08-782-760-5	Sequence 5, Appli
16	604	31.6	927	5	PCT-US96-00995-5	Sequence 5, Appli
17	576	30.1	921	1	US-08-696-139-3	Sequence 3, Appli
18	564	29.5	2128	4	US-09-675-305-13	Sequence 13, Appli
19	564	29.5	2128	4	US-10-200-344-13	Sequence 13, Appli
20	561	29.4	999	2	US-08-860-882A-67	Sequence 67, Appli
21	561	29.4	999	4	US-09-011-769A-50	Sequence 50, Appli
22	561	29.4	1053	2	US-08-860-882A-64	Sequence 64, Appli
23	561	29.4	1053	4	US-09-011-769A-46	Sequence 46, Appli
24	554	29.0	1053	4	US-09-463-451-27	Sequence 27, Appli
25	554	29.0	1053	4	US-09-463-451-28	Sequence 28, Appli
26	554	29.0	1059	2	US-08-860-882A-74	Sequence 74, Appli
27	554	29.0	1059	4	US-09-011-769A-59	Sequence 59, Appli
28	553	28.9	1059	2	US-08-860-882A-77	Sequence 77, Appli
29	553	28.9	1059	4	US-09-011-769A-63	Sequence 63, Appli
30	546	28.6	1200	4	US-09-710-099-7	Sequence 7, Appli
31	546	28.6	1200	4	US-10-200-910-7	Sequence 7, Appli
32	543	28.4	1870	3	US-09-171-945-112	Sequence 112, App
33	528.5	27.7	1050	4	US-09-675-305-11	Sequence 11, Appli
34	528.5	27.7	1050	4	US-10-200-344-11	Sequence 11, Appli
35	519.5	27.2	1311	4	US-09-710-099-5	Sequence 5, Appli
36	519.5	27.2	1311	4	US-10-200-910-5	Sequence 5, Appli
37	513	26.8	1251	3	US-08-640-906-3	Sequence 3, Appli
38	513	26.8	1251	3	US-09-395-936-3	Sequence 1, Appli
39	487.5	25.5	1257	3	US-08-640-906-1	Sequence 1, Appli
40	487.5	25.5	1257	3	US-09-395-936-1	Sequence 1, Appli
41	460.5	24.1	945	4	US-09-710-099-3	Sequence 3, Appli
42	460.5	24.1	945	4	US-09-710-099-11	Sequence 11, Appli
43	460.5	24.1	945	4	US-10-200-910-3	Sequence 3, Appli
44	460.5	24.1	945	4	US-10-200-910-11	Sequence 11, Appli
45	458.5	24.0	2247	4	US-09-710-099-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinlu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 6.66e-227 Length: 1625  
Score: 1849.50 Matches: 355  
Percent Similarity: 94.18% Conservative: 1  
Best Local Similarity: 93.92% Mismatches: 4  
Query Match: 96.78% Indels: 18  
DB: 4 Gaps: 1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

QY	1	MetLyeLeuCyseSerLeuAlaValLeuValProileValLeuPheCysGluGlnHisVal	20
DB	17	ATGAGCTTTTGAGCTTCCTTGACGCTCTTGACCATTTCTTCTTCTGTGAGCAGCATGTC	76
QY	21	PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln	40

Db 77 TTCGGTTTCAGAGTGGCAAGTTCTAGCTGCTCTTCTCTAGAACCTCTAGCAAGTTCAA 136  
Qy 41 ValLeuGlnAenLeuThrThrTyrGluLeuValLeuThrGlnProValThrAlaAsp 60  
Db 137 GTTCTACAGATCTTACTACAAATATGAGATTTGTTCTGCGACCGGTAAACAGCTGAC 196  
Qy 61 LeuLeuValLysLysGlnValHisPhePheValAenAlaSerAspValAsnVal 80  
Db 197 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTGTAAATGATCTGTGTCGACAAATGTG 256  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCATTTAAATGTAGGGGAATTCATGTCAGTGTCTTGCTGGCAGATGTGAAGAT 316  
Qy 101 LeuLeuGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTCAACAGCAGATTTCCAAACACACAGTCAGCCCCCGAGCTCCGCATCGTACTAT 376  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 377 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCAT 436  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 437 CTTGATATGCTTACAAAATCCACATTCGATCCTCATTTGAGAGTACCCACTCTATGTT 496  
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIleTrpIleAspCysGlyIle 180  
Db 497 TTAAGGTTTCTGGAAGAAACACAGCAGCCAAAAATGCCATATGATGATGCTGGAATC 556  
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
Db 557 CATGCCAGAGATGGATCTCTCGCTTTCTGCTTGTGTTTCATAGGCCCAATAATCGAATG 616  
Qy 201 TrpArgLysAsnArgSerPheTyrAlaAenAsnHisCysIleGlyThrAspLeuAsnSer 220  
Db 617 TGGAGAAAGAACCGTTCTTTCTATGCGAACCAATCATTCGATCGGACAGACTGATAGG 676  
Qy 221 AenPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 240  
Db 677 AACTTTGCTTCAAAACACTGGTGTGAGGAAGTGTCATCCAGTTCTCTCATGCTCGAAACC 736  
Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
Db 737 TACTGTGACTTTATCTGAGTCAAGAACAGAAAGTGAAGGAGTGCTAGTTTCTTGAGA 796  
Qy 261 ArgAenIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280  
Db 797 AGAATATCAACAGATTAAGCATACATCAGCATGCATTCATCTACTCCAGCATATAGTG 856  
Qy 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuLeuSerLeuValAla 300  
Db 857 TTTCCATATCTCATACAGAAATAAAGCAAGAACCAACCATGAGGAACCTGCTCTAGTAGCC 916  
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAenThrArgTyrThrHisGlyHis 320  
Db 917 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACAGGATACACATGCGCCAT 976  
Qy 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspTrpIleTyrAspLeuGly 340  
Db 977 GGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGACGATGGATCTATGATTTGGGC 1036  
Qy 341 IleLysTyrSerPhe----- 345  
Db 1037 ATCAAAATATCGTTTACAATTAACCTTCGAGATACGGGCACATACGGATTCTTGTCGCC 1096  
Qy 346 -----ThrSerAenProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1097 GAGCGTTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGGTGTCTCTATAAA 1148

RESULT 2

US-08-869-057-1

; Sequence 1, Application US/08869057

; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/869,057  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washlien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; PUBLICATION INFORMATION:  
; AUTHORS: Eaton, Dan L.  
; AUTHORS: Malloy, Beth E.  
; AUTHORS: Tsai, Siao P  
; AUTHORS: Henzel, William  
; AUTHORS: Drayna, Dennis  
; TITLE: Isolation, Molecular Cloning, and Partial  
; TITLE: Characterization of a No. 5985562zel Carboxypeptidase B  
; JOURNAL: J. Biol. Chem.  
; VOLUME: 266  
; ISSUE: 32  
; PAGES: 21833-21838  
; DATE: No. 5985562 15-1991  
US-08-869-057-1  
Alignment Scores:  
Pred. No.: 7,69e-225 Length: 1272  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.27% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 2 Gaps: 2  
US-09-980-881A-2 (1-360) x US-08-869-057-1 (1-1272)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 1 ATGAAGCTTTGACGCTTCCTTGTAGTCCCTTGTCTCTGTGAGCAGCATGTC 60  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 61 TTCGCGTTTCAGAGTGGCAAGTTCTAGCTGCTCTTCTAGAACCTCTAGCAAGTTCAA 120  
Qy 41 ValLeuGlnAenLeuThrThrTyrGluLeuValLeuThrGlnProValThrAlaAsp 60

Db 121 GTTCTACAGAACTTTACTACACATATGAGATTGTTCTCTGCGACCGGTAAACAGCTGAC 180  
Qy 61 LeuileValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Db 181 CTTATTGTGAAGAAAAACAAGTCCATTTTGTGTAATGTCATCTGATGTGACAAATGTG 240  
Qy 81 LysAlaHisLeuAsnValSerGlyLysProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 241 AAAGCCCATTTAATGTGAGCGGAATTCATGTCAGTGTCTGCTGGCAGAGCTGGAAGAT 300  
Qy 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 301 CTTATTCAACAGCAGATTTCACACAGACAGTCAGCCCGAGCCCTCGCATCGTACTAT 360  
Qy 121 GluGlnTyrHisSerLeuAsnGluLysTyrSerTyrIleGluPheIleThrGluArgHis 140  
Db 361 GAACAGTATCACTCAATAAGAAATCTATTCTGGATAGAAATTTATACTGAGAGGAT 420  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 421 CCGTATATGCTTACAAAATCCCAATTCGATTCCTCATTTGAGAGTACCCACTCTATGT 480  
Qy 161 LeuLysValSerGlyLysGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIle 180  
Db 481 TTAAGGTTTCTGGAAGAAACAAACAGCCAAAATGCCATATGATGACTGTGGAATC 540  
Qy 181 HisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPheIleGlyHis----- 197  
Db 541 CATGCCAGAAATGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATACTCAA 600  
Qy 197 ----- 197  
Db 601 TTCTATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTGTGATTTCTATGTTATG 660  
Qy 198 -----AsnArgMetTyrArgLys 203  
Db 661 CCGGTGGTTAATGTGACGGTTATGACTACTCATCGAAAAAGAAATCGAATGTGGAGAAAG 720  
Qy 204 AsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnSerAsnVal 223  
Db 721 AACCGTTCTTCTATCGAACAATCATTCGATCGGACAGACCTGAAATAGGAACCTTTGCT 780  
Qy 224 SerLysHisTyrCysGluGluGlyAlaSerSerCysSerGluThrTyrCysGly 243  
Db 781 TCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCGGAACCTACTGTGA 840  
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAnile 263  
Db 841 CTTTATCTGAGTCAGAACCCAGAGTGAAGGCGAGTGGCTAGTTCTTGAGAGAAATATC 900  
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283  
Db 901 AACCAATTAAGCATACATACAGCATGCATTCATCTACTCCAGCATATAGTTTTCATAT 960  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303  
Db 961 TCTATACAGAAAGTAAAGCAAGAACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 1020  
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1021 GTTCGTGCTATTGAGAAACCTAGTAAATAATACAGGTATACATACATGCCATGCTCAGAA 1080  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyLysAspAspTyrIleTyrAspLeuGlyIleLysTyr 343  
Db 1081 ACCTTATACCTAGTCTCTGAGGTGGGACGATTCGATCTATGATTTGGGCATCAATAT 1140  
Qy 344 SerPhe-----Th 346  
Db 1141 TCGTTTCAATTAAGACTTCGAGATACGGGCACATACGATTTCTGTGCGGAGCGTTAC 1200  
Qy 346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1201 ATCAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1243

RESULT 3  
US-07-649-591B-2  
; Sequence 2, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161e1 Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: hybridization probe  
; LOCATION: 133 to 178  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: potential clip site  
; LOCATION: 380 to 382  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: signal sequence  
; LOCATION: 41 to 106  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; US-07-649-591B-2  
Alignment Scores: 1.34e-224 Length: 1749  
Pred. No.: 1832.00 Matches: 357  
Score: 86.27% Conservative: 1  
Percent Similarity: 86.02% Mismatches: 2  
Best Local Similarity: 95.87% Indels: 55  
Query Match: 1 Gaps: 2  
DB:  
US-09-980-881A-2 (1-360) x US-07-649-591B-2 (1-1749)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAAGCTTTGACAGCTTGCAGTCTGTACCACTGTTCTTCTGTGAGCAGCATGTC 100

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40  
Db |||||  
101 TTCGGCTTTCAGAGTGGCAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 160  
Qy 41 ValLeuGlnAenLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60  
Db |||||  
161 GTTCTACAGATCTTACTACACATATGAGATTGTTCTTGGCAGCCGGTAACAGCTGAC 220  
Qy 61 LeuIleValIleValLeuGlnValIlePhePheValAlaAlaSerAspValAspAsnVal 80  
Db |||||  
221 CTTATTGTGAAGAAAAACAAGTCCATTTTTTGTAAATGCATCTGATGTCGACAAATGTG 280  
Qy 81 LysAlaHisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db |||||  
281 AAAGCCCATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTGGTGGCAGAGCTGGAAGAT 340  
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db |||||  
341 CTTATTTCACAGCAGATTTCACAGACACATGACGCCCGGAGCTCCGCATCGTACTAT 400  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db |||||  
401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGCAT 460  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db |||||  
461 CCGTATATGCTTACAAAAATCCATTTGGATTCCTCATTTGAGAAAGTACCCCACTCTATGTT 520  
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIle 180  
Db |||||  
521 TTAAGGTTTCTGANAAGAACAAACACGCCAAAATGCCATATGGATTGACTGTGGATC 580  
Qy 181 HisAlaArgGlnTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197  
Db |||||  
581 CATGCCAGAAATGGATCTCTCTGCTTCTCTGCTTCTGCTTCTGCTTCTAGGCCATATAACTCAA 640  
Qy 197 ----- 197  
Db |||||  
641 TTCTATGGGATAATAGGCAATATACCAATCTCTGAGCTTGTGGATTTCTATGTTATG 700  
Qy 198 -----AsnArgMetTrpArgLys 203  
Db |||||  
701 CCGGTGTTAATGTGGACGGTTATGACTACTCATCGGAAAAGAAATCGAATGTGGAGAAAG 760  
Qy 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAenSerAsnPheVal 223  
Db |||||  
761 AACCGTTCTTCTATGCGAACAAATCATTTGCATCGGAACAGACCTGAATAGGAACCTTGCT 820  
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243  
Db |||||  
821 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 880  
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263  
Db |||||  
881 CTTTATCTAGTCTAGAACACAGAGAGTGAAGCAGTGGCTAGTTCTTGAGAGAAATATC 940  
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283  
Db |||||  
941 AACAGATTAAGCATATACATCAGATGATTCATCTACATCCAGCATATAGTGTTCATAT 1000  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303  
Db |||||  
1001 TCCTATACAGAAATGAAAGCAAGACCATAGGAACCTGCTCTAGTAGCCAGTGAAGCA 1060  
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db |||||  
1061 GTTGGTCTATTGAGAAAATAGTAAANAATACAGGATATACATGSCCATGGCTCAGAA 1120  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyCysAspTrpIleTyrAspLeuGlyIleLysTyr 343  
Db |||||  
1121 ACCTTATACCTAGCTCTCTGGAGGTGGGACGATTTGGATCTATGATTTGGGCATCAAAATAT 1180  
Qy 344 SerPhe-----Th 346

Db 1181 TCGTTTACAATTGAATTCGAGATACGGGCACATACGATTTCTTCTGCCGAGCGTTAC 1240  
Qy 346 rSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
Db |||||  
1241 ATCAAAACCCACTGTAGAGAAGCTTTTGGCGCTGTCTCTATAAA 1283  
RESULT 4  
US-08-277-540-2  
; Sequence 2, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Baton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet B.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1CID1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-277-540-2  
Alignment Scores:  
Pred. No.: 1.34e-224 Length: 1749  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.27% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-2 (1-360) x US-08-277-540-2 (1-1749)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db |||||  
41 ATGAAGCTTTTGCAGCCTTGACGCTTGACGCTTTGTGCCCAATGTTCTTCTGTGAGACGATGTC 100  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40  
Db |||||  
101 TTCGGTTTCAGAGTGGCAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 160

Qy 346 rSerAsnProValGluLysLeuProLeuSerLeuLys 360  
Db 1241 ATCAACCCACCTGTAGAGAGCTTTTGGCCGCTGTCTCTAAAA 1283

RESULT 5  
US-08-430-787A-2  
; Sequence 2, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-430-787A-2

Alignment Scores:  
Pred..No.: 1,34e-224 Length: 1749  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.2% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-2 (1-360) x US-08-430-787A-2 (1-1749)

Qy 1 MetLysLeuCySerSerLeuAlaValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAAGCTTTGAGCCTTGCAGCTTCTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 100

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTGCGGCTTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTCTTAGAACCTCTTAGGCAGATTCAA 160





QY 63 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAsnValLysAla 82  
 Db 148 AACCTCACAGTACAGTTCCTCGTGAAGCAGAGATATTTGGCTGGAGAC 207  
 QY 83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 102  
 Db 208 TTTCTGGAGCAGAACTGAATACATAATAGAGTACTATAAACAACCTGAGATCTGTCTC 267  
 QY 103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 122  
 Db 268 GAGGCTCAGTTTGCACAGAGTC-----CGTACCACTGGACACAGATTATGAGAG 318  
 QY 123 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 142  
 Db 319 TACACAACTGGAAACGATCGAGGCTTGACTAGCAAGTCCACAGTGAATCCAGAC 378  
 QY 143 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 162  
 Db 379 CTCATCTCTGGACAGCCATCGCACTACATTTTGGAAACAATATATATACCTCTCAAG 438  
 QY 163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 182  
 Db 439 GTT---GGCAACCTGGACCAATAAGCCTGCCATTTTCATGGACTGGTTTCCATGCC 495  
 QY 183 ArgGluTrpIleSerProAlaPheCysLeuTyrPheIle----- 195  
 Db 496 AGAGAAATGATTTTCCCATGATTTTCCAGTGTGTTGTGAGAGAGGCTGTTCTCACCTAT 555  
 QY 195 ----- 195  
 Db 556 GGATATGAGAGTACATGACAGAAATTCCTCAACAGCTAGACTTTTATGCTTGCCTGTG 615  
 QY 196 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 205  
 Db 616 CTCATATATTGATGGTACATCTACACCTGGACCAAGACCGAATGTGGAGAAAGACCCGC 675  
 QY 206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225  
 Db 676 TTTACCAATGCTGGAACTACCTGCATTTGGCAGACCCCAACAGAAATTTT---GATGCT 732  
 QY 226 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 245  
 Db 733 GGGTGTGGCACAACCTGGAGCTCTACAGACCCCTCGCATGAGACTTTACTGTGATCTGCT 792  
 QY 246 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 265  
 Db 793 GCAGAGTCTGAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACAACTCTCTCTCC 852  
 QY 266 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 285  
 Db 853 ATCAAGCATCTGACGATCCACTCATCTACATGATGATCTCTACCCCTTATCTTCTAT 912  
 QY 286 ThrArgSerLysSerLysAspHisGluGluLeuSerLysValAlaSerGluAlaValArg 305  
 Db 913 GATTACAACTCCCGAGACAACTGCTGAGTTGAATAACCTGGCTAAGGCTGGCGTGA 972  
 QY 306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325  
 Db 973 GAACTT---GCTACACTGTATGGCACCAGATACATACATACCGCCGAGGAGTCAACAATC 1029  
 QY 326 TyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 345  
 Db 1030 TATCTGCTCTGGGGCTCTGATGACTGGGCTTATGACCAAGAAATCAATATTTCTTTC 1089  
 QY 346 Thr 346  
 Db 1090 ACC 1092

RESULT 7  
 US-08-860-882A-56  
 ; Sequence 56, Application US/08860802A  
 ; Patent No. 5985281  
 ; GENERAL INFORMATION:

; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
 ; EGGELTE, HENDRIKUS JOHANNES  
 ; APPLICANT: TARRAGONA-FIOL, ANTONIO  
 ; APPLICANT: RABIN, BRIAN ROBERT  
 ; APPLICANT: BOYLE, FRANCIS THOMAS  
 ; APPLICANT: HENNAM, JOHN FREDERICK  
 ; APPLICANT: BLAKELY, DAVID CHARLES  
 ; APPLICANT: MARSHAM, PETER ROBERT  
 ; APPLICANT: HEATON, DAVID WILLIAM  
 ; APPLICANT: DAVIES, DAVID HUM  
 ; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
 ; NUMBER OF SEQUENCES: 77  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: PILLSBURY, MADISON & SUTRO  
 ; STREET: 1100 NEW YORK AVENUE, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,882A  
 ; FILING DATE: JUNE 23, 1997  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DONALD J. BIRD  
 ; REGISTRATION NUMBER: 25,323  
 ; REFERENCE/DOCKET NUMBER: 9901/238653  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 861-3027  
 ; TELEFAX: (202) 822-0944  
 ; TELEX: 6174627 CUSH  
 ; INFORMATION FOR SEQ ID NO: 56:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1263 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-860-882A-56

Alignment Scores:  
 Pred. No.: 1,258-71 Length: 1263  
 Score: 639.00 Matches: 135  
 Percent Similarity: 53.83% Conservative: 69  
 Best Local Similarity: 35.62% Mismatches: 131  
 Query Match: 33.44% Indels: 44  
 DB: 7 Gaps: 7

US-09-980-881A-2 (1-360) x US-08-860-882A-56 (1-1263)

QY 6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla---PheGln 24  
 Db 4 CTCCTGTTCTGGTGAATCTGGCCCTGGCATCTGCTCATCTGCTGGTGGTGGACACTTTGAA 63  
 QY 25 SerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeuGlnAsn 44  
 Db 64 GCGCAGAGAGGTCTTCGCTTTAACGTTGAAGATGAAATCATCATTAACATAATCCCGAG 123  
 QY 45 LeuThrThrTyrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIleValLys 64  
 Db 124 TTGGCCAGCAGCCAGCCAGGATGACTTCTGGAGCCAGATCTCTGTACACAAATCAACCT 183  
 QY 65 LysLysGlnValHisPheValAsnAlaSerAspValAsnValLysAlaHisLeu 84  
 Db 184 CACAGTACAGTTGACTTCCTGTTAAAGCAGAGATACCTGCTCCTGGAGAATGTTCTA 243  
 QY 85 AsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuGlnGln 104  
 Db 244 AAGCAGAACTGAACTACATACAAAGGTACTGATAAGCAACCTGAGAAATGTGGTGGGCT 303

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QY 105 GlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124
Db 304 CAGTTTGTATAGCCGGTT-----CGTCAACAGGACACAGCTTATGAGAAGTACAAAC 354
QY 125 SerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHisProAspMetLeu 144
Db 355 AAGTGGGAAACGATAGAGCTTGGACTCAACAGTGGCCATGAGATCCAGCCTCATC 414
QY 145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValSer 164
Db 415 TCTCGCAGTGTATCGGAACACATTTGAGGACGCGCTATTACCTCCTGAAGTT--- 471
QY 165 GlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGlu 184
Db 472 GCGAAAGCTGGCAAAATAAGCCTGCCATTTTCATGGAGCTGTGGTTTCCATGCCAGAGAG 531
QY 185 TrpIleSerProAlaPheCysLeuTyrPheIle----- 195
Db 532 TGGATTCTCTGCATTTCTGCAGTGGTTTGTAGAGAGGCTGTTCGTACCTATGGACGT 591
QY 195 ----- 195
Db 592 GAGATCCAAAGTCACAGAGCTTCTCGAACAGTTAGACTTTTATGTCTGCTGTGCTCAAT 651
QY 196 -----GlyHis-----AsnArgMetTrpArgLysAsnArgSerPhe 207
Db 652 ATTGATGCTCATCATACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGCTCCACC 711
QY 208 TyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLysHisTyr 227
Db 712 CATACTGGATCTAGCTGCTGATTTGGACACACCCCAACAGAAATTTT---GATGCTGGTTGG 768
QY 228 CysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247
Db 769 TGTGAATTTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCCGCGAGAG 828
QY 248 SerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLys 267
Db 829 TCTGAAAGGAGAGCAACAGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTCCATCAAG 888
QY 268 AlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArg 287
Db 889 GCATATCTGCACATCCATCTGCTACTCCCAATGATGATCTACCTTACTCATATGCTTAC 948
QY 288 SerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIle 307
Db 949 AAACCTCGGTGAGAACATCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAAGAACTT 1008
QY 308 AspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeu 327
Db 1009 ---GCCCTCAGTCGACGCGCACCAAGTACATATATGCGCGGAGCTTACAACTATATCCT 1065
QY 328 AlaProGlyGlyLysAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPheThr 346
Db 1066 GCTGCTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTCCACC 1122
```

## RESULT 8

US-09-011-769A-38  
Sequence 38, Application US/09011769A  
Patent No. 6436691

## GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.  
BLAKEY, David C.  
DAVIES, David H.  
HENNAM, John F.  
HENNEQUIN, Laurent F.A.  
MARSHAM, Peter R.  
DOWELL, Robert I.  
TITLE OF INVENTION: Chemical Compounds  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011.769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-011-769A-38

Alignment Scores:  
Pred. No.: 1,25e-71 Length: 1263  
Score: 639.00 Matches: 135  
Percent Similarity: 53.83% Conservative: 69  
Best Local Similarity: 35.62% Mismatches: 131  
Query Match: 33.44% Indels: 44  
DB: 4 Gaps: 7

US-09-980-881A-2 (1-360) x US-09-011-769A-38 (1-1263)

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QY 6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla---PheGln 24
Db 4 CTCTTGTTCTGGTGAAGTGGCCCTGCTCATCTGCTCATCTGCTGAGCATTGAA 63
QY 25 SerGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeuGlnAsn 44
Db 64 GCGGAGAGGTGTTCCGTGTTAAGATGAAATCACAATTAACAATAATCCGCGAG 123
QY 45 LeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIleValLys 64
Db 124 TTGCCACGACGACGCCAGATTGACTTCTGGAAGCCAGATTCTGTGCACACAATCAAACT 183
QY 65 LysLysGlnValHisPheValAsnAlaSerAspValaAspValLysAlaHisLeu 84
Db 184 CACAGTACAGTTGACTTCCGTGTTAAAGCAAGAAATGACTGTCTGCTGGAGATGTTCTA 243
QY 85 AsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIleGlnGln 104
Db 244 AAGCAGATGACTACATACAGTACTGATAAGCAACCTGAGAAATGTTGGTGGAGCT 303
QY 105 GlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124
Db 304 CAGTTTGTATAGCCGGTT-----CGTCAACAGGACACAGCTTATGAGAAGTACAAAC 354
QY 125 SerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAspMetLeu 144
Db 355 AAGTGGGAAACGATAGAGGCTTGGACTCAACAGTCCGCTGAGAAATCCAGCCTCATC 414
QY 145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValSer 164
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Best Local Similarity: 33.81% Mismatches: 135
Query Match: 32.00% Indels: 72
DB: 4 Gaps: 11

US-09-980-881A-2 (1-360) x US-10-200-344-9 (1-1311)

Qy 1 MetLysLeuCys-----SerLeuAlaValLeuValProLleValLeuPheCysGluGln 18
Db 43 CTGGCTTTTCTGGCTCTTTTGAAGATTCGCAACG-----GGCCACAGC 90
Qy 19 HisValPhe-----AlaPheGlnSerGlyGlnValLeuAlaLaLeuProArgThrSer 36
Db 91 CACCTTTATAACAACCGCTGCTGGTGATAAAGTATAAGATTATTTCCTCCAAACAGAA 150
Qy 37 ArgGlnValGlnValLeuGlnAsnLeuThrThrThrTyrGluLleValLeuThrGlnPro 56
Db 151 GAGGAAGCATATGCACCTGAGAAAATATCCTATCAACTTAAAGTGGACCTGTGGCAGCC 210
Qy 57 ValThrAlaAspLeuLleValLys-----LysLysGlnValHisPhePheValAsnAla 74
Db 211 AGCAGTATCTCTATGATCAGAGGGAACAGTTACTGATGTCATATCCCCCAAAATGGT 270
Qy 75 SerAspValAspAsnValLysAlaHisLeuAsnValSerGlyLleProCysSerValLeu 94
Db 271 TCCCGAGCC-----CTGTAGCTTCTTACAGGAGCCACATCCAGTACAGGTCTC 324
Qy 95 LeuAlaAspValGluAspLeuLleGlnGlnLleSerAsnAspThrValSerProArg 114
Db 325 ATAGAAGATCTTCAGAAAACACTGAGAGGAAGGAGCAGCTTGCACACCCAGAGAACCGA 384
Qy 115 AlaSerAlaSer-----TyrTyrGluGlnTyrHisSerLeuAsnGluLleTyrSerTrp 132
Db 385 AGATCCCTCTCTGATATATTAATGAAGTTATCACTCTTGAAGAAATTCAAAATGG 444
Qy 133 IleGluPheLleThrGluArgHisProAspMetLeuThrLysLleHisLleGlySerSer 152
Db 445 ATGCATCATCTGAATAAACTCACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCA 504
Qy 153 PheGluLysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsn 172
Db 505 TATGAGGAAGATCTCTTTTATTAAAGCTG---GGCAGCAGCATCAGCACTCAAAAGA 561
Qy 173 AlaLleTrpLleAspCysGlyLleHisAlaArgGluTrpLleSerProAlaPheCysLeu 192
Db 562 GCTGTTGGATAGACTGTGGTATTCATGCAAGAAATGGATTGCTCTGCCTTTTGTGAG 621
Qy 193 TrpPheLle----- 195
Db 622 TGGTTGTAAGAAAGCTCTTCTAATATTAAGAGTGACCCAGCCCATGAGAAAATGTTG 681
Qy 195 ----- 195
Db 682 AATCATCTATATTTCTATATCATCGCTGTGTTTAAACGTCGATGATACCAATTTAGTTGG 741
Qy 196 GlyHisAsnArgMetTrpAtqLysAsnArgSerPheTyrAlaAsnAsnHisCysLleGly 215
Db 742 ACCATGATCATTTTGGAGAAAACAGAGTCAGGAACCTCAAGTTTCGCTGCCGTGGA 801
Qy 216 ThrAspLeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSer 235
Db 802 GTGGATGCCAATAGAACTGGAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCAC 858
Qy 236 SerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaVal 255
Db 859 CCTTGTGATGACATATCTGGGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGGCTGTA 918
Qy 256 AlaSerPheLeuArgArgAsnLleAsnGlnLleLysAlaTyrLleSerMetHisSerTyr 275
Db 919 GCTAACTCTTCGAAAACACAGAAAGCACATTAAGGCTTATCTCTCTCTCATGCAATAT 978
Qy 276 SerGlnHisLleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGlu 295
Db 979 GCTCAGATGTTACTGTATCCCTATCTTACAAATATGCAAAATTCACAAATTTTAGATGT 1038

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296 LeuSerLeuValAlaSerGluAlaValArgAlaLleAspLysThrSerLysAsnThrArg 315  
 1039 GTGAATCTGCAGCTTATAAGCTGTGAATGCACCT---CAGTCAGTATACGGGGTACGA 1095  
 316 TyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrp 335  
 1096 TACAGATATGAGCAGCCTCCACACGTTGTATGTGAGCTCTGGTAGCTCAATGATGG 1155  
 336 IleTyrAspLeuGlyLleLysTyrSerPhe----- 345  
 1156 GCCTACAAAATGCAATACCTTATGCTTTCGAACTACGTGACACTGGATATTTT 1215  
 346 -----ThrSerAsnProProValGluLysLeu 354  
 1216 GGATTTTACTCCAGAGATGCTCATCAAAACCCACCTGTACAGAACTA 1264

RESULT 15  
 US-08-782-760-5  
 ; Sequence 5, Application US/08782760  
 ; Patent No. 5948668  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hartman, Jacob  
 ; APPLICANT: Fulga, Netta  
 ; APPLICANT: Mendelovitch, Simona  
 ; APPLICANT: Gorecki, Marian  
 ; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08782,760  
 ; FILING DATE: 13-JAN-1997  
 ; CLASSIFICATION: 435  
 ; PRIORITY DATA:  
 ; APPLICATION NUMBER: 08/378,233  
 ; FILING DATE: 25-JAN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 0336/43847  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 927 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..927  
 ; US-08-782-760-5

Alignment Scores: 2.28e-67 Length: 927  
 Pred. No.: 604.00 Matches: 125  
 Score: 60.14% Conservative: 44  
 Percent Similarity: 60.14%



Thu Oct 28 07:16:11 2004

```

Best Local Similarity: 44.48%      Mismatches: 72
Query Match:         31.61%      Indels:    41
DB:                  2           Gaps:      5

US-09-980-881A-2 (1-360) x US-08-782-760-5 (1-927)

QY 115 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGlu 134
   |||||
Db 1 GCAGTGGACACAGCTACACCAAGTACAACTGGGAACGATTGAGCGTGGATTCAA 60

QY 135 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 154
   |||||
Db 61 CAAGTTGCCACTGATAATCCACACCTTGTCACTCAGAGCGTCATTGGAAACACACATTGAA 120

QY 155 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 174
   |||||
Db 121 GGACGTAAACATGTATGTCCTCAAGATT--GGTAAACTAGACCGAATAAGCCTGCCATC 177

QY 175 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 194
   |||||
Db 178 TTATCGATTGTGGTTTCCATGCAAGAGAGTGGAATTTCTCTGCATTCTGTCACTGGTTT 237

QY 195 Ile----- 195
   |||
Db 238 GTGAGAGGCTGTCGGTACTATAATCAAGAGATCCACATGAACAGCTTCTAGATGAA 297

QY 196 -----GlyHis----- 197
   |||||
Db 298 CTGGATTCTCTATGTTCTGCTGTGGTCAACATTGATGGCTATGCTTACACCTGGACTAAG 357

QY 198 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 217
   |||||
Db 358 GACAGAAATGTGGAGAAAACCCGCTCTACTATGCTGGTGGAACTCTGCTTGGGTGTAGAC 417

QY 218 LeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 237
   |||||
Db 418 CCCAACAGGAATTTT--AATGCTGGCTGGTGTGAAGTGGAGCTTCTCGAGTCCCTGC 474

QY 238 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 257
   |||||
Db 475 TCTGAAACTTACTGTGGACCGCCAGAGTCTGMAAAAGAGACAAAGCCCTGGCAGAT 534

QY 258 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 277
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Db 535 TTATCCCGCAACAACTCTCCACCATCAAGGCTACTGACCATCCACTCATACTACACAG 594

QY 278 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 297
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Db 595 ATGATGCTCTACCTTACTCTCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654

QY 298 LeuValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThr 317
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Db 655 GCCCTGGTGAAGGTGGCGCAAGAGACTT--GCCACTCTGCATGGCACCACCAAGTACACA 711

QY 318 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 337
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Db 712 TATGGCCCGAGGACTACAAATCTATCTCTGCTGGGGGATCTCAGCACTGCTCTTAT 771

QY 338 AspLeuGlyIleLysTyrSerPheThrSerAsnProValGluLysLeuLeuProLeu 357
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Db 772 GATCAGGGATCAAAATATCTTCTTACCTTTTGAACCT--CCGGGATACAGGCTTCTTTGGCTT 830

QY 358 Ser 358
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Db 831 TCT 833

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Search completed: October 27, 2004, 02:01:06  
Job time : 109.576 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 27, 2004, 01:54:23 ; Search time 1724.49 Seconds  
(without alignments)  
1070.424 Million cell updates/sec

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Perfect score: 1911  
Sequence: 1 MKLCLAVLPVFLVCEQHV.....IKYSFTSPNPVKKLPLSLK 360

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Xgapop 10.0 , Xgapext 0.5  
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Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2.1/USPTO spool\_p/US0980881/runat\_26102004\_084115\_7269/app.query.fasta\_1.1429  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=std.rnpb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=ext -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US0980881.OCGN\_1\_1034.0runat\_26102004\_084115\_7269  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
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Database : Published Applications NA:

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11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
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16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
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20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Query	Description
1	1849.5	96.8	1625	9	US-09-813-133A-1	Sequence 1, Appli
2	1849.5	96.8	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1832	95.9	1728	9	US-09-880-107-2396	Sequence 2386, Ap
4	1808.5	94.6	1344	16	US-10-115-479-69	Sequence 69, Appl
5	1808.5	94.6	1743	16	US-10-115-479-67	Sequence 67, Appl
6	1729	90.5	1272	15	US-10-379-836-1	Sequence 1, Appli
7	1439.5	75.3	1037	16	US-10-115-479-63	Sequence 63, Appl
8	1393.5	72.9	1132	16	US-10-115-479-65	Sequence 65, Appl
9	889	46.5	1400	9	US-09-925-302-24	Sequence 24, Appl
10	889	46.5	1400	10	US-09-925-302-24	Sequence 24, Appl
11	623	32.6	2154	9	US-09-910-059-124	Sequence 124, App
12	621.5	32.5	1332	9	US-09-954-456-1141	Sequence 1141, Ap
13	620.5	32.5	1633	15	US-10-341-434-187	Sequence 187, App
14	620.5	32.5	1740	14	US-10-116-802-95	Sequence 95, Appl
15	619.5	32.4	1254	14	US-10-229-546-3	Sequence 3, Appli
16	619.5	32.4	1622	14	US-10-229-546-1	Sequence 1, Appli
17	619.5	32.4	1622	15	US-10-429-802-21	Sequence 21, Appl
18	619.5	32.4	1622	16	US-10-430-503-12	Sequence 12, Appl
19	619.5	32.4	1622	16	US-10-262-511-71	Sequence 71, Appl
20	619.5	32.4	1622	16	US-10-641-643-1020	Sequence 1020, Ap
21	611.5	32.0	1302	17	US-10-477-515-1	Sequence 1, Appli
22	611.5	32.0	1311	13	US-10-200-344-9	Sequence 9, Appli
23	611.5	32.0	1993	15	US-10-274-639-33	Sequence 33, Appl
24	611.5	32.0	1993	16	US-10-333-574-33	Sequence 33, Appl
25	609.5	31.9	1907	18	US-10-757-262-127	Sequence 127, App
26	591	30.9	416	9	US-09-960-352-14595	Sequence 14595, A
27	564	29.5	2128	13	US-10-200-344-13	Sequence 13, Appl
28	563	29.5	1125	9	US-09-888-615-2	Sequence 2, Appli
29	563	29.5	1332	15	US-10-176-306-75	Sequence 75, Appl
30	563	29.5	1603	15	US-10-176-306-73	Sequence 73, Appl
31	556	29.1	1826	15	US-10-252-157-453	Sequence 453, App
32	546	28.6	1200	14	US-10-200-910-7	Sequence 7, Appli
33	546	28.6	1200	18	US-10-843-130-7	Sequence 7, Appli
34	543	28.4	1870	9	US-09-910-059-112	Sequence 112, App
35	543	28.4	1870	17	US-10-608-710-3	Sequence 3, Appli
36	528.5	27.7	1050	13	US-10-200-344-11	Sequence 11, Appl
37	527.5	27.6	991	16	US-10-383-201-93	Sequence 93, Appl
38	519.5	27.2	1260	16	US-10-257-174-16	Sequence 16, Appl
39	519.5	27.2	1311	14	US-10-200-910-5	Sequence 5, Appli
40	519.5	27.2	1311	16	US-10-257-174-15	Sequence 15, Appli
41	519.5	27.2	1311	17	US-10-451-821-1	Sequence 1, Appli
42	519.5	27.2	1311	18	US-10-843-130-5	Sequence 5, Appli
43	519.5	27.2	1348	16	US-10-072-012-315	Sequence 315, App
44	519.5	27.2	1641	17	US-10-381-820A-5	Sequence 5, Appli
45	514.5	26.9	1295	17	US-10-363-829-148	Sequence 148, App

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1  
Alignment Scores:



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Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
Db 497 TTAAGGTTTCTGGAAGAAAGCAAGCAGCAAAATGCCATATGATGATGACTGTGGAATC 556  
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
Db 557 CATGCCAGAGATGGATCT 616  
Qy 201 TrpArgLysAsnArgSerPheTrpAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220  
Db 617 TGGAGAAAGAACGGTCT 676  
Qy 221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240  
Db 677 AACTTTGCTTCCAAACACACTGGTGTAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 736  
Qy 241 TyrCysGlyLeuTrpProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
Db 737 TACTGTGGACTTATCT 796  
Qy 261 ArgAsnIleAsnGlnIleLysAlaTrpIleSerMetHisSerTrpSerGlnHisIleVal 280  
Db 797 AGAATATACACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTG 856  
Qy 281 PheProTrpSerTrpThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300  
Db 857 TTTCCATATCTCTATACAGAGTAAAGCAAGACCATGAGCAACTGTCTCTAGTAGCC 916  
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTrpThrHisGlyHis 320  
Db 917 AGTGAAGCAGTTCGTCT 976  
Qy 321 GlySerGluThrLeuTrpLeuAlaProGlyGlyAspTrpIleTrpAspLeuGly 340  
Db 977 GGCTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGAGCATGATCTATGATTGGGC 1036  
Qy 341 IleLysTrpSerPhe----- 345  
Db 1037 ATCAATATTTCTTTTACAAATTGAATTCGAGATACGGGCACATACGGATTCTTGTGCGC 1096  
Qy 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1097 GAGCGTTACATCAAAACCCACTGTAGAGAGCTTTTGGCGCTGTCTCTAAAA 1148

RESULT 3  
US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Vockley, Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

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Score: 86.27% Conservative: 1  
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Best Local Similarity: 95.87% Indels: 55  
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Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
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Qy 41 ValLeuGlnAsnLeuThrThrTrpTyrGluIleValLeuTrpGlnProValThrAlaAsp 60  
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Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
Db 200 CTTATTGTGAAGAAAAAACAAGTCCCATTTTTTTTGTAAATGCAATCTGATGTCGACAAATGTG 259  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
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Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTrpTrp 120  
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Db 440 CCTGATATGCTTACAAAAATCCACATTTGGATTCCTCATTTTGAGAAGTACCACCTCTATGTT 499  
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Qy 197 ----- 197  
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Db 680 CCGGTGGTTAATGTGACCGTTATGACTACTCATGCAAAAAGAAATCGAATGTGGAGAAAG 739  
Qy 204 AsnArgSerPheTrpAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223  
Db 740 AACCGTTCTTCTATCGAACAATCATTCATCGAACACAGACCTGAAATAGGAACCTTTGCT 799  
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTrpCysGly 243  
Db 800 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTCTACTGTGA 859  
Qy 244 LeuTrpProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAnile 263  
Db 860 CTTTATCTCTGAGTCAGAACCAAGAGTGAAGGCAAGTGGCTAGTTTCTTTGAGAAGAAATATC 919  
Qy 264 AsnGlnIleLysAlaTrpIleSerMetHisSerTrpSerGlnHisIleValPheProTrp 283  
Db 264 AsnGlnIleLysAlaTrpIleSerMetHisSerTrpSerGlnHisIleValPheProTrp 283

Db 920 AACGAGATTAAAGCATACATCAGCATGCAATTCATACCTCCAGCATATAGTGTTCATAT 979  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303  
Db 980 TCCTATACACGAAGTAAAGCAAGAACCATCAGGAACCTGTCTAGTAGCCAGTGAAGCA 1039  
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1040 GTTCGTGCTATTGTAAGAACTAGTAAATAATACAGGTATACACATGCGCATGGCTCAGAA 1099  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyGlyValAspAspTrpIleTyrAspLeuGlyIleLysTyr 343  
Db 1100 ACCATTATACCTAGCTCTCGAGGTGGGACGATGGATCTAATGATTGGGCATCAATAT 1159  
Qy 344 SerPhe-----Th 346  
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Qy 346. rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360  
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## RESULT 4

US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zethusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710

; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 69  
; LENGTH: 1344  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (31)..(1315)  
US-10-115-479-69  
Alignment Scores:  
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Score: 1808.50 Matches: 355  
Percent Similarity: 84.76% Conservative: 1  
Best Local Similarity: 84.52% Mismatches: 4  
Query Match: 94.64% Indels: 60  
DB: 16 Gaps: 3  
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Db 31 ATGAAGCTTTGCAGCCTTGCAGTCTTGTATCCCATTTCTCTCTCTGTGAGCAGCATGTC 90  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 91 TTCGCGTTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 150  
Qy 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60  
Db 151 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 210  
Qy 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80  
Db 211 CTATTGTTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTGCAATGTG 270  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCyssSerValLeuLeuAlaAspValGluAsp 100  
Db 271 AAGCCCATTTAAATGTGAGCGGAATTCACATGCTGCTCTGGCAGAGCTGGAAGAT 330  
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 331 CTATTCAACAGCAGATTTCACACGACACAGTCAGCCCCCGAGCCTCCGCACTGCTACTAT 390  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
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Db 451 CCTGATATGCTTACAAAAATCCACATTTGGATTCCTCATTTGAGAAGTACCCACTCTATGTT 510  
Qy 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175  
Db 511 TTTAAAGGTTTCTTTTGAGCAGGTTTCTGGAAAAACAAGCAGCAAAATGTCATATGG 570  
Qy 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195  
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Qy 196 GlyHis----- 197  
Db 631 GGCCATATACTCAATCTATGGGATAATAGGGCAATATACCAATCTCTCTGAGGCTTGTG 690  
Qy 198 -----Asn 198  
Db 691 GATTTCATGTTATGTCGCGTGGTTAATGTGATGGTTTGTGACTACTGACTCATGAGAAAAAAGAT 750

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QY 199 ArgMetTTPArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
Db 751 CGAATGTGGAGAAAGAACGGTCTTCTTAAGGAAACAATCATGTGGAACACAGACCTG 810
QY 219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 238
Db 811 AATAGGAACCTTGGCTTCCAAACACATGGTGTGAGGAAGGTGCATCCAGTTCCCTCATGCTCG 870
QY 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValaSerPhe 258
Db 871 GAAACCTACTGTGGACTTTTATCTCAGTACAGAACCAAGAGTGAAGCAGTGGCTAGTTTC 930
QY 259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
Db 931 TTGAGAAGAAATATCAACAGATTAAAGCATATCATCAGCATGCATTCATCTCCAGCAT 990
QY 279 IleValPheProTyrSerTyrThrArgSerLysLysLysLysLysLysLysLysLys 298
Db 991 ATAGTGTTCCTATATCTATACAGAACTAAAGCAAGACCATGAGGAACCTGTCTCTA 1050
QY 299 ValAlaSerGluAlaValAlaGlnIleLysAlaSerLysLysLysLysLysLysLys 318
Db 1051 GTAGCCAGTGAAGCAGTCTGCTGCTATTGAGAAAAATTAGTAAAAATACCAAGTATACAT 1110
QY 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyrAsp 338
Db 1111 GGCCATGGCTCAGAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTTGGATCTATGAT 1170
QY 339 LeuGlyIleLysTyrSerPhe----- 345
Db 1171 TTGGGCATCAATATTCGTTTACAAATTGAACTTCGAGATACGGGCACATACGGAATTCCTG 1230
QY 346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1231 CTGCGGAGGCTTACATCAAAACCCAGCTAGAGAAAGCTTTTGGCGCTGTCTCTAAAA 1288

RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
```

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; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
; US-10-115-479-67

Alignment Scores:
Pred. No.: 6,06e-214 Length: 1743
Score: 1808.50 Matches: 355
Percent Similarity: 84.78% Conservatives: 1
Best Local Similarity: 84.52% Mismatches: 4
Query Match: 94.64% Indels: 60
DB: 16 Gaps: 3

US-09-980-881A-2 (1-360) x US-10-115-479-67 (1-1743)
QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 20 ATGAAGCTTTGCAGGCTTGCAGCTTCCTGTGACCAATTTGTTCTCTCTGTGAGCAGCATGTC 79
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 80 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 139
QY 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
Db 140 GTTCTACAGAACTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 199
QY 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
Db 200 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATGTGCAAAATGTG 259
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 260 AAAGCCCATTTAAATGTGAGCGGAATTCATGAGTGCTTGTCTGGCAGACGTGGGAAGAT 319
QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 320 CTTATTCAACAGCAGATTTCACACACACACAGTCAGCCCGCCGCTCCGATCGTACTAT 379
QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 380 GAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAATTTATACTGAGAGGCAT 439
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 440 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCAATTGAGAAGTACCACCTCTATGTT 499
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QY 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175
Db 500 TTAAGGGTTCTTTGAGCAGGTTCTTGAAAAAGAACAGCAGCCAAAAATGCCATATGG 559
QY 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195
Db 560 ATTGACTGGGATCATCCAGCAAGATGATCTCTCTGCTTCTGCTTCTGTTGTTTATA 619
QY 196 GlyHis----- 197
Db 620 GGCCATAATAACTCAATTCATGGGATAATAGGGCAATATACCAATCTCTCGAGGCTTGTG 679
QY 198 -----Asn 198
Db 680 GATTTCATGTTATGCCAGTGGTTAATGTGGATGTTATGACTACTCATGGAAAAAGAAAT 739
QY 199 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
Db 740 CGAATGTGGAGAAAGACCGTTCTTTCTATGCGAACAATCATTTGCATCGGAACAGACCTG 799
QY 219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 238
Db 800 AATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCG 859
QY 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
Db 860 GAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGCAGTGGCTAGTTTC 919
QY 259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
Db 920 TTGAGAAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCAT 979
QY 279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298
Db 980 ATAGTGTTCCTATATCTTATACAGAAAGTAAAGCAAGACCATGAGGAACTGTCTCTA 1039
QY 299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318
Db 1040 GTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAATATTAGTAAATATACCAGGTATACAT 1099
QY 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAsp 338
Db 1100 GSCCATGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCATTTGCATCTATCAT 1159
QY 339 LeuGlyIleLysTyrSerPhe----- 345
Db 1160 TTGGGCATCAAAATATTCTGTTTACAAATTGAACCTTCGAGATACGGGCACATACGGATTCTTG 1219
QY 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1220 CTGCCGAGGCGTTACATCAACCCACCTGTAGAGAAAGCTTTTGGCCGCTGTCTCTANAA 1277
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## RESULT 6

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US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (1)...(1269)
US-10-379-836-1
Alignment Scores:
Pred. No.: 2,79e-204 Length: 1272
Score: 1729.00 Matches: 338
Percent Similarity: 83.37% Conservative: 8
Best Local Similarity: 81.45% Mismatches: 14
Query Match: 90.48% Indels: 55
DB: 15 Gaps: 2
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US-09-980-881A-2 (1-360) x US-10-379-836-1 (1-1272)

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QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 1 ATGAAGCTTTGCAGCTTTGCAGTCTTGTAGTCCCAATTTCTCTCTGTGACGACGATGTC 60
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
Db 61 TTCGGTTTCAGAGTGGCCAGGTTCTAGTGTCTTCTTAGAACCTCTAGCAAGTTCAA 120
QY 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
Db 121 GTGCTACAGAATCTTACTACAAATATGAGATTGTCTCTGCGACGCGGTAAACAGCGAC 180
QY 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspVal 80
Db 181 CTTATTGAGAGAAAAAACAGTCCATTTTTTTGTAATTCATCTGATGTGCAATGTG 240
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 241 AAAGCCCATTTAATGTGAGCGGAATTCATGTCAGTGTCTGTGTCGCGAGATGTGGAAGAT 300
QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 301 CTTATTCAACAGCAGATTTTCCACGACACATGTCAGCCCCGAGGCTCCGCACTCGTACTAT 360
QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 361 GAAACAGTATCACTCACTAAATGAATCTATTCTTTGGATGAGAACTTATAACTGAGAGAT 420
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 421 CCTGATATGCTTACAAAAATCCACATTTGGATCCTCTATGAGAAAGCACCCACTTTATGTT 480
QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 481 TTAAGGTTTCTGGAAGAAAGAACAAACAGCCAAAAATGCCATGTGATTTGACTGTGGAATC 540
QY 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197
Db 541 CATGCCAGAGAAATGGAATCTCCCTGCTTTCTGCTTTGTGGTTTCATAGGCCATATAACTGAA 600
QY 197 ----- 197
Db 601 TACTACGGGATAATAGGGGAATATACCAATCTTCTGAGGCATGTGGATTTCTATGTTATG 660
QY 198 -----AsnArgMetTrpArgLys 203
Db 661 CCAGTGGTTAATGTGGATGTTTATGACTACTCATGGAAGAAAGAAATCGAATGTGGAAG 720
QY 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
Db 721 AACCGTTCTTTCTATGCGAACAATCGTTGTCATCGAACAGACCTTGAACAGAACTTTCGG 780
QY 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243
Db 781 TCCAAACACTGTTGTGAGGAAGGTGCATCCAGTTTCTCATGCTCGAAAACTTACTGTGA 840
QY 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263
Db 841 CTTTATCTCTGAGTCAGAACCCAGAGCGGTCGCTAATTTCTTGTGAGAGAAATATC 900
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QY 264 AsnGlnIleValAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283  
Db 901 AACCACTTAAGCATACATACATGATGATGATGATGATGATGATGATGATGATGAT 960  
QY 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303  
Db 961 TCTATACCTGAAGCAAAAGCAAGACCAAGAGGATGCTCTAGTAGCAGTGAAGCA 1020  
QY 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1021 GTTCGTGCTATTACAGAAAACCAAGTAAATAATATACAGGTATACATGCGCGTCAGAA 1080  
QY 324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGlyIleTyr 343  
Db 1081 ACCTTATACCTAGCTCTGAGGTGCGAGGATGATGATGATGATGATGATGATGAT 1140  
QY 344 SerPhe-----Th 346  
Db 1141 TCGTTTACAATTGAACCTTCGAGATACGGCAAAATACGGATTCTTGCTGCTGAGCGTTAC 1200  
QY 346 rSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1201 ATCAAAACCACTTTGTAAGACGCTTTTGGCGCTGCTCTAAAA 1243

## RESULT 7

US-10-115-479-63  
; Sequence 63, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687

US-09-980-881A-2 (1-360) x US-10-115-479-63 (1-1037)  
Alignment Scores: 2,07e-168 Length: 1037  
Pred. No.: 1439,50 Matches: 293  
Score: 77.78% Conservative: 1  
Percent Similarity: 77.51% Mismatches: 2  
Best Local Similarity: 75.33% Indels: 82  
Query Match: 16 Gaps: 2  
DB:

QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAAGCTTTGCAGCCTTGCAGCTCTGTACCACTTGTCTCTCTGTGAGCAGCATGTC 100  
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 160  
QY 41 ValLeuGlnAsnLeuThrThrTyrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60  
Db 161 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGAGCCGGTAAACAGCTGAC 220  
QY 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80  
Db 221 CTTATTGTGAGAAAAAACAAGTCCCATTTTTTTGTAATATGTCATCTGATCTCGACAATGTG 280  
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaValGluAsp 100  
Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGAGTGTCTTGTGCGACAGCTGGAGAT 340  
QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 341 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGCCCGAGCCTCCGATCTGTTAT 400  
QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHis 140  
Db 401 GAACAGTATCACTCACTAAATAAATCTATTCTTGGATAGAAATTTATAACTGAGAGCAT 460  
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGlyLysTyrProLeuTyrVal 160  
Db 461 CCGTATATCTTACAAAAATCCACATCGGATCTCTCTTGGAGAGTACCACCTCTATGTT 520  
QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIle 180  
Db 521 TTAAGGTTTCTGGAAGAAACAAGCAGCCAAAATATGCCATATGATGATGATGATGAT 571  
QY 181 HisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPheIleGlyHisAsnArgMet 200  
Db 571 ----- 571  
QY 201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220  
Db 571 ----- 571  
QY 221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 240

Db 571 ----- 571  
 Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValValAlaValAlaSerPheLeuArg 260  
 Db 572 ---TGTGACATTTATCTCTGAGTCAGAACCCAGAGTGAAGGCGAGTGGCTAGTTCTTGAGA 628  
 Qy 261 ArgAnlleAnGlnIleGlyAlaTyrPheSerMetHisSerTyrSerGlnHisIleVal 280  
 Db 629 AGAAATATCAACCCAGATTAAAGCATACATCAGCATGCATTTCATCTCCAGCATATAGTG 688  
 Qy 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300  
 Db 689 TTTTCATATTTCTATACAGAGTAAAGACCAAGCAAGTGAAGTGTCTCTAGTAGCC 748  
 Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320  
 Db 749 AGTGAAGCAGTTCTGCTATTGAGAAATATTAGTAAATAATACAGGTATACATGGCCAT 808  
 Qy 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340  
 Db 809 GGCTCAGAAACCTTATACCTAGCTCTCTGGAGTGGGAGCATTTGGATCTATGATTTGGGC 868  
 Qy 341 IleLysTyrSerPhe----- 345  
 Db 869 ATCAAAATATTTGTTTCAATTTGAACTTCGAGATACGGGCACATACGGATTCTTGTGCGG 928  
 Qy 346 -----ThrSerAnProProValGluLysLeuLeuProLeuSerLeuLys 360  
 Db 929 GAGCGTTACATCAACCCACCTGTAGAGAGCTTTTGGCGTGTCTCTATAAA 980

RESULT 8

US-10-115-479-65  
 ; Sequence 65, Application US/10115479  
 ; Publication No. US2004006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Huihong  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.  
 ; APPLICANT: Furtak, Katarzyna  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Malvanker, Uriel M.  
 ; APPLICANT: Shinkets, Richard A.  
 ; APPLICANT: Taupier, Raymond J.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Mazur, Ann  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
 ; CURRENT APPLICATION NUMBER: US/10/115,479  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 60/281,136  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,863  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,906  
 ; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282,934  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/283,657  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,678  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,687  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,710  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/284,234  
 ; PRIOR FILING DATE: 2001-04-17  
 ; PRIOR APPLICATION NUMBER: 60/285,325  
 ; PRIOR FILING DATE: 2001-04-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SEQ ID NO 65  
 ; LENGTH: 1132  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (41)..(1103)  
 ; US-10-115-479-65  
 Alignment Scores:  
 Pred. No.: 1.27e-162 Length: 1132  
 Score: 1393.50 Matches: 283  
 Percent Similarity: 67.38% Conservative: 0  
 Best Local Similarity: 67.38% Mismatches: 3  
 Query Match: 72.92% Indels: 134  
 DB: 16 Gaps: 4

US-09-980-881A-2 (1-360) x US-10-115-479-65 (1-1132)  
 Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
 Db 41 ATGAAGCTTTGCAGCTTGCAGTCTTGTATCCCATTTGTTCTCTCTGTGAGCAGCATGTC 100  
 Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
 Db 101 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 160  
 Qy 41 ValLeuGlnHisLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 60  
 Db 161 GTTCTACAGATCTTACTACAAATATGAGATTGTTCTCTGCGACCGGTAAACAGCTGAC 220  
 Qy 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
 Db 221 CTTATTGTGAAGAAAAAACAGTCCATTTTGTAAATGATCTGTATGTCGACATGTG 280  
 Qy 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100  
 Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGCGACAGCTGGAAGAT 340  
 Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
 Db 341 CTTATTCAACAGCAGATTTTCCACGACACAGTACGCCCCGAGCTCCGCACTGCTACTAT 400  
 Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
 Db 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGATTTATAAATGAGAGCAT 460  
 Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
 Db 461 CCTGATATGCTTACAAAAATCCATTTGGATTCCTCAITTTGAGAAAGTACCCACTCTATGT 520  
 Qy 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175  
 Db 521 TTAAGGGGTTTCTTTGAGCAGGTTTCTGGAAGAAAGAACAGCAGCAAAATGCCATATGG 580  
 Qy 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195

581 ATTGACTGTGGAATCCATCCAGAGAAATGGATCTCTCTGCTTTCTGCTGTGTTTCATA 640  
QY 196 GlyHis----- 197  
641 GGCACATATAACTCAATTCTATGGGATAATAGGCAATATACCAATCTCTGAGGCTTGTG 700  
QY 198 -----Asn 198  
701 GATTTCATATTATCCCGGTGTTAATGTGGATGTTATGACTACTCATGGAAGAAGAT 760  
QY 199 ArgMetTrpArgGlyAsnArgSerPheTyrAlaAsnAsnHisCysAlleGlyThrAspLeu 218  
761 CGAATGTGAGAAAGAACCGTTCTTCTATGCGAACCAATCAATGCAATCGGAACAGACCTG 820  
QY 219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 238  
821 AATAGGAACCTTTGCTTCCAAACACATGTTGTGAGGAGGTGCATCCATGCTCTGCTCG 880  
QY 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValysAlaValAlaSerPhe 258  
881 GAAACCTACTGTGGACTTTATCTGAG----- 907  
QY 259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278  
907 ----- 907  
QY 279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298  
907 ----- 907  
QY 299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318  
907 ----- 907  
QY 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAsp 338  
908 -----TCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTCGATCATGAT 958  
QY 339 LeuGlyIleLysTyrSerPhe----- 345  
959 TTGGGCATCAATATATTGTTTACAATTGAACCTTCGAGATACGGGCAATACGGAATTCCTTG 1018  
QY 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
1019 CTCCCGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCCGCTGCTCTTAAAA 1076

RESULT 9

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US2002004941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

Alignment Scores:

Pred. No.: 1.06e-99 Length: 1400  
Score: 889.00 Matches: 178  
Percent Similarity: 75.21% Conservative: 1  
Best Local Similarity: 74.79% Mismatches: 3  
Query Match: 46.52% Indels: 56  
DB: 9 Gaps: 2  
US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)  
QY 179 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 197  
DB 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGCTGTGTTTCATAGGCCATATA 69  
QY 197 ----- 197  
DB 70 ACTCAATCTATGGGATAATAGGCAATATACCAATCTCTCTGAGGCTTGTGATTTCTAT 129  
QY 198 -----AsnArgMetTr 201  
DB 130 GTTATGCCGTGTTAATGTGGATGTTATGAACCTACTCATGGAAAAAGAAATCGAATGTG 189  
QY 201 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysAlleGlyThrAspLeuAsnSerAs 221  
DB 190 GAGAAAGAACCGTTCTTCTATGCGAACCAATCAATTCGATCGGAACAGACCTGAATAGGAA 249  
QY 221 nPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 241  
DB 250 CTTTCTCTCCAAACACTGTTGTGAGGAGGTGCATCCAGTTCTCATGCTCGAAACCTTA 309  
QY 241 rCysGlyLeuTyrProGluSerGluProGluValysAlaValAlaSerPheLeuArgAr 261  
DB 310 CTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGCAGTGGCTAGTTCTTGAGAAG 369  
QY 261 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 281  
DB 370 AAATATCAACCGAGTTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGT 429  
QY 281 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 301  
DB 430 TCCATATTCTTATACACGAAGTAAAGCAACACCATGAGGAACCTGTCTCTAGTAGCCAG 489  
QY 301 rGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 321  
DB 490 TGAAGCAGTTCGTGCTATTGAGAAAACCTAGTAAAAATACCAGGTATACACATGGCCATGG 549  
QY 321 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyValAspAspTrpIleTyrAspLeuGlyI 341  
DB 550 CTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGAGCATTTGATTCATGATTTGGGCAT 609  
QY 341 eLysTyrSerPhe----- 345  
DB 610 CAATATTCGTTTACAATTGAACCTTCGAGATACGGSCACATACGGATTCTTGTGCGCGA 669  
QY 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
DB 670 GCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCCGCTGCTCTTAAAA 719

RESULT 10

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Publication No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

Alignment Scores:  
Pred. No.: 1,06e-99 Length: 1400  
Score: 889.00 Matches: 178  
Percent Similarity: 75.21% Conservative: 1  
Best Local Similarity: 74.79% Mismatches: 3  
Query Match: 46.52% Indels: 56  
DB: 10 Gaps: 2

US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

```
Qy 179 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 197
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGTTGTTTCATAGGCCATATA 69
Qy 197 ----- 197
Db 70 ACTCAATTCTATGGGTAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTCTAT 129
Qy 198 -----AsnArgMetTr 201
Db 130 GTTATGCCGGTGTAAATGTGGATGGTTATGNACTACTCATCGGAAAAAGATCGAATGTG 189
Qy 201 pArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnSerAs 221
Db 190 GAGAAAGAACCGTTCTTCTATGTCGAACAATCATTTGCATCGGAACAGACCTGAATAGGAA 249
Qy 221 nPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerSerGluThrTy 241
Db 250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATCTCGGAAACCTA 309
Qy 241 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 261
Db 310 CTGTGGACTTATCTCTAGTCAGAACCAAGAGTGAAGGCAGTGGTAGTCTTCTGAGAG 369
Qy 261 eProlIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValph 281
Db 370 AAATATCAACAGATTAAGCATACATCAGCATGCATTTCATCTCCAGCATATAGTGT 429
Qy 281 eProlIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValph 301
Db 430 TCCATATTCCCTATACACCAAGTAAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCCAG 489
Qy 301 rGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisG1 321
Db 490 TGAACGAGTTCGTGTATTGAGAAACCTAGTAAATAATACCAGGTATACATGAGCCATGG 549
Qy 321 ySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyI 341
Db 550 CTCAGAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTATGATTGGGCAT 609
Qy 341 eLysTyrSerPhe----- 345
Db 610 CAATATTTCGTTTCAATTGAACTTCGAGATACGGGCACATACGGAATTCCTGCTCGCGGA 669
Qy 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360
Db 670 GCGTTACATCAAAACCCACTGCTAGAGAGAGCTTTCCCGCTGCTCTATAA 719
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## RESULT 11

US-09-910-059-124  
; Sequence 124, Application US/09910059  
; Patent No. US20020142359A1  
; GENERAL INFORMATION:

; APPLICANT: Copley, Clive G  
; APPLICANT: Edge, Michael Derek  
; APPLICANT: Emery, Stephen Charles  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,  
; TITLE OF INVENTION: Their Therapeutic use in an Adept System  
; FILE REFERENCE: 1991-209  
; CURRENT APPLICATION NUMBER: US/09/910,059  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 09/171,945  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; PRIOR APPLICATION NUMBER: GB 9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 124  
; LENGTH: 2154  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanised pre-pro HCPB-linker-Fd sequence  
US-09-910-059-124

Alignment Scores:  
Pred. No.: 2,7e-66 Length: 2154  
Score: 623.00 Matches: 132  
Percent Similarity: 53.40% Conservative: 72  
Best Local Similarity: 34.55% Mismatches: 134  
Query Match: 32.60% Indels: 44  
DB: 9 Gaps: 7

US-09-980-881A-2 (1-360) x US-09-910-059-124 (1-2154)

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Qy 3 LeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22
Db 1 ATGTTGGACACTCTGGTTCGTGCTGCTGGCCCTGGCATCTGCTCATCTCATGTGGTGAG 60
Qy 23 ---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal 41
Db 61 CACTTTGAAGCGGAGAGGTGTTCCGTTGAACCTTGAAGATGAATAATCAATTAACATA 120
Qy 42 LeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61
Db 121 ATCCGCGAGTTGGCCAGCAGCACGCCAGATTGACTTCTGGAAGCCAGATTCTGTACACAA 180
Qy 62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81
Db 181 ATCAAACTCACATACAGTTGACTTCGTTTAAAGCAGAGATATCTGTCTGTGTGAG 240
Qy 82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValIgluAspLeu 101
Db 241 AATGTTCTAAAGCAGAGTGAAGTACTACAAAGTACTGATAAGCAACCTGAGAAATGTG 300
Qy 102 IleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
Db 301 GTGGAGGCTCAGTTTGTATAGCCGGTT-----CGTGCACAGGACACACAGATTATGAG 351
Qy 122 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141
Db 352 AAGTACAAACAGTGGGAAACGATAGAGCTTGGACTCAACAAAGTCGCCACTGAGAAATCCA 411
Qy 142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
Db 412 GCCCTCATCTCCGAGTGTATTCGGAACACACATTTGAGGGACCGCGCTATTATTACTCTG 471
Qy 162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181
Db 472 AAGGTT---GGCAAAAGCTGGACAAAATAAGCCTCCCATTTTCATGGACTTGTGGTTCCAT 528
Qy 182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
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; PRIORITY FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1141
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1141

Alignment Scores:
Pred. No.: 1,866-66 Length: 1332
Score: 621.50 Matches: 134
Percent Similarity: 53.66% Conservative: 71
Best Local Similarity: 35.08% Mismatches: 132
Query Match: 32.52% Indels: 45
DB: 9 Gaps: 8

US-09-980-881A-2 (1-360) x US-09-954-456-1141 (1-1332)

QY 3 LeuCySerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22
DB 24 ATGTTGGCACCTCTGTTCTGGTACCTGGCCCTGGCATCTGCTCATCATGTTGGTGGAG 83
QY 23 ---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal 41
DB 84 CACTTTGAAGCGCGAGAGGTTCCTGCTTAACTGTTGAAGTGAAGATGAAAAATCACATTAA 143
QY 42 LeuGlnAenLeuThrThrThrTyrluileValLeuTyrGlnProValThrAlaLeu 61
DB 144 ATCCCGAGTGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 203
QY 62 ileValLysLysLysGlnValHisPhePheValAenAlaSerAspValAspValLys 81
DB 204 ATCAAACTCACAGTACAGTTCCTGCTGTTAAAGCAGAGATACCTGCTCACTGTGGAG 263
QY 82 AlaHisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluLeu 101
DB 264 AATGTTCTAAAGCAGAACTGAATACAACTGATGATGATGATGATGATGATGATGATG 323
QY 102 IleGlnGlnIleSerAenAspThrValSerProArgAlaSerAlaSerTyrrGlu 121
DB 324 GTGGAGGCTCAGTTGATAGCCGGGT-----CGTGCACAGCAGCAGCAGCAGCAG 374
QY 122 GlnTyHisSerLeuAenGluIleTyrrSerTrpIleGluPheIleThrGluArgHisPro 141
DB 375 AGTACACAACTGGGAAACGATAGAGGCTTGAGCTCAACAAGTCGCCACTGAGAAATCCA 434
QY 142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrrProLeuTyrrVal 161
DB 435 GCCCTCATCTCTCGCAGTGTATCGGAACACATTTGAGGGAGCGCGCTATTTACCTCTG 494
QY 162 LysValSerGlyLysGluGlnThrAlaLysAenAlaIleTrpIleAspCysGlyIleHis 181
DB 495 AAGGTT---GGCAAAGCTGGACAAATAAGCCCTGCCATTTTCATGGACTGTGTTTCCAT 551
QY 182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
DB 552 GCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTTGTAAAGAGAGGCTGTTCTGATCC 611
QY 195 ----- 195
DB 612 TATGGACGTGAGATCCAACTGACAGAGCTTCTCGACAACTTAGACTTTTATGTCCTGCC 671
QY 196 -----GlyHis-----AsnArgMetTrpArgLysAen 204
DB 672 GTGCTCAATATTGATGGCTACATCTACCTGACCAAGAGCGGATTTTGGAGAAAGACT 731
QY 205 ArgSerPheTyrrAlaAenAenHisCysIleGlyThrAspLeuAenSerAenPheValSer 224
DB 732 CGCTCCACCCTACTGGATCT---AGCATTTGGCAGACAGCCCAACAGAAATTTT---GAT 785
QY 225 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrrCysGlyLeu 244
```

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529 GCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTGTAAGAGAGGCTGTTGCTACC 588
195 ----- 195
589 TATGGACGTGAGATCCAACTGACAGAGCTTCTCGACAACTTAGACTTTTATGCTGCTC 648
196 -----GlyHis-----AsnArgMetTrpArgLysAen 204
649 GTGCTCAATATTGATGGCTACATCTACCTGACCAAGAGCGGATTTTGGAGAAAGACT 708
205 ArgSerPheTyrrAlaAenAenHisCysIleGlyThrAspLeuAenSerAenPheValSer 224
709 CGCTCCACCCTACTGGATCTAGCTGCTGCAATTCGCCAGACAGCCCAACAGAAATTTT---GAT 765
225 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrrCysGlyLeu 244
766 GCTGGTGGTGGTGAATTTGGAGCCTCTCGAAACCCCTGTGATGAAACTTTACTGTGGACT 825
245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAenIleAen 264
826 GCCGAGAGTGTGAAGAGAGACCAAGGCCCTGGCTGATTTTCATCCGCAACAACTCTCT 885
265 GlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPheProTyrrSer 284
886 TCCATCAAGCATATCTGACATCTGACTGCTACTCCCAATGATGATCTACCTTACTCA 945
285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304
946 TATGCTTTACAACTCGGTGAGAACATGCTGAGTTGATGCTGCTGCTGCTGCTGCTGCTG 1005
305 ArgAlaIleAspLysThrSerLysAenThrArgTyrrThrHisGlyHisGlySerGluThr 324
1006 AAGAAACTT---GCCCTACTGACGGCAGCAGACATGATGATGATGATGATGATGATGATG 1062
325 LeuTyrrLeuAlaProGlyGlyAspAspTrpIleTyrrAspLeuGlyIleLysTyrrSer 344
1063 ATCTATCTCTGCTGGACTTCTAAAGACTGGCTTATGACCAAGAAATCAGATATTC 1122
345 PheThr 346
1123 TTCACC 1128

RESULT 12
US-09-954-456-1141
; Sequence 1141, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
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Db 786 C T G G T T G G T G A A T T G G A C C T C T C G A A A C C C C T G T G A T G A A A C T T A C T G G A C C T 845  
 Qy 245 T y r P r o G l u S e r G l u P r o G l u V a l l y A l a S e r P h e L e u A l a S e r P h e L e u A r g A s n I l e A s n 264  
 Db 846 C C C G A G A G T C T G A A A G A G A C C A A G C C C T G G T G A T T C A T C C G C A A C A A A C T C T C T 905  
 Qy 265 G l n l e y s A l a T y r I l e S e r M e t H i s S e r T y r S e r G l n H i s I l l e V a l P h e P r o T y r S e r 284  
 Db 906 T C C A T C A A G G C A T A T C T G A C A A T C C A C T C G T A C T C C C A A A T G A T G A T C A C C C T T A C T C A 965  
 Qy 285 T y r T h r A r g S e r L y s S e r L y s A s p H i s G l u L e u S e r L e u V a l A l a S e r G l u A l a V a l 304  
 Db 966 T A T C T T A C A A C T C G G T G A G A A C A A T G C T G A G T T G A T G C C T G G C T T A A G C T A C T G T G 1025  
 Qy 305 A r g A l a l e A s p L y s T h r S e r L y s A s n T h r A r g T y r T h r H i s G l y H i s G l y S e r G l u T h r 324  
 Db 1026 A A G A A C T T - - - G C T C A C T C A C G G C A C C A A G T A C A C A T A T G G C C G G G A G C T A C A C A 1082  
 Qy 325 L e u T y r L e u A l a P r o G l y G l y A s p A s o T r p I l e T y r A s p L e u G l y I l l e V a l P h e T y r S e r 344  
 Db 1083 A T C T A T C T G T G T G G G G C T C T G A C G A C T G G G C T T A T G A C C A A G G A A T C A G A T A T T C C 1142  
 Qy 345 P h e T h r 346  
 Db 1143 T T C A C C 1148  
 RESULT 13  
 US-10-341-434-187  
 ; Sequence 187, Application US/10341434  
 ; Publication No. US20030215835A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Origene Technologies  
 ; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes  
 ; FILE REFERENCE: 90 204 205 R1  
 ; CURRENT APPLICATION NUMBER: US/10/341.434  
 ; PRIOR FILING DATE: 2003-07-18  
 ; PRIOR APPLICATION NUMBER: US 60/348,164  
 ; PRIOR FILING DATE: 2002-01-15  
 ; PRIOR APPLICATION NUMBER: US 60/348,119  
 ; PRIOR FILING DATE: 2002-01-15  
 ; NUMBER OF SEQ ID NOS: 238  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 187  
 ; LENGTH: 1633  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (12)..(1262)  
 ; OTHER INFORMATION:  
 US-10-341-434-187  
 Alignment Scores:  
 Pred. No.: 3.48e-66 Length: 1633  
 Score: 620.50 Matches: 130  
 Percent Similarity: 54.19% Conservative: 77  
 Best Local Similarity: 34.03% Mismatches: 128  
 Query Match: 32.47% Indels: 47  
 DB: 15 Gaps: 8  
 US-09-980-881a-2 (1-360) x US-10-341-434-187 (1-1633)  
 Qy 5 S e r L e u A l a V a l L e u V a l P r o I l e V a l l e u P h e C y s G l u G l n H i s V a l P h e A l a - - - - - 22  
 Db 9 A C C A T G A G C T C A T C T G C C T G T G G T T G A T T G C T A C C A C T C T T G C A A T T G C T C C T G T C 68  
 Qy 23 - - - P h e G l n S e r G l y G l n V a l L e u A l a L a l e u P r o A r g T h r S e r A r g G l n V a l G l n V a l 41  
 Db 69 C G C T T T G A C G G G A G A G A G G T T C C G C G T G A A G C C C C A G G A T G A A A A C A A C A G A C A T C 128  
 Qy 42 L e u G l n A s n L e u T h r T h r T y r G l u I l l e V a l L e u T r p G l n P r o V a l T h r A l a A s p L e u 61  
 Db 129 A T A A A G A C T T T G C C A A A A C C A A T G A G C T T G A C T T C T G T A T C C A G G T G C C A C C C A C C A C 188

Qy 62 I l e V a l l y S y s L y s G l n V a l H i s P h e P h e V a l A s n A l a S e r A s p V a l A s p A s n V a l l y s 81  
 Db 189 G T A G C T C T A A T A T G A T G T G G A T T T C C G A G T T A G T G A A G A A G A A T C C C A A G C C A G C C A G 248  
 Qy 82 A l a H i s L e u A s n V a l S e r G l y I l l e P r o C y s S e r V a l L e u L e u A l a A s p V a l G l u A s p L e u 101  
 Db 249 T C T G C C T T G A T C A A A T A A A A T G C A C T A T G A A A T C T T G A T C A T G A T C T A C A A G A A G A G 308  
 Qy 102 I l e G l n G l n I l l e S e r - - - A s n A s p T h r V a l S e r P r o A r g A l a S e r A l a S e r T y r T y r 120  
 Db 309 A T T G A G A A C A G T T T G A T T T A A A G A A G A T A T C C A G G C A G G C A C A G C - - - - - T A C 359  
 Qy 121 G l u G l n T y r H i s S e r L e u A s n G l u I l l e T y r S e r T r p I l e G l u P h e I l l e T h r G l u A r g H i s 140  
 Db 360 G C A A A A T A C A A T A A T T G G G A A A G A T T G T G C T T G G A C T G A A A G A T G A T G A T A A G A T 419  
 Qy 141 P r o A s p M e t L e u T h r L y s I l l e H i s I l l e G l y S e r S e r P h e G l u L y s T y r P r o L e u T y r V a l 160  
 Db 420 C C T G A A A T G T C T C T G A T T A A A A T T G G A T T A C T A C T T G A A G A T A T C C A C T A T A T G T T 479  
 Qy 161 L e u L y s V a l S e r G l y L y s G l u G l n T h r A l a L y s A s n A l a I l e T r p I l e A s p C y s G l y I l l e 180  
 Db 480 C T G A A G A T T - - - G G G G A A A A G A A T G A A A G A A A G C T A T T T T A T G G A T T G T G C A T T 536  
 Qy 181 H i s A l a A r g G l u T r p I l l e S e r P r o A l a P h e C y s L e u T r p P h e I l l e - - - - - 195  
 Db 537 C A C G C A C G A A T G G G T C T C C C A G C A T T C C C A G T G T T G T C T A T A C A G G C A A C A A A 596  
 Qy 195 - - - - - 195  
 Db 597 A C T T A T G G G A A A C A A A A T T A T G A C C A A A C T C T T G G A C C G A A T G A A T T T T A C A T T C T T 656  
 Qy 196 - - - - - G l y H i s - - - - - A n A r g M e t T r p A r g L y s 203  
 Db 657 C C T G T G T T C A A T G T T G A T G A T A T A T T T G C T A T G G A C A A A A G A A C C G C A T G T G G A G A A A 716  
 Qy 204 A s n A r g S e r P h e T y r A l a A s n A s n H i s C y s I l l e G l y T h r A s p L e u A s n S e r A s n P h e V a l 223  
 Db 717 A A T C G T T C C A A G A A C C A A A A C T C C A A T G C A T C G G C A C T G A C C T C A A C A G A A T T T T - - - 773  
 Qy 224 S e r L y s H i s T r p C y s G l u G l u G l y A l a S e r S e r S e r C y s S e r G l u T h r T y r C y s G l y 243  
 Db 774 A A T G C T T C A T G G A A C T C C A T T C C T A C A C C A A T G A C C C A T G T G C A G A T A C T A T C G G G C 833  
 Qy 244 L e u T y r P r o G l u S e r G l u P r o G l u V a l l y A l a V a l A l a S e r P h e L e u A r g A r g A s n I l e 263  
 Db 834 T C T G C A C C A G A T C C G A G A A A G A G A C G A A A G C T G T C A T A A T T T C A T T A G A A G C C A C C T G 893  
 Qy 264 A s n G l n I l l e L y s A l a T y r I l l e S e r M e t H i s S e r T y r S e r G l n H i s I l l e V a l P h e P r o T y r 283  
 Db 894 A A T G A A A T C A A G G T T T A C A T C A C C T T C C A T T C C T A C T C C C A G A T G C T A T T G T T T C C C T A T 953  
 Qy 284 S e r T y r T h r A r g S e r L y s S e r L y s A s p H i s G l u L e u S e r L e u V a l A l a S e r G l u A l a 303  
 Db 954 G G A T A T A C A T C A A A A C T G C C A C C A C C A T A C C A T G A G A C T T G C C A A A G T T G C A A A G A T T G G C 1013  
 Qy 304 V a l a r g A l a l e A s p L y s T h r S e r L y s A s n T h r A r g T y r T h r H i s G l y H i s G l y S e r G l u 323  
 Db 1014 A C T G A T G T T C T A - - - T C A A C T C G A T A T G A A A C C G C T A C A T C T A T G C C C A A T A G A A T C A 1070  
 Qy 324 T h r L e u T y r L e u A l a P r o G l y G l y A s p A s o T r p I l l e T y r A s p L e u G l y I l l e V a l P h e T y r 343  
 Db 1071 A C A A T T T A C C G A T A T C A G G T T C T T C T T A G A C T G G C T T A T G A C C T G G G C A T C A A A C A C 1130  
 Qy 344 S e r P h e 345  
 Db 1131 A C A T T T 1136  
 RESULT 14  
 US-10-116-802-95  
 ; Sequence 95, Application US/10116802  
 ; Publication No. US20030065157A1

```

; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 95
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1656674CB1
US-10-116-802-95

Alignment Scores:
Pred. No.: 3,876-66 Length: 1740
Score: 620.50 Matches: 130
Percent Similarity: 54.19% Conservative: 77
Best Local Similarity: 34.03% Mismatches: 128
Query Match: 32.47% Indels: 47
DB: 14 Gaps: 8

US-09-980-881A-2 (1-360) x US-10-116-802-95 (1-1740)

QY 5 SerLeuAlaValLeuValProLeuPheCysGluGlnHisValPheAla----- 22
DB 3 ACCATGAGGCTCATCTGCTGCTGGTGTGATGTGCTACCATCTTGCATTTGCTCCTGTC 62
QY 23 ---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal 41
DB 63 CGCTTTGACAGGAGAGAGGTGTTCCGCGTGAAGCCCGAGGATGAAAGAACAGCAGCATC 122
QY 42 LeuGlnAsnLeuThrThrThrThrGluLeuValLeuValLeuValProValThrAlaAspLeu 61
DB 123 ATAAAGGACTTGGCCAAAACCAATGAGCTTGACTTCTGTATCCAGGTCGCCACCCACCAC 182
QY 62 IleValLyLysLysGlnValHisPheValAsnAlaSerValAspValValLys 81
DB 183 GTAGCTGCTAATATGATGTGGATTTCCAGTTAGTGAGAGGAATCCCAAGCCATCCAG 242
QY 82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101
DB 243 TCTGCCTTGCATCAAAATAAATGCATATGAAATCTTGATTCATGATCTACAAGAAGAG 302
QY 102 IleGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerThrTy 120
DB 303 ATTGAGAAACAGTTTGTGTTAAAGAAGATATCCCGAGGAGGACACAGC-----TAC 353
QY 121 GluGlnTyHisSerLeuAsnGluIleTySerTriPheIleGluPheIleThrGluArgHis 140
DB 354 GCAAAATACAAATAATTCGGAAAGATTTGGCTTGAGCTGAAAGATGATGATAAGTAT 413
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTyVal 160
DB 414 CCTGAATGCTCTCTCGTATTAATTTGGATCTACTGTTGAAGATAATCCACTATATGTT 473
QY 161 LeuLyValSerGlyLysGluGlnThrAlaLysAlaIleThrIleAspCysGlyIle 180
DB 474 CTGAAGATT---GGGGAAGAAATGAAGAAGAGGCTATTTTATGATTTGTGCAATT 530
QY 181 HisAlaArgGluThrIleSerProAlaPheCysLeuThrPheIle----- 195
DB 531 CACGCACGAGATGGGTCTCCCGAGCATTTCTGCCAGTGGTTGTCTATCAGGCAACCAA 590
QY 195 ----- 195
DB 591 ACTTATGGGAGAAACAAATATGACCACCAACTCTTGACCGAATGAATTTTACATTTCTT 650
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QY 196 -----GlyHis-----AsnArgMetTrpArgLys 203
DB 651 CCTGTGTTCAATGTTGATGATATATTTGGTGTATGAGCAAGAACCGCATGTGGAGAAA 710
QY 204 AsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
DB 711 AATCGTTTCCAAGAACCAAACTCCAAATGTCATCGGCACTGACCTCAACAGAAATTTT 767
QY 224 SerLyHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyCysGly 243
DB 768 AATGCTTCATGGAACCTCCATTCCTAAACCAATGACCCATGTCAGATACTATCGGGGC 827
QY 244 LeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263
DB 828 TCTGCACAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTTATTAGAACCCACCTG 887
QY 264 AsnGlnIleLysAlaTyIleSerMetHisSerTySerGlnHisIleValPheProTy 283
DB 888 AATGAAATCAAGGTTTACATCCCTTCATTCCTACCTCCAGATGCTATTTTCCCTAT 947
QY 284 SerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
DB 948 GGATATATCATCAAACTCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAGATTGGC 1007
QY 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyThrHisGlySerGlu 323
DB 1008 ACTGATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGACCTGGCCCAATGAATCA 1064
QY 324 ThrLeuTyLeuAlaProGlyGlyAspAspTrpIleTyAspLeuGlyIleLysTy 343
DB 1065 ACAATTTTACCAGATATCAGGTTCTTTTATGACTGGGCTTATGACCTGGGCATCAACAC 1124
QY 344 SerPhe 345
DB 1125 ACATTT 1130

RESULT 15
US-10-229-546-3
; Sequence 3, Application US/10229546
; Publication No. US20030082649A1
; GENERAL INFORMATION:
; APPLICANT: Weich, Nadine S.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR
; FILE REFERENCE: MP101-156P1RNM
; CURRENT APPLICATION NUMBER: US/10/229,546
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/316,575
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1254)
US-10-229-546-3

Alignment Scores:
Pred. No.: 2,996-66 Length: 1254
Score: 619.50 Matches: 130
Percent Similarity: 54.07% Conservative: 76
Best Local Similarity: 34.12% Mismatches: 128
Query Match: 32.42% Indels: 47
DB: 14 Gaps: 8

US-09-980-881A-2 (1-360) x US-10-229-546-3 (1-1254)

QY 6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla----- 22
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:31:47 ; Search time 18.2606 Seconds  
(without alignments)  
1227.533 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 338  
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYSPTSNPPVEKLLPLSLK 338

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/prodata/1/1aa/PTUS\_COMB.pep: \*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	55.0	386	4	US-09-813-133A-2
2	175	51.8	423	1	US-07-649-591B-3
3	175	51.8	423	1	US-08-277-540-3
4	175	51.8	423	1	US-08-430-787A-3
5	175	51.8	423	2	US-08-869-057-2
6	146	43.2	423	4	US-09-813-133A-4
7	31	9.2	37	1	US-07-649-591B-1
8	31	9.2	37	1	US-08-277-540-1
9	31	9.2	37	1	US-08-430-787A-1
10	15	4.4	417	1	US-07-649-591B-7
11	15	4.4	417	1	US-08-277-540-7
12	15	4.4	417	1	US-08-430-787A-7
13	12	3.6	247	4	US-09-675-305-6
14	12	3.6	247	4	US-10-200-344-6
15	12	3.6	350	4	US-09-675-305-12
16	12	3.6	350	4	US-10-200-344-12
17	12	3.6	437	4	US-09-675-305-10
18	12	3.6	437	4	US-10-200-344-10
19	11	3.3	86	4	US-09-270-767-56648
20	11	3.3	89	4	US-09-513-999C-7648
21	11	3.3	216	4	US-09-270-767-41427
22	11	3.3	307	2	US-08-782-760-6
23	11	3.3	307	5	PCT-US96-00995-6
24	11	3.3	329	4	US-09-011-769A-51
25	11	3.3	349	4	US-09-011-769A-47
26	11	3.3	349	4	US-09-011-769A-60
27	11	3.3	349	4	US-09-011-769A-64

28	11	3.3	396	1	US-07-649-591B-4	Sequence 4, Appli
29	11	3.3	396	1	US-08-277-540-4	Sequence 4, Appli
30	11	3.3	396	1	US-08-430-787A-4	Sequence 4, Appli
31	11	3.3	415	2	US-08-860-882A-57	Sequence 57, Appl
32	11	3.3	415	4	US-09-011-769A-39	Sequence 39, Appl
33	11	3.3	424	4	US-09-011-769A-56	Sequence 56, Appl
34	11	3.3	613	3	US-09-171-945-113	Sequence 113, App
35	11	3.3	716	3	US-09-171-945-125	Sequence 125, App
36	10	3.0	417	1	US-07-649-591B-6	Sequence 6, Appli
37	10	3.0	417	1	US-08-277-540-6	Sequence 6, Appli
38	10	3.0	417	1	US-08-430-787A-6	Sequence 66, Appl
39	10	3.0	417	4	US-09-517-254-66	Sequence 66, Appl
40	9	2.7	162	4	US-09-248-796A-14973	Sequence 14973, A
41	9	2.7	417	1	US-07-649-591B-8	Sequence 8, Appli
42	9	2.7	417	1	US-08-277-540-8	Sequence 8, Appli
43	9	2.7	417	1	US-08-430-787A-8	Sequence 8, Appli
44	8	2.4	282	3	US-09-412-102-2	Sequence 2, Appli
45	8	2.4	282	3	US-09-217-787-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2  
  
Query Match 55.0%; Score 186; DB 4; Length 386;  
Best Local Similarity 99.7%; Pred. No. 1.8e-175;  
Matches 286; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	FQSGQVLAALPRTSRQVQLNLT	TTT	Y	E	I	V	L	W	Q	P	T	A	D	L	I	V	K	K	Q	V	H	F	F	N	A	S	D	V	N	V	K	A	60														
Db	23	FQSGQVLAALPRTSRQVQLNLT	TTT	Y	E	I	V	L	W	Q	P	T	A	D	L	I	V	K	K	Q	V	H	F	F	N	A	S	D	V	N	V	K	A	82														
QY	61	HLNVSGIPCSVLLADVEDLI	QQQ	I	S	N	D	T	V	S	P	R	A	S	A	S	Y	E	O	V	H	S	L	N	E	I	S	W	I	E	F	I	T	E	R	H	P	120										
Db	83	HLNVSGIPCSVLLADVEDLI	QQQ	I	S	N	D	T	V	S	P	R	A	S	A	S	Y	E	O	V	H	S	L	N	E	I	S	W	I	E	F	I	T	E	R	H	P	142										
QY	121	MLTKIHIGSSF	E	K	P	L	Y	V	L	V	K	S	G	E	O	T	A	K	N	A	I	W	D	C	G	I	H	A	R	E	W	I	S	P	A	F	C	L	W	I	G	H	N	M	W	180		
Db	143	MLTKIHIGSSF	E	K	P	L	Y	V	L	V	K	S	G	E	O	T	A	K	N	A	I	W	D	C	G	I	H	A	R	E	W	I	S	P	A	F	C	L	W	I	G	H	N	M	W	202		
QY	181	KNRSFYANNHCIT	G	D	L	N	R	N	F	A	S	K	H	W	C	E	G	A	S	S	S	S	S	C	S	E	T	C	G	L	Y	P	E	S	E	P	E	V	K	A	V	A	S	F	L	R	N	240
Db	203	KNRSFYANNHCIT	G	D	L	N	R	N	F	A	S	K	H	W	C	E	G	A	S	S	S	S	S	C	S	E	T	C	G	L	Y	P	E	S	E	P	E	V	K	A	V	A	S	F	L	R	N	262
QY	241	INOIKAYISMHSY	Q	H	I	V	P	P	Y	S	T	R	S	K	S	K	D	H	E	L	S	L	V	A	S	E	A	V	R	A	I	E	K	287														
Db	263	INOIKAYISMHSY	Q	H	I	V	P	P	Y	S	T	R	S	K	S	K	D	H	E	L	S	L	V	A	S	E	A	V	R	A	I	E	K	309														

RESULT 2  
US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:

;; APPLICANT: Dennis Drayna and Daniel Eaton  
;; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
;; NUMBER OF SEQUENCES: 8  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 460 Point San Bruno Blvd  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: patin (Genentech)

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/649,591B

;; FILING DATE: 19910201

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hasak, Janet E.

;; REGISTRATION NUMBER: 28,616

;; REFERENCE/DOCKET NUMBER: 689

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 415/266-1896

;; TELEFAX: 415/952-9881

;; TELEX: 910/371-7168

;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 423 amino acids

;; TYPE: AMINO ACID

;; TOPOLOGY: linear

US-07-649-591B-3

Query Match 51.8%; Score 175; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.5e-164;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTTADLVKKQVHFFVNASDNDVKA 60

Db 23 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTTADLVKKQVHFFVNASDNDVKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 120

Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKPYLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 175

Db 143 MLTKIHGSSFEKPYLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 197

## RESULT 3

US-277-540-3

;; Sequence 3, Application US/08277540

;; Patent No. 547901

;; GENERAL INFORMATION:

;; APPLICANT: Drayna, Dennis T., Eaton, Dan L.

;; TITLE OF INVENTION: No. 547901el Plasma Carboxypeptidase

;; NUMBER OF SEQUENCES: 8

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Genentech, Inc.

;; STREET: 460 Point San Bruno Blvd

;; CITY: South San Francisco

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94080

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: patin (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/277,540  
;; FILING DATE: 19-JUL-1994  
;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/167727

;; FILING DATE: 15-DEC-1993

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 07/959944

;; FILING DATE: 14-OCT-1992

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 07/649591

;; FILING DATE: 01-FEB-91

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hasak, Janet E.

;; REGISTRATION NUMBER: 28,616

;; REFERENCE/DOCKET NUMBER: 689D1C1D1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 415/225-1896

;; TELEFAX: 415/952-9881

;; TELEX: 910/371-7168

;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 423 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

US-08-277-540-3

Query Match 51.8%; Score 175; DB 1; Length 423;

Best Local Similarity 100.0%; Pred. No. 1.5e-164;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTTADLVKKQVHFFVNASDNDVKA 60

Db 23 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTTADLVKKQVHFFVNASDNDVKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 120

Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKPYLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 175

Db 143 MLTKIHGSSFEKPYLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 197

## RESULT 4

US-08-430-787A-3

;; Sequence 3, Application US/08430787A

;; Patent No. 5593674

;; GENERAL INFORMATION:

;; APPLICANT: Drayna, Dennis T., Eaton, Dan L.

;; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase

;; NUMBER OF SEQUENCES: 8

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Genentech, Inc.

;; STREET: 460 Point San Bruno Blvd

;; CITY: South San Francisco

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94080

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: patin (Genentech)

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/430,787A

;; FILING DATE: 27-APR-1995

;; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/277,540

;; FILING DATE: 19-JUL-1994

APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-3

Query Match 51.8%; Score 175; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.5e-164;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTDLIIVKKQVHFFVNASDVNDVKA 60  
DB 23 FSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTDLIIVKKQVHFFVNASDVNDVKA 82

QY 61 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 120  
DB 83 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 142

QY 121 MLTKIHGSSFEKPYLYVLKVSQKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 175  
DB 143 MLTKIHGSSFEKPYLYVLKVSQKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 197

RESULT 5  
US-08-869-057-2  
Sequence 2, Application US/08869057  
Patent No. 5985562  
GENERAL INFORMATION:  
APPLICANT: Morser, Michael J  
APPLICANT: Nagashima, Mariko  
TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
TITLE OF INVENTION: Risk  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
TISSUE TYPE: Plasma  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 23..401  
US-08-869-057-2

Query Match 51.8%; Score 175; DB 2; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.5e-164;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTDLIIVKKQVHFFVNASDVNDVKA 60  
DB 23 FSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTDLIIVKKQVHFFVNASDVNDVKA 82

QY 61 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 120  
DB 83 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 142

QY 121 MLTKIHGSSFEKPYLYVLKVSQKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 175  
DB 143 MLTKIHGSSFEKPYLYVLKVSQKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 197

RESULT 6  
US-09-813-133A-4  
Sequence 4, Application US/09813133A  
Patent No. 6455294  
GENERAL INFORMATION:  
APPLICANT: Gan, Weinu et al  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL001173  
CURRENT APPLICATION NUMBER: US/09/813,133A  
CURRENT FILING DATE: 2001-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 423  
TYPE: PRT  
ORGANISM: Human  
US-09-813-133A-4

Query Match 43.2%; Score 146; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 6.7e-136;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTDLIIVKKQVHFFVNASDVNDVKA 60  
DB 23 FSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTDLIIVKKQVHFFVNASDVNDVKA 82

QY 61 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 120  
DB 83 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 142

QY 121 MLTKIHGSSFEKPYLYVLKVSQKEQ 146  
DB 143 MLTKIHGSSFEKPYLYVLKVSQKEQ 168

RESULT 7  
US-07-649-591B-1  
Sequence 1, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:

```
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-649-591B-1

Query Match          9.2%; Score 31; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.4e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQSGQVLAALPRTSRQVQLNLTITTYEIVL 31
Db      1 FQSGQVLAALPRTSRQVQLNLTITTYEIVL 31

RESULT 8
US-08-277-540-1
; Sequence 1, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-277-540-1

Query Match          9.2%; Score 31; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.4e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQSGQVLAALPRTSRQVQLNLTITTYEIVL 31
Db      1 FQSGQVLAALPRTSRQVQLNLTITTYEIVL 31

RESULT 9
US-08-430-787A-1
; Sequence 1, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
```

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-1

Query Match 9.2%; Score 31; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 3.4e-23; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSGQVLAALPRTSRQVQLQLTTTYEIVL 31  
Db 1 FQSGQVLAALPRTSRQVQLQLTTTYEIVL 31

RESULT 10  
US-07-649-591B-7  
Sequence 7, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:  
APPLICANT: Dennis Drayna and Daniel Eaton  
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-649-591B-7

Query Match 4.4%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 DCGIHAREWISPAFC 169  
Db 172 DCGIHAREWISPAFC 186

RESULT 11  
US-08-277-540-7  
Sequence 7, Application US/08277540  
Patent No. 5474901  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.

TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,540  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-277-540-7

Query Match 4.4%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 DCGIHAREWISPAFC 169  
Db 172 DCGIHAREWISPAFC 186

RESULT 12  
US-08-430-787A-7  
Sequence 7, Application US/08430787A  
Patent No. 5593674  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A

```

, FILING DATE: 27-APR-1995
, CLASSIFICATION: 514
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/277,540
, FILING DATE: 19-JUL-1994
, APPLICATION NUMBER: 08/167727
, FILING DATE: 15-DEC-1993
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 07/959944
, FILING DATE: 14-OCT-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 07/649591
, FILING DATE: 01-FEB-91
, ATTORNEY/AGENT INFORMATION:
, NAME: Haseak, Janet E.
, REGISTRATION NUMBER: 28,616
, REFERENCE/DOCKET NUMBER: 689D1C1D1
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 415/225-1896
, TELEFAX: 415/952-9981
, TELEX: 910/371-7168
, INFORMATION FOR SEQ ID NO: 7:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 417 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
US-08-430-787A-7

```

```
Query Match      4.4%; Score 15; DB 1; Length 417;
Best Local Similarity 100.0%; Fred.No. 2.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels
```

---

```
QY    155 DCGIHAREWISPAFC 169
       ||| ||||| |||||
Db     172 DCGIHAREWISPAFC 186
```

```

RESULT 13
US-09-675-305-6
; Sequence 6, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRt
; ORGANISM: homo sapiens
US-09-675-305-6

```

```

Query Match      3.6%; Score 12; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      153 WIDCGIHAREWI 164
         |||||
Db       190 WIDCGIHAREWI 201

```

RESULT 14

```

US-10-200-344-6
; Sequence 6, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-200-344-6

```

```

Query Match      3.6%; Score 12; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WIDCGIHAREWI 164
      |||||
Db 190 WIDCGIHAREWI 201

```

```

RESULT 15
US-09-675-305-12
; Sequence 12, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 350
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-12

```

Query Match	3.8%;	Score 12;	DB 4;	Length 350;
Best Local Similarity	100.0%;	Pred. No.	0.0016;	
Matches 12;	Conservative	0;	Mismatches	0;
Indels				
Gaps				
Qy	153	WIDCGIHAREWI	164	
Db	190	WIDCGIHAREWI	201	

Search completed: October 27, 2004, 01:53:58  
Job time : 18.2606 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:41:12 ; Search time 44.3983 Seconds  
(without alignments)  
2464.743 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 338  
Sequence: 1 FOSGQVLAALPRTSRQVQL.....IKYSFTSNPPVKKLLPLSLK 338

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1364641 seqs, 323758627 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	55.0	386	9 US-09-813-133A-2	Sequence 2, Appli
2	186	55.0	386	14 US-10-212-877-2	Sequence 2, Appli
3	175	51.8	423	14 US-10-379-836-17	Sequence 17, Appl
4	149	44.1	211	9 US-09-925-302-467	Sequence 467, App
5	149	44.1	211	10 US-09-925-302-467	Sequence 467, App
6	146	43.2	322	15 US-10-115-479-64	Sequence 64, Appl
7	146	43.2	322	9 US-10-115-479-64	Sequence 4, Appli
8	146	43.2	423	14 US-09-813-133A-2	Sequence 4, Appli
9	140	41.4	354	15 US-10-115-479-66	Sequence 66, Appl
10	140	41.4	428	15 US-10-115-479-68	Sequence 68, Appl
11	140	41.4	428	15 US-10-115-479-70	Sequence 70, Appl
12	60	17.8	423	14 US-10-379-836-2	Sequence 2, Appli
13	27	8.0	422	14 US-10-379-836-18	Sequence 18, Appl

14	26	7.7	422	14	US-10-379-836-16	Sequence 16, Appl
15	12	3.6	210	16	US-10-363-829-401	Sequence 401, App
16	12	3.6	247	13	US-10-200-344-6	Sequence 6, Appli
17	12	3.6	315	9	US-09-888-615-60	Sequence 60, Appl
18	12	3.6	350	13	US-10-200-344-12	Sequence 12, Appl
19	12	3.6	434	16	US-10-477-515-2	Sequence 2, Appli
20	12	3.6	437	13	US-10-200-344-10	Sequence 10, Appl
21	12	3.6	437	14	US-10-274-639-12	Sequence 12, Appl
22	12	3.6	437	15	US-10-333-574-12	Sequence 128, App
23	12	3.6	437	17	US-10-757-262-128	Sequence 274, App
24	11	3.3	118	15	US-10-074-978A-274	Sequence 48, Appl
25	11	3.3	231	15	US-10-074-978A-48	Sequence 50, Appl
26	11	3.3	231	15	US-10-074-978A-50	Sequence 52, Appl
27	11	3.3	231	15	US-10-074-978A-52	Sequence 46, Appl
28	11	3.3	349	15	US-10-074-978A-46	Sequence 20, Appl
29	11	3.3	402	14	US-10-379-836-20	Sequence 266, App
30	11	3.3	416	15	US-10-074-978A-266	Sequence 267, App
31	11	3.3	417	15	US-10-074-978A-267	Sequence 268, App
32	11	3.3	417	15	US-10-074-978A-268	Sequence 3, Appli
33	11	3.3	417	16	US-10-477-515-3	Sequence 113, App
34	11	3.3	613	9	US-09-910-059-113	Sequence 4, Appli
35	11	3.3	613	16	US-10-608-710-4	Sequence 125, App
36	11	3.3	716	9	US-09-910-059-125	Sequence 6143, Ap
37	10	3.0	180	14	US-10-106-698-6143	Sequence 54, Appl
38	10	3.0	231	15	US-10-074-978A-54	Sequence 1959, Ap
39	10	3.0	286	16	US-10-408-765A-1959	Sequence 20, Appl
40	10	3.0	310	16	US-10-470-390A-20	Sequence 61, Appl
41	10	3.0	374	9	US-09-888-615-61	Sequence 270, App
42	10	3.0	416	15	US-10-074-978A-270	Sequence 2, Appli
43	10	3.0	417	14	US-10-229-546-2	Sequence 9, Appli
44	10	3.0	417	14	US-10-229-546-9	Sequence 188, App
45	10	3.0	417	14	US-10-341-434-188	

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match 55.0%; Score 186; DB 9; Length 386;  
Best Local Similarity 99.7%; Pred. No. 5.1e-171;  
Matches 286; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	FOSGQVLAALPRTSRQVQLNLTYYEIVLPQVTADLVKKQVHFFVFNASDVNVKA	60
Db	23	FOSGQVLAALPRTSRQVQLNLTYYEIVLPQVTADLVKKQVHFFVFNASDVNVKA	82
Qy	61	HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYRQYHSLNIYWIETTERHPD	120
Db	83	HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYRQYHSLNIYWIETTERHPD	142
Qy	121	MLTKIHGSGFEPKYPYLVKVSKEQTAKNAWIDCGIHAREWISPAFCWPIGHNRMWR	180
Db	143	MLTKIHGSGFEPKYPYLVKVSKEQTAKNAWIDCGIHAREWISPAFCWPIGHNRMWR	202

Qy	181	KNRSFYANNHCIGTDLNRNFASKHWCBEGASSSSCSCTETCGLYPESEPEVKAVASFLRRN	240
Db	203	KNRSFYANNHCIGTDLNRNFASKHWCBEGASSSSCSCTETCGLYPESEPEVKAVASFLRRN	262
Qy	241	INQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEK	287
Db	263	INQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEK	309

RESULT 2

US-10-212-877-2

; Sequence 2, Application US/10212877

; Publication No. US20030017574A1

; GENERAL INFORMATION:

; APPLICANT: GAN, Weiniu et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001173DIV

; CURRENT APPLICATION NUMBER: US/10/212,877

; CURRENT FILING DATE: 2002-08-07

; PRIOR APPLICATION NUMBER: 09/813,133

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 386

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-212-877-2

Query Match	55.0%;	Score 186;	DB 14;	Length 386;
Best Local Similarity	99.7%;	Pred. No. 5,1e-171;		
Matches 286;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	FQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTADLIYKKQVHFVNASDVNDVKA	60
Db	23	FQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTADLIYKKQVHFVNASDVNDVKA	82
Qy	61	HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD	120
Db	83	HLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD	142
Qy	121	MLTKIHIGSSPEKPYLYVLKVSQKEQTAKNAIWDICGIIHAREWISPAFCLWFIHNRWVR	180
Db	143	MLTKIHIGSSPEKPYLYVLKVSQKEQAQNAIWDICGIIHAREWISPAFCLWFIHNRWVR	202
Qy	181	KNRSFYANNHCIGTDLNRNFASKHWCBEGASSSSCSCTETCGLYPESEPEVKAVASFLRRN	240
Db	203	KNRSFYANNHCIGTDLNRNFASKHWCBEGASSSSCSCTETCGLYPESEPEVKAVASFLRRN	262
Qy	241	INQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEK	287
Db	263	INQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEK	309

RESULT 3

US-10-379-836-17

; Sequence 17, Application US/10379836

; Publication No. US20030215850A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON

; TITLE OF INVENTION: TAFI

; FILE REFERENCE: D0214NP

; CURRENT APPLICATION NUMBER: US/10/379,836

; CURRENT FILING DATE: 2003-03-04

; PRIOR APPLICATION NUMBER: U.S. 60/361,523

; PRIOR FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 17

; LENGTH: 423



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; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

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Best Local Similarity 100.0%; Pred. No. 1.8e-135;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 NWRKRSFYANNHCIGTDLNRNFASKWCEGASSSSCSSTCYCGLYPESEPEVKAVAS 235
    |||
Db 23 NWRKRSFYANNHCIGTDLNRNFASKWCEGASSSSCSSTCYCGLYPESEPEVKAVAS 82
    |||

QY 236 FLRRNINQIKAYISMHSYQHIVFPYSTRSKSKOHEELSLVASEAVRAIEKTSKNTRYT 295
    |||
Db 83 FLRRNINQIKAYISMHSYQHIVFPYSTRSKSKOHEELSLVASEAVRAIEKTSKNTRYT 142
    |||

QY 296 HGGSETLYLAPGGDDWIYDLGIKYSFT 324
    |||
Db 143 HGGSETLYLAPGGDDWIYDLGIKYSFT 171
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RESULT 6
US-10-115-479-64
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytak, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678

; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-64

Query Match      43.2%; Score 146; DB 15; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSGQVLAALPRTSRQVQLNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDNDVKA 60
    |||
Db 23 FQSGQVLAALPRTSRQVQLNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDNDVKA 82
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QY 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120
    |||
Db 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142
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QY 121 MLTKIHIGSSFEEKYPLYVLKVSQKEQ 146
    |||
Db 143 MLTKIHIGSSFEEKYPLYVLKVSQKEQ 168
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RESULT 7
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: Gan, Weinui et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Query Match      43.2%; Score 146; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.6e-132;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSGQVLAALPRTSRQVQLNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDNDVKA 60
    |||
Db 23 FQSGQVLAALPRTSRQVQLNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDNDVKA 82
    |||

QY 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120
    |||
Db 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142
    |||

QY 121 MLTKIHIGSSFEEKYPLYVLKVSQKEQ 146
    |||
Db 143 MLTKIHIGSSFEEKYPLYVLKVSQKEQ 168
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RESULT 8
US-10-212-877-4
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; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: NUCLEATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: ISOLATED ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-10-212-877-4

Query Match 43.2%; Score 146; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.6e-132;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNVKA 60
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNVKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKPYLYLVKVSREQ 146
Db 143 MLTKIHGSSFEKPYLYLVKVSREQ 168

RESULT 9
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkers, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
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; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-66

Query Match 41.4%; Score 140; DB 15; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.4e-126;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNVKA 60
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNVKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKPYLYLVK 140
Db 143 MLTKIHGSSFEKPYLYLVK 162

RESULT 10
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
```

```

; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Query Match          41.4%; Score 140; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.7e-126; Indels 0; Gaps 0;
Matches 140; Conservative 0; Mismatches 0;

QY 1 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDVNVKA 60
DB 23 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDVNVKA 82

QY 61 HLNVSIGPCSVLLADVDELIOQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 120
DB 83 HLNVSIGPCSVLLADVDELIOQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 142

QY 121 MLTKIHIGSSFKEKYPYLVK 140
DB 143 MLTKIHIGSSFKEKYPYLVK 162

RESULT 11
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Hainong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.

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; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera E.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-70

Query Match          41.4%; Score 140; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.7e-126; Indels 0; Gaps 0;
Matches 140; Conservative 0; Mismatches 0;

QY 1 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDVNVKA 60
DB 23 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTADLIIVKKQVHFFVNASDVNVKA 82

QY 61 HLNVSIGPCSVLLADVDELIOQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 120
DB 83 HLNVSIGPCSVLLADVDELIOQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 142

QY 121 MLTKIHIGSSFKEKYPYLVK 140
DB 143 MLTKIHIGSSFKEKYPYLVK 162

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US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523

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; PRIOR FILING DATE: 2002-03-04  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 2  
 ; LENGTH: 423  
 ; TYPE: PRT  
 ; ORGANISM: Papio hamadryas  
 US-10-379-836-2

Query Match 17.8%; Score 60; DB 14; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-49;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 75 SDVNVKALNVSGIPCSVLADVEDLIQQOISNDTVSPRASASYEQYHSLNLIYSWIE 134

RESULT 13

; Sequence 18, Application US/10379836  
 ; Publication No. US20030215850A1  
 ; GENERAL INFORMATION:  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
 ; TITLE OF INVENTION: TAFI  
 ; FILE REFERENCE: D0214NP  
 ; CURRENT APPLICATION NUMBER: US/10/379,836  
 ; CURRENT FILING DATE: 2003-03-04  
 ; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
 ; PRIOR FILING DATE: 2002-03-04  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent in version 3.2  
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 ; LENGTH: 422  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-379-836-18

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 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 NDTVSPRASASYEQYHSLNLIYSWIE 112  
 Db 107 NDTVSPRASASYEQYHSLNLIYSWIE 133

RESULT 14

; Sequence 16, Application US/10379836  
 ; Publication No. US20030215850A1  
 ; GENERAL INFORMATION:  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
 ; TITLE OF INVENTION: TAFI  
 ; FILE REFERENCE: D0214NP  
 ; CURRENT APPLICATION NUMBER: US/10/379,836  
 ; CURRENT FILING DATE: 2003-03-04  
 ; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
 ; PRIOR FILING DATE: 2002-03-04  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent in version 3.2  
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 ; LENGTH: 422  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-379-836-16

Query Match 7.7%; Score 26; DB 14; Length 422;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 KNAIWIDCGIHAREWISPAFLWFIG 174  
 Db 170 KNAIWIDCGIHAREWISPAFLWFIG 195

RESULT 15

US-10-363-829-401  
 ; Sequence 401, Application US/10363829  
 ; Publication No. US20040142331A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;  
 ; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;  
 ; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;  
 ; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;  
 ; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;  
 ; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;  
 ; APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;  
 ; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;  
 ; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;  
 ; APPLICANT: Gerstin, Jr., Edward H.; Beralta, Careyna H.;  
 ; APPLICANT: David, Marie H.; Panzer, Scott R.;  
 ; APPLICANT: Flores, Vincent Z.; Daifo, Abel;  
 ; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;  
 ; APPLICANT: Chang, Simon C.; Au, Alan P.;  
 ; APPLICANT: Inman, Rebekah R.  
 ; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT  
 ; FILE REFERENCE: PT-1183 USN  
 ; CURRENT APPLICATION NUMBER: US/10/363,829  
 ; CURRENT FILING DATE: 2003-03-05  
 ; PRIOR APPLICATION NUMBER: PCT/US01/27628  
 ; PRIOR FILING DATE: 2001-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/229,751  
 ; PRIOR FILING DATE: 2000-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/229,749  
 ; PRIOR FILING DATE: 2000-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/229,750  
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 ; PRIOR APPLICATION NUMBER: US 60/229,747  
 ; PRIOR FILING DATE: 2000-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/229,748  
 ; PRIOR FILING DATE: 2000-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/230,583  
 ; PRIOR FILING DATE: 2000-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/230,517  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: US 60/230,610  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: US 60/230,597  
 ; PRIOR FILING DATE: 2000-09-06  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 401  
 ; LENGTH: 210  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No: LG:366783.1.orf1:2000SEP08  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: 102  
 ; OTHER INFORMATION: unknown or other  
 ; OTHER INFORMATION: unknown or other  
 US-10-363-829-401

Query Match 3.6%; Score 12; DB 16; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 0.005;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WIDCGIHAREWI 164  
 Db 48 WIDCGIHAREWI 59

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Job time : 45.3983 secs



GenCore version 5.1.6  
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Perfect score: 338  
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Searched: 824507 seqs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1643622

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	186	55.0	1625	US-09-813-133A-1	Sequence 1, Appli
2	175	51.8	1272	US-08-869-057-1	Sequence 1, Appli
3	175	51.8	1749	US-07-649-591B-2	Sequence 2, Appli
4	175	51.8	1749	US-08-277-540-2	Sequence 2, Appli
5	175	51.8	1749	US-08-430-787A-2	Sequence 2, Appli
6	68	20.1	55827	US-09-813-133A-3	Sequence 3, Appli
7	12	3.6	741	US-09-675-305-5	Sequence 5, Appli
8	12	3.6	741	US-10-200-344-5	Sequence 5, Appli
9	12	3.6	1050	US-09-675-305-11	Sequence 11, Appli
10	12	3.6	1050	US-10-200-344-11	Sequence 11, Appli
11	12	3.6	1311	US-09-675-305-9	Sequence 9, Appli
12	12	3.6	1311	US-10-200-344-9	Sequence 9, Appli

13	12	3.6	2128	4	US-09-675-305-13	Sequence 13, Appli
14	12	3.6	2128	4	US-10-200-344-13	Sequence 13, Appli
15	11	3.3	258	4	US-09-270-767-25119	Sequence 25119, A
16	11	3.3	359	4	US-09-513-999C-3571	Sequence 3571, Ap
17	11	3.3	927	2	US-08-782-760-5	Sequence 5, Appli
18	11	3.3	927	5	PCT-US96-00995-5	Sequence 5, Appli
19	11	3.3	999	2	US-08-860-882A-67	Sequence 67, Appli
20	11	3.3	999	4	US-09-011-769A-50	Sequence 50, Appli
21	11	3.3	1053	2	US-08-860-882A-64	Sequence 64, Appli
22	11	3.3	1053	4	US-09-011-769A-46	Sequence 46, Appli
23	11	3.3	1053	4	US-09-463-451-27	Sequence 27, Appli
24	11	3.3	1053	4	US-09-463-451-28	Sequence 28, Appli
25	11	3.3	1059	2	US-08-860-882A-74	Sequence 74, Appli
26	11	3.3	1059	2	US-08-860-882A-77	Sequence 77, Appli
27	11	3.3	1059	4	US-09-011-769A-59	Sequence 59, Appli
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33	11	3.3	1284	4	US-09-011-769A-55	Sequence 55, Appli
34	11	3.3	1870	3	US-09-171-945-112	Sequence 112, App
35	11	3.3	2154	3	US-09-171-945-124	Sequence 124, App
36	10	3.0	1622	4	US-09-023-655-1020	Sequence 1020, Ap
37	9	2.7	486	4	US-09-248-796A-870	Sequence 870, App
38	8	2.4	873	4	US-09-583-110-2322	Sequence 2322, Ap
39	8	2.4	882	4	US-09-252-991A-11174	Sequence 11174, A
40	8	2.4	918	4	US-09-252-991A-11018	Sequence 11018, A
41	8	2.4	1113	4	US-09-252-991A-11239	Sequence 11239, A
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44	8	2.4	1347	3	US-09-412-102-1	Sequence 1, Appli
45	8	2.4	1347	3	US-09-217-787-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinliu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 4.61e-187 Length: 1625  
Score: 186.00 Matches: 322  
Percent Similarity: 98.77% Conservative: 0  
Best Local Similarity: 98.77% Mismatches: 2  
Query Match: 55.03% Indels: 4  
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

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Qy	21	GlnAsnLeuThrThrThrTyrGluLeuValLeuTrpGlnProValThrAlaLeuLeu	40

Db 143 CAGAACTCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTACACAGCTGACCTTATT 202  
Qy 41 VallyslylsGlnValHisPhePheValAsnAlaSerValAspAsnValLysAla 60  
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Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTACAAAAATCCCAATGGATCTCTATTGAGAAGTACCCACTCTATGTTTTAAAG 502  
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Db 503 GTTCTCGAAAGAACAAAGC-AGCCAAAATGCCATATGGATTGACTGTGAATCCATGC 561  
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Db 562 CAGAGAATGGATCTCTCTGCTTCTGTTGTTGATAGGCCATATCGAATGTGGAG 621  
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Db 622 AAGAAGCGTTCCTTCTATGGAACAATCATTTGATCGGAACAGACCTGGAATGAAGACTT 681  
Qy 200 eAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCy 220  
Db 682 TGCTTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTG 741  
Qy 220 sGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAs 240  
Db 742 TGGACTTTATCTCTGAGTCAGAACAGAGAGTGAAGCAGTGGCTAGTGTCTTGAAGAAA 801  
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Db 981 CAGAAACCTTATACCTAGCTCTGAGGTGGGACGATTTGATCTATGATTTGGGCATCA 1040  
Qy 320 yTyrSerPheThr 324  
Db 1041 AATATTCGTTTACA 1054

## RESULT 2

US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; PUBLICATION INFORMATION:  
; AUTHORS: Eaton, Dan L.  
; AUTHORS: Malloy, Beth E.  
; AUTHORS: Tsai, Siao P.  
; AUTHORS: Henzel, William  
; AUTHORS: Dravna, Dennis  
; TITLE: Isolation, Molecular Cloning, and Partial  
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B  
; JOURNAL: J. Biol. Chem.  
; VOLUME: 266  
; ISSUE: 32  
; PAGES: 21833-21838  
; DATE: No. 5985562 15-1991  
; US-08-869-057-1

Alignment Scores:  
Pred. No.: 1.59e-175 Length: 1272  
Score: 175.00 Matches: 175  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.78% Indels: 0  
DB: 2 Gaps: 0

US-09-980-881A-3 (1-338) x US-08-869-057-1 (1-1272)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 67 TTTCAGAGTGGCCAAAGTCTAGTGTCTTCTTAGAACCTCTTAGGCAAGTTCAGGTCTA 126  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuile 40  
Db 127 CAGAACTTACTACACATATGAGATTGTTCTCTGGCAGCGGTACAGCTGACCTTATT 186  
Qy 41 VallyslylsGlnValHisPhePheValAsnAlaSerValAspAsnValLysAla 60  
Db 187 GTGAAGAAAAACAAGTCCATTTTTTTTGAATGCATCTGATGTGCAATGTGAAAGCC 246  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuile 80  
Db 247 CATTTAAATGTGACGGAATTCATGAGTGTCTTGTGCGACGCTGGAAGATCTTATT 306  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100



Db 307 CAACAGCAGATTTCACAGACACAGCTCAGCCCGGAGCTCGCATCTGCTATGAAACAG 366  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 367 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAAATGAGAGGATCCCTGAT 426  
Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 427 ATGCTTACAAAATACCATGAGTCCCTATTGAGAGTACCCACTCTATGTTTAAAG 486  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 487 GTTCTGGAAAAGAAACAAACAGCCAAAATGCGATATGATGACTGTGGAATCCATGCC 546  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 547 AGAGAATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCAT 591

## RESULT 3

US-07-649-591B-2

; Sequence 2, Application US/07649591B  
; Patent No. 5206161

; GENERAL INFORMATION:

; APPLICANT: Dennis Drayna and Daniel Eaton

; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/649,591B

; FILING DATE: 19910201

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 689

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/266-1896

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1749 bases

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: hybridization probe

; LOCATION: 133 to 178

; IDENTIFICATION METHOD:

; OTHER INFORMATION:

; FEATURE:

; NAME/KEY: potential clip site

; LOCATION: 380 to 382

; IDENTIFICATION METHOD:

; OTHER INFORMATION:

; FEATURE:

; NAME/KEY: signal sequence

; LOCATION: 41 to 106

; IDENTIFICATION METHOD:

## OTHER INFORMATION:

US-07-649-591B-2

Alignment Scores:

Pred. No.: 2,188-175 Length: 1749

Score: 175.00 Matches: 175

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 51.78% Indels: 0

DB: 1 Gaps: 0

US-09-980-881A-3 (1-338) x US-07-649-591B-2 (1-1749)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTCCAGAGTGGCCCAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166  
Qy 21 GlnAsnLeuThrThrThrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 167 CAGAACTTTACTACAAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226  
Qy 41 ValIleLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 227 GTGAGAGAAAAACAAAGTCCATTTTTTTGTAATGCAATCTGATGTCACAAATGTGAAGCC 286  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 287 CATTTAAATGTGAGCGGAATTCATGCACTGCTTGTGGCAGAGCTGGAAGATCTTATT 346  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTCACAGACACACAGTCCAGCCCGGAGCTCCGCACTCGTACTATGAACAG 406  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAAATGAGAGGATCTCTGAT 466  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 467 ATGCTTACAAAATCCACATTCCTCATTTGAGAAAGTACCACCTCTATGTTTAAAG 526  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 527 GTTCTGGAAAAGAAACAAACAGCCAAAATGCGATATGATGACTGTGGAATCCATGCC 586  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 587 AGAGAATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCAT 631

## RESULT 4

US-08-277-540-2

; Sequence 2, Application US/08277540

; Patent No. 5474901

; GENERAL INFORMATION:

; APPLICANT: Drayna, Dennis T., Eaton, Dan L.

; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/277,540

; FILING DATE: 19-JUL-1994

; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-277-540-2

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Alignment Scores:
Pred. No.: 2.18e-175 Length: 1749
Score: 175.00 Matches: 175
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.78% Indels: 0
DB: 1 Gaps: 0

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US-09-980-881A-3 (1-338) x US-08-277-540-2 (1-1749)

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Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 107 TTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166

Qy 21 GlnAsnLeuThrThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40
Db 167 CAGAATCTTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226

Qy 41 VallysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db 227 GTGAAGAAAAACAAGTCCATTTTTTTGTAATGCATCTGATGTCGACAAATGTGAAAGCC 286

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80
Db 287 CATTTAAATGAGCGGAAATTCATGACAGTCTCTGCGCAGACGTGGAAAGATCTTATT 346

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTCACACGACACAGTCAGCCCGCAGCCTCCGCATCCGTACTATGAACAG 406

Qy 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheLeuThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAATCTATTCTTTGGATGAATTTATTAACCTGAGAGCATCTCTGAT 466

Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 467 ATGCTTACAAAAATCCATTGGATTCCTCATTTGAGAAAGTACCCACTCTATGTTTTTAAG 526

Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 527 GTTTCTGAAAGAAACAAACAGCCAAATATGCCATATGATGATTGACTGTGGAATCCATGCC 586

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175
Db 587 AAGAATGGATCTCTCTCGCTTCTTGCTTGGTTTTCATAGGCCAT 631

RESULT 5
US-08-430-787A-2

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; Sequence 2, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-430-787A-2

Alignment Scores:
Pred. No.: 2.18e-175 Length: 1749
Score: 175.00 Matches: 175
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.78% Indels: 0
DB: 1 Gaps: 0

US-09-980-881A-3 (1-338) x US-08-430-787A-2 (1-1749)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 107 TTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166

Qy 21 GlnAsnLeuThrThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40
Db 167 CAGAATCTTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226

Qy 41 VallysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db 227 GTGAAGAAAAACAAGTCCATTTTTTTGTAATGCATCTGATGTCGACAAATGTGAAAGCC 286

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80

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Db 287 CATTAAATGTGAGCGGAATTCATGACGTGCTTCTGGCAGAGTGGGAAGATCTTATT 346  
Qy 81 GlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTCACAGACACAGTCAGCCCCCGAGCTCCGCATCGTACTATGACAG 406  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAATTATTAAGTGAAGGCATCCTGAT 466  
Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 467 ATGCTTACAAAATCCACATTCGATCCTCATTTGAGAGTACCCTCTATGTTTTAAAG 526  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 527 GTTCTGGAAAAGAACAAACAGCCAAAATGCCATATGATGACTGTGGAATTCATGCC 586  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 587 AGAGAAATGGATCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 631

## RESULT 6

US-09-813-133A-3  
; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:

; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 55827  
; TYPE: DNA  
; ORGANISM: Human

Alignment Scores:  
Pred. No.: 1,19e-60 Length: 55827  
Score: 68.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.12% Indels: 0  
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-813-133A-3 (1-55827)

Qy 207 GluGluGlyValaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 226  
Db 48643 GAGGAAGTGATCCAGTCTCTATGCTGGAACCTACTGTGACTTTTATCTGAGTCA 48702  
Qy 227 GluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 246  
Db 48703 GAACCAAGAGTGAAGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAAGATTAAGCA 48762  
Qy 247 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 266  
Db 48763 TACATCAGCATGATTTCTATCATCTCCAGCATATAGTGTTCATATTCCTATACACGAAGT 48822  
Qy 267 LysSerLysAspHisGluGluLeu 274  
Db 48823 AAAAGCAAAACACCATGAGGAAGT 48846

## RESULT 7

US-09-675-305-5  
; Sequence 5, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: NO. 6441153el Human Carboxypeptidases and  
; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 741  
; TYPE: DNA  
; ORGANISM: homo sapiens

US-09-675-305-5

Alignment Scores:  
Pred. No.: 0.00304 Length: 741  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.55% Indels: 0  
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-675-305-5 (1-741)

Qy 153 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 164

Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGATT 603

## RESULT 8

US-10-200-344-5  
; Sequence 5, Application US/10200344  
; Patent No. 6780640  
; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: NO. 6780640el Human Carboxypeptidases and  
; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/10/200,344  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 741  
; TYPE: DNA  
; ORGANISM: homo sapiens

US-10-200-344-5

Alignment Scores:  
Pred. No.: 0.00304 Length: 741  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.55% Indels: 0  
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-200-344-5 (1-741)

Qy 153 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 164



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US-10-200-344-9
Alignment Scores:
Pred. No.: 0.00535 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.55% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-200-344-9 (1-1311)
Qy 153 TptileAspCysGlyIleHisAlaArgGluTrpIle 164
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 13
US-09-675-305-13
; Sequence 13, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambricwicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-13

Alignment Scores:
Pred. No.: 0.00865 Length: 2128
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.55% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-675-305-13 (1-2128)
Qy 153 TptileAspCysGlyIleHisAlaArgGluTrpIle 164
Db 933 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 968

RESULT 14
US-10-200-344-13
; Sequence 13, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambricwicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
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; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-13

Alignment Scores:
Pred. No.: 0.00865 Length: 2128
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.55% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-200-344-13 (1-2128)
Qy 153 TptileAspCysGlyIleHisAlaArgGluTrpIle 164
Db 933 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 968

RESULT 15
US-09-270-767-25119
; Sequence 25119, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25119
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-25119

Alignment Scores:
Pred. No.: 0.0122 Length: 258
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.25% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-270-767-25119 (1-258)
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAla 167
Db 127 GGCATCCACGCCCGCAATGGATCAGCCCCCGC 159

Search completed: October 27, 2004, 06:09:16
Job time : 111.797 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 27, 2004, 04:49:14 ; Search time 455.441 Seconds  
(without alignments)  
3805.390 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 338  
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYFTSNPPVEXKLPLSLK 338

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues  
Word size: 1

Total number of hits satisfying chosen parameters: 6817637

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Published Applications NA -QWMT=fastap -SUFFIX=oli.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1  
-ALIGN=15 -MODES=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US0980881@cgn\_1\_1034\_@runat\_26102004\_084213\_7638  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FQAPOP=6 -FQAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA: \*  
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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq: \*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq: \*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq: \*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq: \*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq: \*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq: \*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq: \*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq: \*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq: \*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq: \*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq: \*  
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16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq: \*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq: \*  
18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq: \*  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq: \*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq: \*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

\*

Result No.	Score	Match	Length	DB ID	Description
1	186	55.0	1625	9	US-09-813-133A-1
2	186	55.0	1625	14	US-10-212-877-1
3	175	51.8	1728	9	US-09-880-107-2396
4	149	44.1	1400	9	US-09-925-302-24
5	149	44.1	1400	10	US-09-925-302-24
6	146	43.2	1037	16	US-10-115-479-63
7	140	41.4	1132	16	US-10-115-479-65
8	140	41.4	1344	16	US-10-115-479-69
9	140	41.4	1743	16	US-10-115-479-67
10	68	20.1	55827	9	US-09-813-133A-3
11	68	20.1	55827	14	US-10-212-877-3
12	60	17.8	1272	15	US-10-379-836-1
13	43	12.7	1547	13	US-10-027-632-265133
14	43	12.7	1547	13	US-10-027-632-265134
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16	43	12.7	1547	13	US-10-027-632-265136
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19	43	12.7	1547	15	US-10-027-632-265135
20	43	12.7	1547	15	US-10-027-632-265136
21	19	5.6	60	10	US-09-908-975-8511
22	17	5.0	416	9	US-09-960-352-14595
23	16	4.7	65	10	US-09-908-975-26009
24	14	4.1	431	9	US-09-917-800A-468
25	13	3.8	65	10	US-09-908-975-25938
26	12	3.6	741	13	US-10-200-344-5
27	12	3.6	948	9	US-09-888-615-1
28	12	3.6	1050	13	US-10-200-344-11
29	12	3.6	1187	14	US-10-198-846-13457
30	12	3.6	1295	17	US-10-363-829-148
31	12	3.6	1302	17	US-10-477-515-1
32	12	3.6	1311	13	US-10-200-344-9
33	12	3.6	1907	18	US-10-757-262-127
34	12	3.6	1993	15	US-10-274-639-33
35	12	3.6	1993	16	US-10-333-574-33
36	12	3.6	2128	13	US-10-200-344-13
37	11	3.3	230	14	US-10-060-036-3042
38	11	3.3	230	14	US-10-060-036-3068
39	11	3.3	230	14	US-10-060-036-3096
40	11	3.3	230	14	US-10-060-036-3131
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42	11	3.3	230	14	US-10-060-036-3153
43	11	3.3	230	14	US-10-060-036-3164
44	11	3.3	230	14	US-10-060-036-3168
45	11	3.3	230	14	US-10-060-036-3175

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:

Pred. No.: 6.58e-184 Length: 1625  
Score: 186.00 Matches: 322  
Percent Similarity: 98.77% Conservative: 0  
Best Local Similarity: 98.77% Mismatches: 2  
Query Match: 55.03% Indels: 4  
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTCCAGAGTGCCAAAGTTCTAGTCTCTCTAGAACCTCTAGCAAGTTCAAGTTCTA 142

Qy 21 GlnAsnLeuThrThrThrGluLeuValLeuProGlnProValThrAlaAspLeu 40  
Db 143 CAGAACTCTACTACCAACATATGAGATTCTCTGCGCAGCCGGTAACAGCTGACCTTATT 202

Qy 41 VallysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLeuAla 60  
Db 203 GTGAAGAAAAAACAAGTCCATTTTTTGTAAATGCACTGATGCGACAAATGTGAAGCC 262

Qy 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGAGCGGAATCCATGCTGCTGCGCAGATGTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCACGACACAGTCAGCCCCCGAGCCTCCGATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCACTCACTAATGAATCTATTCTTGGATAGAAATTTATTAACCTGAGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAAATCCATTTGGATCTCTATTGAGAAAGTACCCACTCTATGTTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAl 160  
Db 503 GTTTCTGGAAGAAACAAGC-AGCCAAAAATGCCATATGGAATGCACTGTGGAATCCATGC 561

Qy 160 aArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpAr 180  
Db 562 CAGAAATGGATCTCTCTGCTTTCTGCTTGTGTTCTATAGCCATAATCGAATGTGGAG 621

Qy 180 gLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPh 200  
Db 622 AAAGAACCGTTCTTTCTATGCGAACATCAATTCATCGAACAGACCTGGAATAGGAACCTT 681

Qy 200 eAlaSerLysHisTrpCysGluGluGlyValAspSerSerSerCysSerGluThrTyrCy 220  
Db 682 TGCTTTCCAAACACATGGTGTGAGGAGGTGCATCCAGTTTCCTCATGCTCGGAAACCTACTG 741

Qy 220 sGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAs 240  
Db 742 TGGACTTTATCTGAGTCAGAACCCAGAGTGAAGCAGTGGCTAGTTTCTTGAGAGNAA 801

Qy 240 nIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePr 260  
Db 802 TATCAACAGATTTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCCTCC 861

Qy 260 oTyrSerTyrThrArgSerLysSerLysAspHisGluLysSerLeuValAlaSerGl 280  
Db 862 ATATTCTTATACGAAGTAAAGCAAGACCATGAGGAATCTCTCTAGTAGCCAGTGA 921

Qy 280 uAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrThrHisGlyHisGlyS 300  
Db 922 AGCAGTTCTGCTATTGAGAAAAAT-AGTAAAAATACCGAGTATACATCGCCATGGCT 980

Qy 300 eGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleL 320  
Db 981 CAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTGGATCTATGATTTGGGCATCA 1040

Qy 320 ySTyrSerPheThr 324  
Db 1041 AATATTCTGTTTACA 1054

RESULT 2  
US-10-212-877-1  
; Sequence 1, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinui et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-877-1

Alignment Scores:  
Pred. No.: 6.58e-184 Length: 1625  
Score: 186.00 Matches: 322  
Percent Similarity: 98.77% Conservative: 0  
Best Local Similarity: 98.77% Mismatches: 2  
Query Match: 55.03% Indels: 4  
DB: 14 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-212-877-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTCCAGAGTGCCAAAGTTCTAGTCTCTCTAGAACCTCTAGCAAGTTCAAGTTCTA 142

Qy 21 GlnAsnLeuThrThrThrGluLeuValLeuProGlnProValThrAlaAspLeu 40  
Db 143 CAGAACTCTACTACCAACATATGAGATTCTCTGCGCAGCCGGTAACAGCTGACCTTATT 202

Qy 41 VallysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLeuAla 60  
Db 203 GTGAAGAAAAAACAAGTCCATTTTTTGTAAATGCACTGATGCGACAAATGTGAAGCC 262

Qy 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGAGCGGAATCCATGCTGCTGCGCAGATGTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCACGACACAGTCAGCCCCCGAGCCTCCGATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCACTCACTAATGAATCTATTCTTGGATAGAAATTTATTAACCTGAGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAAATCCATTTGGATCTCTATTGAGAAAGTACCCACTCTATGTTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAl 160  
Db 503 GTTTCTGGAAGAAACAAGC-AGCCAAAAATGCCATATGGAATGCACTGTGGAATCCATGC 561

Qy 160 aArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpAr 180  
Db 562 CAGAAATGGATCTCTCTGCTTTCTGCTTGTGTTCTATAGCCATAATCGAATGTGGAG 621

Qy 180 gLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPh 200  
Db 622 AAAGAACCGTTCTTTCTATGCGAACATCAATTCATCGAACAGACCTGGAATAGGAACCTT 681

Qy 200 eAlaSerLysHisTrpCysGluGluGlyValAspSerSerSerCysSerGluThrTyrCy 220  
Db 682 TGCTTTCCAAACACATGGTGTGAGGAGGTGCATCCAGTTTCCTCATGCTCGGAAACCTACTG 741

Qy 220 sGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAs 240  
Db 742 TGGACTTTATCTGAGTCAGAACCCAGAGTGAAGCAGTGGCTAGTTTCTTGAGAGNAA 801

Qy 240 nIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePr 260  
Db 802 TATCAACAGATTTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCCTCC 861

Qy 260 oTyrSerTyrThrArgSerLysSerLysAspHisGluLysSerLeuValAlaSerGl 280  
Db 862 ATATTCTTATACGAAGTAAAGCAAGACCATGAGGAATCTCTCTAGTAGCCAGTGA 921

Qy 280 uAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrThrHisGlyHisGlyS 300  
Db 922 AGCAGTTCTGCTATTGAGAAAAAT-AGTAAAAATACCGAGTATACATCGCCATGGCT 980

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Db 622 AAGAACCGTCTTCTATCGCAACAATCATTCATCGCAAGACCTGAAATAGGAACCT 681  
Qy 200 eAlaSerLysHisTrpCysGluGluAlaSerSerCysSerGluThrTyrcy 220  
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Qy 220 sGlyLeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuAtgAtgAs 240  
Db 742 TGGACTTATCTCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTCTTCTTGAGAGAAA 801  
Qy 240 nileAsnGlnIleLysAlaTyrlleSerMetHisSerTyrsrGlnHisIleValPhePr 260  
Db 802 TATCAACAGATTAAAGCATACATCAGCATGCTATTCATCTCCAGCATATAGTGTTC 861  
Qy 260 oTyrsrTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGl 280  
Db 862 ATATTCTCTATACACGAAGTAAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCCAGTGA 921  
Qy 280 uAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyThrHisGlyHisGlys 300  
Db 922 AGCAGTTCGTGTATTGAGAAATT-AGTAAATAATACCAAGGTATACATGSCCATGGCT 980  
Qy 300 exGluThrLeuTyrlleuAlaProGlyGlyGlyAspTrpIleTyAspLeuGlyIleL 320  
Db 981 CAGAAACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTTGGGCATCA 1040  
Qy 320 YeTyrsrPheThr 324  
Db 1041 AATATTCTGTTTACA 1054

RESULT 3

US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherif, Uwe  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

Alignment Scores:  
Pred. No.: 2,12e-172 Length: 1728  
Score: 175.00 Matches: 175  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.78% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-880-107-2396 (1-1728)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 86 TTTTCAGAGTGGCCAAAGTCTAGCTGCTCTCTCCAGAACCTCTAGGAAGTCAAGTTCTA 145  
Qy 21 GlnAsnLeuThrThrThrTyThrTyGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40

Db 146 CAGAATCTTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTTGACCTTATT 205  
Qy 41 VallyslyslvsGlnValHisPhePheValAsnAlaSerAspValAspAsnVallyeAla 60  
Db 206 GTGAAGAAAAAACAAAGTCCATTTTTTTGTAATGCACTGATGTCGACATGTGNAAGCC 265  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 266 CATTTAAATGTGCGGGAATTCATGTCAGTGTCTTGTGGCAGACGCTGGAAGATCTTATT 325  
Qy 81 GlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyTyTyGluGln 100  
Db 326 CAACAGCAGATTTCCAAACGACACATCAGTCCAGCCCCGAGCCTCCGCATCTGTACTATGAACAG 385  
Qy 101 TyHisSerLeuAsnGluIleTySerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 386 TATCACTCCTAAATGAATCTATCTTGGATAGATTTATTAACATGAGAGCATCTGAT 445  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTyTyValLeuLys 140  
Db 446 ATGCTTACAAAAATCCACATTTGGATCTCTCAITTTGAGAAAGTACCCCACTCTATGTTTTAAAG 505  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 506 GTTTCGTGAAAGAAACAAACAGCCAAAAATGCCATATGATGATTTGACTGTGGAATCCATGCC 565  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 566 AGAGAAATGGATCTCTCTCTGCTTTTCGCTTGGTTTCATAGGCCAT 610

RESULT 4

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

Alignment Scores:  
Pred. No.: 2,42e-145 Length: 1400  
Score: 149.00 Matches: 149  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 44.08% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)

Qy 176 AsnArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAsp 195  
Db 179 ATTCGATGTGGAGAAGAACCGTCTTCTATGCGAACCAATCATTTGCATCGGAACAGAC 238  
Qy 196 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 215

Db 239 CTGAATAGGAACCTTTGGCTTCCAAACACATGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 298  
Qy 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 235  
Db 299 TCGGAACCTACTGTGGACTTTATCTCCTGAGTCAGAACCCAGAGTGAAGCCAGTGGCTAGT 358  
Qy 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255  
Db 359 TTCCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATACCTCCAG 418  
Qy 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275  
Db 419 CATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGACCATGAGGAAGTGTCT 478  
Qy 276 LeuValAlaSerGluValAlaArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295  
Db 479 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACCTAGTAAATAATACCAGGTATACA 538  
Qy 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 315  
Db 539 CATGCCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 598  
Qy 316 AspLeuGlyIleLysTyrSerPheThr 324  
Db 599 GATTGGGCATCAATATTCGTTTACA 625

## RESULT 5

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Publication No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

## Alignment Scores:

Pred. No.:	2,42e-145	Length:	1400
Scores:	149.00	Matches:	149
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	44.08%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)

Qy 176 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 195  
Db 179 AATCGAATGTGAGAAAGAACCGTTCTTTCTATGCGAACATCATTCATGCGAACACAC 238  
Qy 196 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 215  
Db 239 CTGAATAGGAACCTTTGGCTTCCAAACACATGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 298  
Qy 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 235  
Db 299 TCGGAACCTACTGTGGACTTTATCTCCTGAGTCAGAACCCAGAGTGAAGCCAGTGGCTAGT 358

Qy 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255  
Db 359 TTCCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATACCTCCAG 418  
Qy 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275  
Db 419 CATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGACCATGAGGAAGTGTCT 478  
Qy 276 LeuValAlaSerGluValAlaArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295  
Db 479 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACCTAGTAAATAATACCAGGTATACA 538  
Qy 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 315  
Db 539 CATGCCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 598  
Qy 316 AspLeuGlyIleLysTyrSerPheThr 324  
Db 599 GATTGGGCATCAATATTCGTTTACA 625

## RESULT 6

US-10-115-479-63

; Sequence 63, Application US/10115479

; Publication No. US20040006205A1

; GENERAL INFORMATION:

; APPLICANT: Li, Li

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Liu, Xiaohong

; APPLICANT: Miller, Charles E.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Zethusen, Bryan D.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Zhong, Haihong

; APPLICANT: Smithson, Glendda

; APPLICANT: Casman, Stacie J.

; APPLICANT: Boldog, Perenc L.;

; APPLICANT: Voss, Edward

; APPLICANT: Vernet, Corine

; APPLICANT: MacDougall, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Anderson, David W.

; APPLICANT: Zhong, Mei

; APPLICANT: Mezes, Peter S.

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Malyanker, Uriel M.

; APPLICANT: Shinkets, Richard A.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-322 B (Cura 622 PT)

; CURRENT APPLICATION NUMBER: US/10/115,479

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 60/281,136

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281,863

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/281,906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282,934

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/283,657

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,678

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,687

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,710

; PRIOR FILING DATE: 2001-04-13

```
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.: 2,47e-142 Length: 1037
Score: 146.00 Matches: 146
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.20% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-115-479-63 (1-1037)

QY 1 PheGlnSerGlyGlnValLeuAlaLeuProAtgThrSerArgGlnValGlnValLeu 20
DB 107 TTTCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166
QY 21 GlnAsnLeuThrThrThrTyrGluLeValLeuTrpGlnProValThrAlaAspLeu 40
DB 167 CAGAATCTTACTACACATATGAGATTGTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226
QY 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
DB 227 GTCAAGAAAAAACAAGTCCATTTTTTTGTAAATGTCATCTGATGTCACAAATGTGAAGCC 286
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80
DB 287 CATTTAAATGTGAGCGGAATTCATGAGTGCTTCTGTCGACAGCTGGAGATCTTATT 346
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
DB 347 CAACAGCAGATTTCACACGACACAGTCAGCCCCGAGCCTCGCATCGTACTATGAACAG 406
QY 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
DB 407 TATCACTCACTAAATGAAATCTATTCTTGATAGAATTTATATACTGAGAGGCATCCTGAT 466
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
DB 467 ATGCTTACAAAAATCCATCGGATCTCTATTGAGAAAGTACCCTCTATGTTTAAAG 526
QY 141 ValSerGlyLysGluGln 146
DB 527 GTTTCTGGAAGAAAGACAA 544

RESULT 7
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Sytek, Kimberly A.
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
```

```
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Patturajan, Meera
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1103)
US-10-115-479-65
```

```
Alignment Scores:
Pred. No.: 4,93e-136 Length: 1132
Score: 140.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.42% Indels: 0
DB: 16 Gaps: 0
```

US-09-980-881A-3 (1-338) x US-10-115-479-65 (1-1132)

```
QY 1 PheGlnSerGlyGlnValLeuAlaLeuProAtgThrSerArgGlnValGlnValLeu 20
DB 107 TTTCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166
QY 21 GlnAsnLeuThrThrThrTyrGluLeValLeuTrpGlnProValThrAlaAspLeu 40
DB 167 CAGAATCTTACTACACATATGAGATTGTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226
QY 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
DB 227 GTCAAGAAAAAACAAGTCCATTTTTTTGTAAATGTCATCTGATGTCACAAATGTGAAGCC 286
```

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Qy 61 HisLeuAenValSerGlyVileProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 287 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGGCAGACGTTGGAAGATCTTATT 346
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTCCACGACACAGTCAGCCCGCGGCTCCGATCGTACTATGACAG 406
Qy 101 TyrHisSerLeuAenGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAATCTATTCTTGGATAGATTTATATACTGAGAGCATCTTGAT 466
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 467 ATGCTTACAAAAATCCACATTTGGATTCCTATTGAGAAGTAGTACCACCTCTATGTTTAAAG 526

RESULT 8
US-10-115-479-69
; Sequence 69, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel W.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69
Alignment Scores:
Pred. No.: 5,79e-136 Length: 1344
Score: 140.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.42% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-115-479-69 (1-1344)
Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 97 TTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAAACCTCTAGGCAAGTTCAAGTTCTA 156
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 157 CAGAATCTTACTACACATATGAGATTGTCTCTGGCAGCGGTAACAGCTGACCTTATT 216
Qy 41 VallyslyslsGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
Db 217 GTGAAGAAAAACAAGTCCATTTTGTGTAATGCATCTGATGTCGACAAATGTGAAAGCC 276
Qy 61 HisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 277 CAITTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGGCAGACGTGGAAGATCTTATT 336
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 337 CAACAGCAGATTTTCCAAACGACACACAGTCAGCCCCCGACCTCCGCATCGTACTATGAACAG 396
Qy 101 TyrHisSerLeuAenGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 397 TATCACTCACTAAATGAATCTATTCTTGGATAGATTTTATACTAGAGAGCATCTTGAT 456
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 457 ATGCTTACAAAAATCCACATTTGGATCTCTCATTTTGAGAAGTACCACCTCTATGTTTAAAG 516

RESULT 9
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
```

```

; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
US-10-115-479-67

Alignment Scores:
Pred. No.: 7,398-136 Length: 1743
Score: 140.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.42% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-115-479-67 (1-1743)

QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
DB 86 TTTCAGAGTGGCCAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 145
QY 21 GlnAsnLeuThrThrThrGluLeuValLeuThrGlnProValThrAlaAspLeuLeu 40
DB 146 CAGAACTTACTACAACATATGAGATTGTCTCTGGCAGCCGGTAACAGCTGACCTTATT 205
QY 41 VallyValysGlnValHisPheValAsnAlaSerAspValAlaAspVallyAla 60
DB 206 GTGAAGAAAAACAAGTCCATTTTGTAAATGTCATCTGTGTCGACAGTGGGAAGCC 265
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80
DB 266 CATTAAATGTCAGCGGAATTCCTAGTGTCTGTGTCGACAGCTGGGAAGATCTTATT 325
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
DB 326 CAACAGCAGATTTCACACGACACAGTCAGCCCCCGAGCCTCCGATCTGTAATGACAG 385
QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120

```

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DB 386 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTATTAACAGAGCATCCTGAT 445
QY 121 MetLeuThrIysIleHisIleGlySerSerPheGluIysTyrProLeuTyrValleuLys 140
DB 446 ATGCTTACAAAAATCCACATTTGGATTCCTCAITTTGAGAAAGTACCCACACTCTATGTTTAAAG 505
RESULT 10
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Publication No. US20020131719A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinlu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Alignment Scores:
Pred. No.: 2,838-59 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.12% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-813-133A-3 (1-55827)

QY 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 226
DB 48643 GAGGAAGTGTCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCTGAGTCA 48702
QY 227 GluProGluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 246
DB 48703 GAACCAAGATGAAGCGAGTGGCTAGTTCTTTGAGAAGAAATATCAACAGATTAAGCA 48762
QY 247 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 266
DB 48763 TACATCAGATGATTCATATCCTCCAGCATATAGTGTTCATATTCCTATATACACAGAGT 48822
QY 267 LysSerLysAspHisGluGluLeu 274
DB 48823 AAAAGCAAGACCATGAGGAAGCTG 48846
RESULT 11
US-10-212-877-3
; Sequence 3, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinlu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens

```

## US-10-212-877-3

## Alignment Scores:

Pred. No.: 2,83e-59 Length: 55827  
Score: 68.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.12% Indels: 0  
DB: 14 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-212-877-3 (1-55827)

Qy 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 226  
Db 48643 GAGGAAGTGATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCTTGAGTCA 48702  
Qy 227 GluProGluValLysAlaValAlaSerPheLeuArgArgAniLeAAsnGlnIleLysAla 246  
Db 48703 GAACCAAGTGAAGGCAAGTGGTAGTTCTTGAGAGAATATCAACCAATTAAAGCA 48762  
Qy 247 TyrLeSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 266  
Db 48763 TACATCAGATGCATTCATCTACTCCAGCATATAGTGTTCATATTCATATACACGAAGT 48822  
Qy 267 LysSerLysAspHisGluGluLeu 274  
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

## RESULT 12

US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1272  
; TYPE: DNA  
; ORGANISM: Papio hamadryas  
; NAME/KEY: CDS  
; LOCATION: (1)..(1269)  
US-10-379-836-1

## Alignment Scores:

Pred. No.: 1.81e-52 Length: 1272  
Score: 60.00 Matches: 60  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 17.75% Indels: 0  
DB: 15 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-379-836-1 (1-1272)

Qy 53 SerAspValAspAsnValLysAlaHisLeuAsnValSerGlyIleProCysSerValLeu 72  
Db 223 TCTGATGTCGCAATGTGAAGGCCCATTTAAATGTGAGCGGAATTCATGCGAGTCTCTG 282  
Qy 73 LeuAlaAspValGluAspLeuIleGlnGlnIleSerAsnAspThrValSerProArg 92  
Db 283 CTGGCAGATGTGAAGATCTTATTCAACAGCAGATTTCCACAGCACAGTCAGCCCCCGA 342  
Qy 93 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 112  
Db 343 GCCTCCGCGTACTATGAACAGATATCACTCACTAAATGAATCTATTCTTGGATAGAA 402

## RESULT 13

US-10-027-632-265133  
; Sequence 265133, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 265133  
; LENGTH: 1547  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1547)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-265133

## Alignment Scores:

Pred. No.: 1.21e-34 Length: 1547  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.72% Indels: 0  
DB: 13 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-027-632-265133 (1-1547)

Qy 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 226  
Db 1417 GAGGAAGTGATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCTTGAGTCA 1476  
Qy 227 GluProGluValLysAlaValAlaSerPheLeuArgArgAniLeAAsnGlnIleLysAla 246  
Db 1477 GAACCAAGTGAAGGCAAGTGGCTAGTTCTTGAGAGAATATCAACCAATTAAAGCA 1536  
Qy 247 TyrLeSer 249  
Db 1537 TACATCAGC 1545

## RESULT 14

US-10-027-632-265134  
; Sequence 265134, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12

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; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265134
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265134

Alignment Scores:
Pred. No.: 1,21e-34 Length: 1547
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.72% Indels: 0
DB: 13 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-027-632-265134 (1-1547)
QY 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrcysGlyLeuTyProGluSer 226
Db 1417 GAGGAAGGTGCATCCAGTTCTCATGCTCGGAACCTACTGTGGACTTTATCTGAGTCA 1476
QY 227 GluProGluVallyslalAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 246
Db 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536
QY 247 TyrIleSer 249
Db 1537 TACATCAGC 1545

Search completed: October 27, 2004, 09:21:14
Job time : 501.441 secs
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; SEQ ID NO 265135
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265135

Alignment Scores:
Pred. No.: 1,21e-34 Length: 1547
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.72% Indels: 0
DB: 13 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-027-632-265135 (1-1547)
QY 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrcysGlyLeuTyProGluSer 226
Db 1417 GAGGAAGGTGCATCCAGTTCTCATGCTCGGAACCTACTGTGGACTTTATCTGAGTCA 1476
QY 227 GluProGluVallyslalAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 246
Db 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536
QY 247 TyrIleSer 249
Db 1537 TACATCAGC 1545

Search completed: October 27, 2004, 09:21:14
Job time : 501.441 secs
```





Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	57	3	2	19	3	US-09-309-317-5	Sequence 5, Appli
2	42.5	2.4		16	4	US-09-541-345-44	Sequence 44, Appl
3	40	2.2		18	4	US-09-693-822B-19	Sequence 19, Appl
4	40	2.2		19	4	US-09-693-822B-8	Sequence 8, Appli
5	40	2.2		19	4	US-09-693-822B-23	Sequence 23, Appl
6	40	2.2		19	4	US-09-693-822B-24	Sequence 24, Appl
7	39.5	2.2		13	4	US-09-402-641-1	Sequence 1, Appli
8	39.5	2.2		15	3	US-08-142-590B-5	Sequence 5, Appli
9	39.5	2.2		18	2	US-08-747-915-4	Sequence 4, Appli
10	39.5	2.2		18	3	US-08-467-023-211	Sequence 211, App
11	39.5	2.2		18	3	US-08-142-590B-4	Sequence 4, Appli
12	39.5	2.2		18	3	US-08-142-590B-24	Sequence 24, Appl
13	39.5	2.2		18	4	US-09-285-783-4	Sequence 4, Appli
14	39	2.2		13	2	US-08-596-387B-6	Sequence 6, Appli
15	39	2.2		13	3	US-09-067-615-6	Sequence 6, Appli
16	39	2.2		13	5	PCT-US93-09816A-6	Sequence 6, Appli
17	39	2.2		17	1	US-08-428-733A-55	Sequence 55, Appl
18	39	2.2		18	4	US-08-634-332A-2	Sequence 2, Appli
19	39	2.2		19	4	US-09-693-822B-25	Sequence 25, Appl
20	38.5	2.1		17	4	US-09-622-624-20	Sequence 20, Appl
21	38	2.1		14	2	US-08-685-589A-198	Sequence 198, App
22	38	2.1		16	4	US-09-340-620A-47	Sequence 47, Appl
23	38	2.1		17	2	US-08-685-589A-140	Sequence 140, App
24	38	2.1		17	4	US-08-182-967-25	Sequence 25, Appl
25	38	2.1		18	5	PCT-US93-0374B-10	Sequence 10, Appl
26	38	2.1		19	1	US-08-382-013A-59	Sequence 59, Appl
27	38	2.1		19	1	US-08-382-013A-71	Sequence 71, Appl

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CEA binding
; OTHER INFORMATION: polypeptide
US-09-541-345-44

Query Match          2.4%; Score 42.5; DB 4; Length 16;
Best Local Similarity 43.8%; Pred. No. 5.1e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 152 IWIDCGIHAREWISPA 167
Db 1 IW-DCNLFKNQWFCPA 15

RESULT 3
US-09-693-822B-19
; Sequence 19, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-19

Query Match          2.2%; Score 40; DB 4; Length 18;
Best Local Similarity 38.1%; Pred. No. 1.2e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
Db 2 HHC-----YKRFPEKHCHRG 18

RESULT 4
US-09-693-822B-8
; Sequence 8, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-8

Query Match          2.2%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
```

```
Db 2 HHC-----YKRFPEKHCHRG 18

RESULT 5
US-09-693-822B-23
; Sequence 23, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-23

Query Match          2.2%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
Db 2 HHC-----YKRFPEKHCHRG 18

RESULT 6
US-09-693-822B-24
; Sequence 24, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-24

Query Match          2.2%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
Db 2 HHC-----YKRFPEKHCHRG 18

RESULT 7
US-09-402-641-1
; Sequence 1, Application US/09402641
; Patent No. 6528619
; GENERAL INFORMATION:
; APPLICANT: BUERGLE, Markus
; APPLICANT: GRAEPF, Heinrich
```

```
; APPLICANT: KESSLER, Horst
; APPLICANT: MAGDOLEN, Viktor Robert
; APPLICANT: KOENIG, Bernhard
; APPLICANT: KOPPIZ, Marcus
; APPLICANT: RIEMER, Christoph
; APPLICANT: SCHMITT, Manfred
; APPLICANT: WEIDLE, Ulrich
; APPLICANT: WILHELM, Olaf
; TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR
; FILE REFERENCE: Case 20367US
; CURRENT APPLICATION NUMBER: US/09/402,641
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: EP97106024.9
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/EP98/02178
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide "cyclo
; OTHER INFORMATION: 19.31 UPA 19-31"; Figure 3A
US-09-402-641-1

Query Match      2.2%; Score 39.5; DB 4; Length 13;
Best Local Similarity 37.5%; Pred. No. 7.8e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 191 CIGTDLNRNPFASKHWC 206
Db 1 CVS---NKYFSNIHWC 13

RESULT 8
US-08-142-590B-5
; Sequence 5, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and GOETINCK,
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-142-590B-5

Query Match      2.2%; Score 39.5; DB 3; Length 15;
Best Local Similarity 37.5%; Pred. No. 9.8e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 191 CIGTDLNRNPFASKHWC 206
Db 2 CVS---NKYFSNIHWC 14

RESULT 9
US-08-747-915-4
; Sequence 4, Application US/08747915
; Patent No. 5942492
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.
; APPLICANT: Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
; TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,915
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 32904-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEFAX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-747-915-4

Query Match      2.2%; Score 39.5; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 191 CIGTDLNRNPFASKHWC 206
Db 3 CVS---NKYFSNIHWC 15

RESULT 10
US-08-467-023-211
; Sequence 211, Application US/08467023
; Patent No. 6090386
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; APPLICANT: Pollock, Joanne;
```

APPLICANT: Bond, Julian P.;  
APPLICANT: Garman, Richard D;  
APPLICANT: Kuo, Mei-Chang;  
APPLICANT: Yeung, Siu-mei H.;  
APPLICANT: Brauer, Andrew;  
APPLICANT: Exley, Mark A.;  
APPLICANT: Powers, Steven P.  
TITLE OF INVENTION: Allergenic Proteins And Peptides From  
TITLE OF INVENTION: Japanese Cedar Pollen  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
STREET: 610 Lincoln St  
CITY: Waltham  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424.  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 211:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-023-211

Query Match 2.2%; Score 39.5; DB 3; Length 18;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 144 KEOTAKNAIWD 155  
Db 2 KERTATN-IWD 12

RESULT 11  
US-08-142-590B-4  
Sequence 4, Application US/08142590B  
Patent No. 6120765  
GENERAL INFORMATION:  
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and  
TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,590B  
FILING DATE: 25-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,318  
FILING DATE: 02-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: MGP-009CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-142-590B-4

Query Match 2.2%; Score 39.5; DB 3; Length 18;  
Best Local Similarity 37.5%; Pred. No. 1.3e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 191 CIGTDLNRNFASKHWC 206  
Db 5 CVS---NKYFSNIHWC 17

RESULT 12  
US-08-142-590B-24  
Sequence 24, Application US/08142590B  
Patent No. 6120765  
GENERAL INFORMATION:  
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and  
TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,590B  
FILING DATE: 25-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,318  
FILING DATE: 02-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: MGP-009CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-142-590B-24



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; APPLICATION NUMBER: US/09/067,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,387
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-09-067-615-6

Query Match      2.2%; Score 39; DB 3; Length 13;
Best Local Similarity 58.3%; Pred. No. 8.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      63 NVSGIPCSVLIA 74
Db      1 NLCNIPCSALLS 12

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Search completed: October 27, 2004, 01:31:43  
Job time : 18.5445 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:13:21 ; Search time 42.6081 Seconds  
(without alignments)  
2568.304 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 1798  
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYFSTNPPEVKLPLSLK 338

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 260209

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	57	3.2	19	9 US-09-799-760-5	Sequence 5, Appli
2	48	2.7	11	16 US-10-343-509-10	Sequence 10, Appl
3	46	2.6	11	15 US-10-410-764-87	Sequence 87, Appl
4	42.5	2.4	16	10 US-09-825-517A-44	Sequence 44, Appl
5	41	2.3	13	15 US-10-469-304-55	Sequence 55, Appl
6	41	2.3	18	16 US-10-742-379-90	Sequence 90, Appl
7	40	2.2	14	15 US-10-436-715-431	Sequence 431, App
8	39.5	2.2	13	16 US-10-756-289-3	Sequence 3, Appli
9	39.5	2.2	15	16 US-10-756-289-2	Sequence 2, Appli
10	39.5	2.2	18	14 US-10-349-543-4	Sequence 4, Appli
11	39.5	2.2	19	10 US-09-791-524-1	Sequence 1, Appli
12	39	2.2	13	9 US-09-848-164-6	Sequence 6, Appli
13	39	2.2	13	9 US-09-957-674-5	Sequence 5, Appli

14	39	2.2	13	9 US-09-900-379-6	Sequence 6, Appli
15	39	2.2	19	10 US-09-791-524-2	Sequence 2, Appli
16	38.5	2.1	17	9 US-09-822-624-20	Sequence 20, Appl
17	38	2.1	16	9 US-09-728-721-47	Sequence 47, Appl
18	38	2.1	16	14 US-10-295-981-47	Sequence 47, Appl
19	38	2.1	18	14 US-10-125-869A-23	Sequence 23, Appl
20	38	2.1	18	15 US-10-462-262-247	Sequence 247, App
21	38	2.1	18	16 US-10-364-645A-54	Sequence 54, Appl
22	38	2.1	19	8 US-08-817-832B-25	Sequence 25, Appl
23	38	2.1	19	15 US-10-440-435-25	Sequence 25, Appl
24	37.5	2.1	15	14 US-10-034-974-32	Sequence 32, Appl
25	37.5	2.1	17	15 US-10-624-153-66	Sequence 66, Appl
26	37.5	2.1	18	16 US-10-712-447-22	Sequence 22, Appl
27	37	2.1	13	15 US-10-469-304-56	Sequence 56, Appl
28	37	2.1	14	9 US-09-740-211-15	Sequence 15, Appl
29	37	2.1	14	13 US-10-007-968-15	Sequence 15, Appl
30	37	2.1	14	14 US-10-293-400-15	Sequence 15, Appl
31	37	2.1	15	14 US-10-371-540-30	Sequence 30, Appl
32	37	2.1	15	16 US-10-327-598-74	Sequence 74, Appl
33	37	2.1	16	14 US-10-225-567A-1864	Sequence 1864, Ap
34	37	2.1	16	14 US-10-083-768-15	Sequence 15, Appl
35	37	2.1	16	15 US-10-609-217-75	Sequence 75, Appl
36	37	2.1	16	15 US-10-632-388-75	Sequence 75, Appl
37	37	2.1	16	15 US-10-651-723-75	Sequence 75, Appl
38	37	2.1	16	15 US-10-645-761-75	Sequence 75, Appl
39	37	2.1	16	15 US-10-666-696-75	Sequence 75, Appl
40	37	2.1	16	15 US-10-653-048-75	Sequence 75, Appl
41	37	2.1	18	14 US-10-105-232-194	Sequence 194, App
42	37	2.1	18	14 US-10-189-437-181	Sequence 181, App
43	37	2.1	19	9 US-09-864-761-41546	Sequence 41546, A
44	37	2.1	19	10 US-09-931-325A-25	Sequence 25, Appl
45	37	2.1	19	10 US-09-563-222-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1  
US-09-799-760-5  
; Sequence 5, Application US/09799760  
; Patent No. US20010021771A1  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley  
; APPLICANT: Tremblay, Patrick  
; APPLICANT: Moore, Richard  
; APPLICANT: Westaway, David  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Lee, Inyoul  
; TITLE OF INVENTION: PrP-like Gene  
; FILE REFERENCE: 6510-130CON  
; CURRENT APPLICATION NUMBER: US/09/799,760  
; CURRENT FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 09/309,317  
; PRIOR FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized peptide  
US-09-799-760-5

Query Match 3.2%; Score 57; DB 9; Length 19;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 189 NHCIGTDLNRFASKHWC 206  
||| : : : : :  
Db 1 NHCFGAEGNRYAANYIC 18

```
RESULT 2
US-10-343-509-10
; Sequence 10, Application US/10343509
; Publication No. US20040101865A1
; GENERAL INFORMATION:
; APPLICANT: BASF
; TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
; FILE REFERENCE: 0050/51654
; CURRENT APPLICATION NUMBER: US/10/343,509
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Euglena gracilis
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = (Phe/Tyr)
US-10-343-509-10

Query Match      2.7%; Score 48; DB 16; Length 11;
Best Local Similarity 70.0%; Pred. No. 5,1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 309 GGDWYDLG 318
Db 1 GGDGWYDIG 10

RESULT 3
US-10-410-764-87
; Sequence 87, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; FILE REFERENCE: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520MNM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zinc carboxypeptidase zinc-binding region 2
US-10-410-764-87

Query Match      2.6%; Score 46; DB 15; Length 11;
Best Local Similarity 63.6%; Pred. No. 8,1e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 251 HSYSQHIVFPY 261
Db 1 HSYSQMLMPY 11

RESULT 4
US-09-825-517A-44
; Sequence 44, Application US/09825517A
; Publication No. US20030203415A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
; FILE REFERENCE: DYX-016.1 (3421, 1005-001)
; CURRENT APPLICATION NUMBER: US/09/825,517A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/541,345
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEA binding polypeptide
US-09-825-517A-44

Query Match      2.4%; Score 42.5; DB 10; Length 16;
Best Local Similarity 43.8%; Pred. No. 3,1e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 152 IWIDGIIHAREWISPA 167
Db 1 IW-DCNLFKNQWFCPA 15

RESULT 5
US-10-469-304-55
; Sequence 55, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
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US-10-469-304-55

Query Match 2.3%; Score 41; DB 15; Length 13;  
Best Local Similarity 42.1%; Pred. No. 3.2e+03;  
Matches 8; Conservative 2; Mismatches 1; Indels 8; Gaps 1;

Qy 31 LWQPVTDLVKKKGVHFF 49  
Db 2 LWQP-----KRSCHFF 12

RESULT 6

US-10-742-379-90  
; Sequence 90, Application US/10742379  
; Publication No. US20040181033A1  
; GENERAL INFORMATION:  
; APPLICANT: Han, HQ  
; APPLICANT: Min, Hosung  
; APPLICANT: Boone, Thomas Charles  
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN  
; FILE REFERENCE: A-828 (US)  
; CURRENT APPLICATION NUMBER: US/10/742,379  
; PRIOR FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: US 60/435,923  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 634  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 90  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Myostatin Binding Peptide  
US-10-742-379-90

Query Match 2.3%; Score 41; DB 16; Length 18;  
Best Local Similarity 83.3%; Pred. No. 5.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 204 HMCQG 209  
Db 2 HMCQG 7

RESULT 7

US-10-436-715-431  
; Sequence 431, Application US/10436715  
; Publication No. US20040018976A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,  
; TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF  
; FILE REFERENCE: D0262 NP  
; CURRENT APPLICATION NUMBER: US/10/436,715  
; CURRENT FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: U.S. 60/380,336  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 431  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-436-715-431

Query Match 2.2%; Score 40; DB 15; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.5e+03;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 NLATTVIVLWQ 33  
Db 3 DLATGYDVVLWK 14

RESULT 8

US-10-756-289-3  
; Sequence 3, Application US/10756289  
; Publication No. US20040138110A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Horst  
; APPLICANT: Graeff, Heinrich  
; APPLICANT: Schmitt, Manfred  
; APPLICANT: Magdolen, Viktor  
; APPLICANT: Wilhelm, Olaf G.  
; APPLICANT: Riemer, Christoph  
; APPLICANT: Burgle, Markus  
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
; FILE REFERENCE: 100564-09040  
; CURRENT APPLICATION NUMBER: US/10/756,289  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US/09/402,464  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: EP 97 106 024.9  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 1...12  
; OTHER INFORMATION: D-amino acids may be substituted for corresponding L-  
; OTHER INFORMATION: amino acids at  
; OTHER INFORMATION: positions 1,2,3,9, 11, and 12.  
US-10-756-289-3

Query Match 2.2%; Score 39.5; DB 16; Length 13;  
Best Local Similarity 37.5%; Pred. No. 4.6e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 191 CIGTDLNENFASKWC 206  
Db 1 CVS---NKYFSNIHWC 13

RESULT 9

US-10-756-289-2  
; Sequence 2, Application US/10756289  
; Publication No. US20040138110A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Horst  
; APPLICANT: Graeff, Heinrich  
; APPLICANT: Schmitt, Manfred  
; APPLICANT: Magdolen, Viktor  
; APPLICANT: Wilhelm, Olaf G.  
; APPLICANT: Riemer, Christoph  
; APPLICANT: Burgle, Markus  
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
; FILE REFERENCE: 100564-09040  
; CURRENT APPLICATION NUMBER: US/10/756,289  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US/09/402,464  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: EP 97 106 024.9  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-756-289-2

Query Match 2.2%; Score 39.5; DB 16; Length 15;

Best Local Similarity 37.5%; Pred. No. 5.6e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Oy 191 CIGTDLNRFASKHC 206  
Db 2 CVS---NKYFSNIHWC 14

RESULT 10

US-10-349-543-4  
; Sequence 4, Application US/10349543  
; Publication No. US200301665141  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Terence R.  
; Haney, David N.  
; Varga, Janos  
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RADER, FISHMAN & GRAUER  
; STREET: 1233 20TH STREET NW, SUITE 501  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/349,543  
; FILING DATE: 22-Jan-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285,783  
; FILING DATE: 05-Apr-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LIVNAT, SHMUEL  
; REGISTRATION NUMBER: 33,949  
; REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 955-8787  
; TELEFAX: (202) 955-3751  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-349-543-4

Query Match 2.2%; Score 39.5; DB 14; Length 18;  
Best Local Similarity 37.5%; Pred. No. 7.3e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Oy 191 CIGTDLNRFASKHC 206  
Db 3 CVS---NKYFSNIHWC 15

RESULT 11

US-09-791-524-1  
; Sequence 1, Application US/09791524  
; Publication No. US20030143209A1  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharmaceuticals Products Inc.  
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery of Heterologous Genes  
; FILE REFERENCE: A3319A  
; CURRENT APPLICATION NUMBER: US/09/791,524  
; CURRENT FILING DATE: 2001-02-22

; PRIOR APPLICATION NUMBER: 60/09828  
; PRIOR FILING DATE: 1998-08-27  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Adenovirus  
; US-09-791-524-1

Query Match 2.2%; Score 39.5; DB 10; Length 19;  
Best Local Similarity 37.5%; Pred. No. 7.9e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Oy 191 CIGTDLNRFASKHC 206  
Db 6 CVS---NKYFSNIHWC 18

RESULT 12

US-09-848-164-6  
; Sequence 6, Application US/09848164  
; Patent No. US20020034513A1  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; Jiao, Jin-An  
; Burkhardt, Martin  
; Wong, Hing  
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dade International, Inc.  
; STREET: 1717 Deerfield Road  
; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/848,164  
; FILING DATE: 03-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/067,615  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/382,454  
; FILING DATE: 01-FEB-1995  
; APPLICATION NUMBER: US 08/283,302  
; FILING DATE: 29-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pearson, Louise S.  
; REGISTRATION NUMBER: 32,369  
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708) 267-5300  
; TELEFAX: (708) 267-5376  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-848-164-6

Query Match 2.2%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.1e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 63 NVSGIPCSVILLA 74  
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 Db 1 NLCNIPCSALLS 12

RESULT 13  
 US-09-957-674-5  
 ; Sequence 5, Application US/09957674  
 ; Patent No. US20020120948A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Medical Research Council  
 ; TITLE OF INVENTION: Methods for Expressing Gene Products  
 ; FILE REFERENCE: 18396/2072  
 ; CURRENT APPLICATION NUMBER: US/09/957,674  
 ; CURRENT FILING DATE: 2001-09-20  
 ; PRIOR APPLICATION NUMBER: GB990736  
 ; PRIOR FILING DATE: 1999-03-30  
 ; PRIOR APPLICATION NUMBER: PCT/GB00/01225  
 ; PRIOR FILING DATE: 2000-03-30  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Chicken  
 US-09-957-674-5

Query Match 2.2%; Score 39; DB 9; Length 13;  
 Best Local Similarity 58.3%; Pred. No. 5.1e+03;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 63 NVSGIPCSVILLA 74  
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 Db 1 NLCNIPCSALLS 12

RESULT 14  
 US-09-900-379-6  
 ; Sequence 6, Application US/09900379  
 ; Publication No. US20020198144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wong, Hing C.  
 ; Rhode, Peter R.  
 ; Widanz, Jon A.  
 ; Grammer, Susan  
 ; Edwards, Ana C.  
 ; Chavallaz, Pierre-Andre  
 ; Jiao, Jin-An  
 ; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 123  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dade International, Inc.  
 ; STREET: 1717 Deerfield Road  
 ; CITY: Deerfield  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60015  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/900,379  
 ; FILING DATE: 06-Jul-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/776,084  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: PCT/US95/09816  
 ; FILING DATE: 31-JUL-1995  
 ; APPLICATION NUMBER: US 08/382,454  
 ; FILING DATE: 01-FEB-1995

APPLICATION NUMBER: US 08/283,302  
 FILING DATE: 29-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pearson, Louise S.  
 REGISTRATION NUMBER: 32,369  
 REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (708) 267-5300  
 TELEFAX: (708) 267-5376  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-900-379-6

Query Match 2.2%; Score 39; DB 9; Length 13;  
 Best Local Similarity 58.3%; Pred. No. 5.1e+03;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 63 NVSGIPCSVILLA 74  
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 Db 1 NLCNIPCSALLS 12

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 US-09-791-524-2  
 ; Sequence 2, Application US/09791524  
 ; Publication No. US20030143209A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aventis Pharmaceuticals Products Inc.  
 ; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes  
 ; FILE REFERENCE: A3319A  
 ; CURRENT APPLICATION NUMBER: US/09/791,524  
 ; CURRENT FILING DATE: 2001-02-22  
 ; PRIOR APPLICATION NUMBER: 60/09828  
 ; PRIOR FILING DATE: 1998-08-27  
 ; NUMBER OF SEQ ID NOS: 150  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Adenovirus  
 US-09-791-524-2

Query Match 2.2%; Score 39; DB 10; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 8.9e+03;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 197 NRPASKHWC 206  
 : : : : :  
 Db 9 NKYFSNIHWC 18

Search completed: October 27, 2004, 01:43:16  
 Job time : 42.6081 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 27, 2004, 01:43:22 ; Search time 88.7966 Seconds  
(without alignments)  
2705.583 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 1798  
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYSFTSNPPVKKLLPLSLK 338

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALLGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
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6: /cgn2\_6/prodata/1/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1749.5	97.3	1625	US-09-813-133A-1	Sequence 1, Appli
2	1732	96.3	1272	US-08-869-057-1	Sequence 1, Appli
3	1732	96.3	1749	US-07-649-591B-2	Sequence 2, Appli
4	1732	96.3	1749	US-08-277-540-2	Sequence 2, Appli
5	1732	96.3	1749	US-08-430-787A-2	Sequence 2, Appli
6	646.5	36.0	1215	US-08-696-139-1	Sequence 1, Appli
7	637.5	35.5	1263	US-08-860-882A-56	Sequence 56, Appli
8	637.5	35.5	1283	US-09-011-769A-38	Sequence 38, Appli
9	637.5	35.5	1284	US-08-860-882A-71	Sequence 71, Appli
10	637.5	35.5	1284	US-09-011-769A-55	Sequence 55, Appli
11	622	34.6	1622	US-09-023-655-1020	Sequence 1020, Ap
12	619.5	34.5	1311	US-09-675-305-9	Sequence 9, Appli

13	619.5	34.5	1311	4	US-10-200-344-9	Sequence 9, Appli
14	619.5	34.5	2154	3	US-09-171-945-124	Sequence 124, App
15	610	33.9	927	2	US-08-782-760-5	Sequence 5, Appli
16	610	33.9	927	5	PCT-US96-00995-5	Sequence 5, Appli
17	582	32.4	921	1	US-08-696-139-3	Sequence 3, Appli
18	571.5	31.8	921	4	US-09-675-305-13	Sequence 13, Appl
19	571.5	31.8	2128	4	US-10-200-344-13	Sequence 13, Appl
20	567	31.5	999	2	US-08-860-882A-67	Sequence 67, Appl
21	567	31.5	999	4	US-09-011-769A-50	Sequence 50, Appl
22	567	31.5	1053	2	US-08-860-882A-64	Sequence 64, Appl
23	567	31.5	1053	4	US-09-011-769A-46	Sequence 46, Appl
24	560	31.1	1053	4	US-09-463-451-27	Sequence 27, Appl
25	560	31.1	1053	4	US-09-463-451-28	Sequence 28, Appl
26	560	31.1	1059	2	US-08-860-882A-74	Sequence 74, Appl
27	560	31.1	1059	4	US-09-011-769A-59	Sequence 59, Appl
28	559	31.1	1059	2	US-08-860-882A-77	Sequence 77, Appl
29	559	31.1	1059	4	US-09-011-769A-63	Sequence 63, Appl
30	554	30.8	1200	4	US-09-710-099-7	Sequence 7, Appli
31	554	30.8	1200	4	US-10-200-910-7	Sequence 7, Appli
32	549	30.5	1870	3	US-09-171-945-112	Sequence 112, App
33	534.5	29.7	1050	4	US-09-675-305-11	Sequence 11, Appl
34	534.5	29.7	1050	4	US-10-200-344-11	Sequence 11, Appl
35	527.5	29.3	1311	4	US-09-710-099-5	Sequence 5, Appli
36	527.5	29.3	1311	4	US-10-200-910-5	Sequence 5, Appli
37	516.5	28.7	1251	3	US-08-640-906-3	Sequence 3, Appli
38	516.5	28.7	1251	3	US-09-395-936-3	Sequence 3, Appli
39	491.5	27.3	1257	3	US-08-640-906-1	Sequence 1, Appli
40	491.5	27.3	1257	3	US-09-395-936-1	Sequence 1, Appli
41	467.5	26.0	945	4	US-09-710-099-3	Sequence 3, Appli
42	467.5	26.0	945	4	US-09-710-099-11	Sequence 11, Appl
43	467.5	26.0	945	4	US-10-200-910-3	Sequence 3, Appli
44	467.5	26.0	945	4	US-10-200-910-11	Sequence 11, Appl
45	465.5	25.9	2247	4	US-09-710-099-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-09-813-133A-1

; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 3,19e-215 Length: 1625  
Score: 1749.50 Matches: 336  
Percent Similarity: 94.38% Conservative: 0  
Best Local Similarity: 94.38% Mismatches: 2  
Query Match: 97.30% Indels: 18  
DB: 4 Gaps: 1

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

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QY	21	GlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle	40

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Qy 41 VallyslyslsGlnValHisPhePheValAsnAlaSerAspValAspAsnVallyAla 60
Db 203 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAGCC 262
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80
Db 263 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTGTGGCAGATGTGGAAGATCTTATT 322
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
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Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 383 TATCACTCACATAATGAATCTATTCTTGGATGAATTTATAACTGAGAGCATCTTGAT 442
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Qy 141 ValSerGlyLysGluGlnThrAlaIleAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 503 GTTTCGGAAGAAGAACAGACGACCAAAATGCCATATGGATTGACTGTGGAATCCATGCC 562
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180
Db 563 AGAAGATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATAATCGAATGTGGAGA 622
Qy 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200
Db 623 AAGAACCGTCTTCTATGCGAACAATCATTTGCAATCGGAACAGACCTGAAATAGGAACTTT 682
Qy 201 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCys 220
Db 683 GCTTCCAAACACTGGTGTGAGNAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGT 742
Qy 221 GlyLeuTyrProGluSerGluProGluVallyslsAlaValAlaSerPheLeuArgAsn 240
Db 743 GGACTTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTCTTCTGAGAAGAAAT 802
Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260
Db 803 ATCAACAGATTAAGACATACATCAGCATGATTCATCTACTCCAGCATATAGTGTTCGA 862
Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280
Db 863 TATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACGTCTCTAGTAGCCAGTGAA 922
Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300
Db 923 GCAGTTCGTGCTATTGAGAAAAATTAGTAAAAATACCAGGTATACACATGGCCATGGCTCA 982
Qy 301 GluThrLeuTyrLeuAlaProGlyGlyIleAspAspTrpIleTyrAspLeuGlyIle 320
Db 983 GAAACCTTATACCTAGCTCTCGAGAGGTGGGACCATGATGATTTGGGCATCAAA 1042
Qy 321 TyrSerPhe----- 323
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Qy 324 -ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 338
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RESULT 2
US-08-869-057-1
; Sequence 1, Application US/08869057
; Patent No. 5985562
; GENERAL INFORMATION:
; APPLICANT: Morser, Michael J
; APPLICANT: Nagashima, Mariko
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247 CATTAAATGTGACGGAAATTCATGCAGTGTCTTGCTGGCAGACGCTGGAAGATCTTATT 306  
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307 CAACAGCAGATTTCCACGACACACATGTCAGCCCGAGCCTCCGCATCGTACTATGAAACAG 366  
101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
367 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATACTGAGAGCATCTTGAT 426  
121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
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141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
487 GTTCTGGAAGAAGAACCAACGACCAAAATGCCATATGGATTGACTGGGAATCCATGCC 546  
161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175  
547 AGAAGATGGAATCTCTCTGCTTCTGCTTGGTTTCATAGGCCATATACTCAATCTTAT 606  
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607 GCGATAATAGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGTG 666  
176 ----- 176  
667 GTTAATGTGACGGTTATGACTACTCATGGAAGAAAGATCGAATGTGGAAGAAACCGT 726  
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204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
787 CACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTTAT 846  
224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243  
847 CCTGAGTCAGAACCAAGAGAGTGAAGCAGTGGCTAGTTCTTGAGAGAAATATCAACAG 906  
244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
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967 ACACGAAGTAAAGCAAGCAACCATGAGGAACGTCTCTAGTAGCCAGTGAAGCAGTTCT 1026  
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1027 GCTATTGAGAAAACTAGTAAAAATACAGGATGATACATGCGCATGGCTCAGAAACCTTA 1086  
304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323  
1087 TACCTAGCTCTGAGAGTGGGACGATTTGAUCTATGATTTGGGCATCAAAATATCGTTT 1146  
324 -----ThrSerAs 326  
1147 ACAATTTGAATTCGAGATAGGGCACATACGGATTCTTGTGCGGAGCGTTATACATCAA 1206  
326 nProProValGluLysLeuLeuProLeuSerLeuLys 338  
1207 CCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1243  
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; Sequence 2, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
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APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: hybridization probe  
LOCATION: 133 to 178  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: potential clip site  
LOCATION: 380 to 382  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: 41 to 106  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
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Score: 1732.00 Matches: 338  
Percent Similarity: 86.01% Conservative: 0  
Best Local Similarity: 86.01% Mismatches: 0  
Query Match: 96.33% Indels: 55  
DB: 2

US-09-980-881A-3 (1-338) x US-07-649-591B-2 (1-1749)  
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DB 167 CAGAATCTTACTACAAACATATGAGATTGTTCTCTGGCAGCCGGTAAACAGCTGACCTTATT 226  
QY 41 ValLysLysGluValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
DB 227 GTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGCAATCTGATGTCACATATGTGAAGCC 286

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Qy 61 HisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 287 CATTTAAATGTAGCGGAATTCATGCGAGTGTCTTGCGGAGAGCTGGAAGATCTTATT 346
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTCCACGACACACAGTACGCCCCGAGCTCCGATCGTACTATGACAG 406
Qy 101 TyrHisSerLeuAenGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTAATACTAGAGGATCTCGAT 466
Qy 121 MetLeuThrIleHisIleGlySerSerPheGluIleTyrProLeuTyrValLeuIlys 140
Db 467 ATGCTTACAAAATCCCAATTGGATCCCTATTGAGAAAGTACCCCACTCTATGTTTTAAAG 526
Qy 141 ValSerGlyIysGluGlnThrAlaIysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 527 GTTCTGAAAAGAACAAACAGCCAAATGCCATATGGATTGACTGTGGAAATCCATGCC 586
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175
Db 587 AGAGAAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATATAAATCAATTTCTAT 646
Qy 175 ----- 175
Db 647 GGGTAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706
Qy 176 -----AsnArgMetTrpArgIysAsnArg 183
Db 707 GTTAATGTGGACGGTTATGACTACTCATCGTGAAGAAAGATCAATGTGGAGAAAGACCGT 766
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerIys 203
Db 767 TCTTTCTATGCGAAACAATCAATTGCTATCGAAGACAGACCTGAATAGGAATTTGCTTCCAAA 826
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 827 CACTGGTGTAGGAAGGTGCATCCAGTTCTCATGCTCGGAACCTACTGTGGACTTTAT 886
Qy 224 ProGluSerGluProGluValIysAlaValAlaSerPheLeuArgAsnIleAsnGln 243
Db 887 CCTGAGTCAGAACACAGAGTGAAGCAGTGCAGTCTTCTTGAGAGAAATATCAACAG 946
Qy 244 IleIysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 947 ATTAAGCATATACATCAGCATGCATTCATPACTCCAGCATATAGTGTTCATATTCCTAT 1006
Qy 264 ThrArgSerIysSerIysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 1007 ACAGAAAGTAAAGCAAGACATGAGGAATGTTCTCTAGTAGCCAGTGAAGCAGTTCGT 1066
Qy 284 AlaIleGluIysThrSerIysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1067 GCTATTGAGAAACTAGTAAATATACAGGTATACACATGCCATCGCTCAGAAACCTTA 1126
Qy 304 TyrLeuAlaProGlyGlyAspTrpIleTyrAspLeuGlyIleIysTyrSerPhe 323
Db 1127 TACCTAGCTCCTGGAGGTGGGACGATGGATCTATGATTTGGGCATCAAAATATTCGTTT 1186
Qy 324 -----ThrSerAs 326
Db 1187 ACAATTGAACCTCGAGATACGGGCACATACGAGTTCTTGCTGCCGAGCGTTATACATAA 1246
Qy 326 nProProValGluIysLeuLeuProLeuSerLeuIlys 338
Db 1247 CCCACCTGTAGAGAGCTTTTGCCGCTGTCTCTRAAA 1283
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## RESULT 4

US-08-277-540-2

; Sequence 2, Application US/08277540

; Patent No. 5474901

; GENERAL INFORMATION:

```
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-277-540-2

Alignment Scores:
Pred. No.: 6,58e-213 Length: 1749
Score: 1732.00 Matches: 338
Percent Similarity: 86.01% Conservative: 0
Best Local Similarity: 86.01% Mismatches: 0
Query Match: 96.33% Indels: 55
DB: 1 Gaps: 2

US-09-980-881A-3 (1-338) x US-08-277-540-2 (1-1749)
Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 107 TTTTCAGAGTGCCCAAGTCTAGCTGCTCTTCTAGAACCTCTAGCAAGTTCAGATCTTA 166
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 167 CAGAACTCTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTGACCTTATT 226
Qy 41 VallysIysIysGlnValHisPhePheValAsnAlaSerAspValAsnValIysAla 60
Db 227 GTGAAGAAAAACAAGTCCATTTTTTTGTAATGTCATGTGTCGACAAATGTGAAGCC 286
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 287 CATTTAAATGTGACCGGAATTCATGATGATGCTTGTGGCAGACGTGGGAAGATCTTATT 346
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTCCACAGCACACAGTACGCCCCGAGCTCCGATCGTACTATGACAG 406
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QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGATCTCTGAT 466
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 467 ATGCTTACAAAATTCACATTGGATCCCTATTGAGAGTACCCACTCTATGTTTTAAAG 526
QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 527 GTTCTGGAAAAAGAACCAACGCCAAAATGCGATATGATGATGACTGTGGAATCCATGCC 586
QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175
Db 587 AGAGAAATGGATCTCTCTGCTTTCTGCTTGTGTTGTCATAGGCCATATAACTCAATCTTAT 646
QY 175 ----- 175
Db 647 GGGATAATAGGCAATATACCAATCTCTGAGGCTTGTGATTTCTATGTTATGCCGGTG 706
QY 176 -----AsnArgMetTrpArgLysAsnArg 183
Db 707 GTTAATGTGGACGGTTATCACTACTCATGCAAAAAGAAATCGAATGCGAGAAAGAACCGT 766
QY 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 767 TCTTTCTATGCGAACAATCATTCGATCGGAACAGACCTGAATAGGAACCTTCTGTTCCAAA 826
QY 204 HisTrpCysGluGluGlnValAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 827 CACTGTGTGAGAGAGTGCATCCAGTTCTCTATGCTCGGAACCTACTGTGACTTTAT 886
QY 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243
Db 887 CCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTTCTTGTGAGAGAAATATCAACACAG 946
QY 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 947 ATTAAGCATACATCATGATGCAATCATATCTCCAGCATATAGTGTTCATATTCCTAT 1006
QY 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 1007 ACACGAAGTAAAGCAAGCAAGCCATGAGGAAGTCTCTAGTAGCCAGTGAAGCAGTTCTG 1066
QY 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1067 GCTATTGAGAAAACCTAGTAAATAATACAGGTATACATGCGCCATGGCTCAGAAAACCTTA 1126
QY 304 TyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db 1127 TACCTAGCTCCTGGAGGTGGGAGCATGATGATCTATGATTTGGGCATCAAAATTCGTTT 1186
QY 324 -----ThrSerAs 326
Db 1187 ACAATTGAACCTCGAGATCGGCACATACCGGATTTCTGTGCGGAGCGTTACATCAAA 1246
QY 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1247 CCCACCTGTAGAGAGCTTTTGGCGGTGCTCTCTAAA 1283
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## RESULT 5

US-08-430-787A-2

; Sequence 2, Application US/08430787A

; Patent No. 5593674

; GENERAL INFORMATION:

; APPLICANT: Drayna, Dennis T., Eaton, Dan L.

; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

```
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-430-787A-2
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Alignment Scores:
Pred. No.: 6,58e-213 Length: 1749
Score: 1732.00 Matches: 338
Percent Similarity: 86.01% Conservative: 0
Best Local Similarity: 86.01% Mismatches: 0
Query Match: 96.33% Indels: 55
DB: 1 Gaps: 2
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US-09-980-881A-3 (1-338) x US-08-430-787A-2 (1-1749)

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QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 107 TTTCAGAGTGGCCAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166
QY 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 167 CAGAATCTTACTACAAATATGAGATTGTTCTCTGGCAGCCGCTAACAGCTGACCTTATT 226
QY 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db 227 GTGAGAAAAAACAAGTCCATTTTTTTGTAATATGTCATCTGATGTCACAAATGGAAGCC 286
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 287 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTCTGGCAGACCGCTGGAAGATCTTATT 346
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTCCTCAACGACACAGTCAGCCCCCGAGCCCTCCGATCTACTATGACAG 406
QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAAATCTATTCTTGATAGAATTTTATAACTGAGAGGATCTCTGAT 466
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174 QY -----GlyHis-----AsnArgMetTyrArgLysAsnArg 183  
Db CTCAATATTGATGCTACATACACCTGGACCAAGAGCCGATTTTGAGAAAGACTCGC 705  
184 QY SerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db TCCACCATACCTGATCTAGCTGATGGACACACCCCAACAGAAATTTT---GATGCT 762  
204 QY HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db GGTGGTGTGAATTTGAGCCCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCC 822  
224 QY ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243  
Db GCAGAGTCTGAAAGGAGCAACAGCCCTGGCTGATTTTCATCCGCAACAACTCTCTCC 882  
244 QY IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db ATCAGGCATATCTGACATCCACTCGTACTCCCAATGATGATCTACCCCTTACTCATAT 942  
264 QY ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db GCTTACAACTCGGTGAGAACATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1002  
284 QY AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db GAATCT---GCCTCACTGACCGCACCAAGTACACATATGGCCGGGAGCTTACAACT 1059  
304 QY TyrLeuAlaProGlyGlyGlyAspTyrIleTyrAspLeuGlyIleLysTyrSerPhe 323  
Db TATCTGCTGCTGGGGCTCTGACGACTGGCTTATGACCAAGGANTCAGATATCTCTTC 1119  
324 Thr 324  
1120 ACC 1122

## RESULT 8

US-09-011-769A-38  
; Sequence 38, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; BLAKEY, David C.  
; DAVIES, David H.  
; HENNAM, John F.  
; HENNEQUIN, Laurent F.A.  
; MARSHAM, Peter R.  
; DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011,769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2

; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1263 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-011-769A-38

Alignment Scores: 7.07e-72 Length: 1263  
Pred. No.: 637.50 Matches: 130  
Score: 54.85% Conservative: 68  
Percent Similarity: 36.01% Mismatches: 120  
Best Local Similarity: 35.46% Indels: 43  
Query Match: 4 Gaps: 6

US-09-980-881A-3 (1-338) x US-09-011-769A-38 (1-1263)

QY 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 58 TTTGAAGCGCAGAGGTGTTCCGTGTTAAGCTTGAAGTGAATCAATTAACATAATC 117  
QY 21 GlnAsnLeuThrThrThrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 118 CGCAGTGGCCAGCAGCCAGATTTCTTGGAAAGCCAGATTCTGTGCACACAAATC 177  
QY 41 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAspValLysAla 60  
Db 178 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAAGATACTGTCTGTGGAGAT 237  
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 238 GTTCTAAAGCAGATGAACTACATAAGGTACTGATAGCAACCTGAGAAATGGTG 297  
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 298 GAGGCTCAGTTTGATAGCCGGT-----CGTCAACACAGCAGACAGTATAGAAAG 348  
QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 349 TACAACAGTGGGAAACGATAGAGCTTGAGCTCAACAGCTGGCCACTGAGATCCAGCC 408  
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 409 CTCATCTCTGCAGTGTATTATCGGAACACATTTGAGGAGCGCGCTATTACTCTCTGAAG 468  
QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 469 GTT---GCCAAAGCTGGACAAATAAGCTGCCATTTTCATGGACTGTGGTTTCCATGCC 525  
QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173  
Db 526 AGAGAGTGGATTTCTCTGCTATCTCCAGTGGTTTGTAAAGAGAGCGCTTTCGTACTAT 585  
QY 173 ----- 173  
Db 586 GGACGTGAGATCCAAGTGACAGAGCTTCTCGCAAGTTAGACTTTTATGTCTCTGCTGTG 645  
QY 174 -----GlyHis-----AsnArgMetTyrArgLysAsnArg 183  
Db 646 CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCGGATTTTGAGAAAGACTCGC 705  
QY 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 706 TCCACCATACTGATCTAGCTGATGGACACACCCCAACAGAAATTTT---GATGCT 762  
QY 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223

Db 763 GGTGGTGTGAATGGAGCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCC 822  
Qy 224 ProGluSerGluProGluValValAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 823 GCAGAGTCTGAAGAGAAACCAAGGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTCC 882  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 883 ATCAGGCATATCTGCATCCACTCGTACTCTCCAAATGATGATCTACCTTACTCATAT 942  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 943 GCTTACAACTCGGTGAGAACAACTGCTGAGTTGAATGCCCTGCCTAAAGCTACTGTGAAA 1002  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1003 GAACCTT--GCCTCACTGCACGCCACCAAGTACACATATGGCCCGGAGCTACAAATC 1059  
Qy 304 TyrLeuAlaProGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyrSerPhe 323  
Db 1060 TATCTGCTGCTGGGGGCTCTGACGACTGGCTTATGACCAAGGAATCAGATATTCCTTC 1119  
Qy 324 Thr 324  
Db 1120 ACC 1122

RESULT 9

US-08-860-882A-71  
; Sequence 71, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGLESTE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HOW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860, 882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1284 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-860-882A-71  
Alignment Scores:  
Pred. No.: 7,27e-72 Length: 1284  
Score: 537.50 Matches: 130  
Percent Similarity: 54.85% Conservative: 68  
Best Local Similarity: 36.01% Mismatches: 120  
Query Match: 35.46% Indels: 43  
DB: 2 Gaps: 6  
US-09-980-881A-3 (1-338) x US-08-860-882A-71 (1-1284)  
Qy 1 PheGlnSerGlyGlnValValAlaValAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 85 TTTGAAGCGGAGAGGTGTTCCGTGTTAAAGTGAAGATGAAAAATCAATTAACATAATC 144  
Qy 21 GlnAsnLeuThrThrTyrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuLeu 40  
Db 145 CGCGAGTTGGCCAGCAGCCAGATTGACTTCTGGAAGCCAGATCTCTGTACACAATC 204  
Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 205 AAACCTCACAGTACAGTTGACTTCGTGCTTAAAGCAGAAGATGACTGTCTGCTGAGAAT 264  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80  
Db 265 GTTCTAAAGCAGAAATGAACATAACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 324  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 325 GAGGCTCAGTTGATAGCGGGTT-----CGTGAACAGGACACAGATTATGAGAG 375  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 376 TACAACAAGTGGAAACCGATAGAGCTTGGACTCAACAAGTCGCCACTGAGAAATCCAGCC 435  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 436 CTCATCTCTCGCAGTGTATCGAAACACATTTGAGGGACGCGCTATTTACCTCTCTGAAG 495  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIleHisAla 160  
Db 496 GTT--GGCAAGCTGGACAAATAAGCTGCTCATTTTCATGACTGTGTTTCCATGCC 552  
Qy 161 ArgGluTyrIleSerProAlaPheCysLeuTyrPheIle----- 173  
Db 553 AGAGAGTGGATTTCTCTCGCATCTTCCAGTGTGTTGTAAGAGAGGCTGTCTGTACCTAT 612  
Qy 173 ----- 173  
Db 613 GCAGGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGCTGCTGCTGTG 672  
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183  
Db 673 CTCAATATTGATGGCTACATCTACCTGGACAAGCGCGATTTTGGAGAAAGACTCGC 732  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 733 TCACCCATCTGGATCTAGCTGATGTCATGGCACAGACCCCAACAGAAATTTT---GATGCT 789  
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 790 GGTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGACCTGCC 849  
Qy 224 ProGluSerGluProGluValValAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 850 GCAGAGTCTGAAAGGAGAGACCAAGGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTCC 909  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 910 ATCAAGGCATATCTGCAATCTGACTCTGCTACTCCCAATATGATGATCTACCTTACTCATAT 969  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283



Db	1030	GAAC	TTT---	GCCT	CAC	TGC	ACG	GAC	CA	AGT	AC	A	TAT	TG	CCG	GAG	AGT	AC	A	CA	A	ATC	1086
Qy	304	Tyr	Leu	Ala	Pro	Gly	Gly	Asp	Asp	Trp	Ile	Tyr	Asp	Leu	Gly	Val	Leu	Tyr	Ser	Phe	323		
Dh	1087	TAT	CCG	TGC	TGC	TGC	GGG	GGT	TGA	CGA	TGG	CTT	TAT	GAC	CA	AG	AA	T	C	A	T	1146	

RESULT 11  
US-09-023-655-1020  
; Sequence 1020, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1020:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1622 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g179933  
US-09-023-655-1020

Qy	21	GlnAsnLeuThrThrThyTyrGluIleValLeuTprGlnProValThrAlaAspLeuIle	40
Db	121	AGGGACTTTGGCCAAACCAACATGAGCTTGACTCTCGTATCCAGGTGCCACCCACACGTA	180
Qy	41	VallysLysGlnValHisPheValAsnAlaSerAspValAspAsnValbysAla	60
Db	181	GCTGCTAAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCAAAGCCATCCAGTCT	240
Qy	61	HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle	80
Db	241	GCCTTGGATCAAAATAAATGCACTATGAAATCTTGATTCATGATCTCAAGAAGAGATT	300
Qy	81	GlnGlnIleSer--AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu	99
Db	301	GAGAAACATTTGATGTTAAAGAGATATCCGAGCAGGCACAGC-----TACGCA	351
Qy	100	GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro	119
Db	352	AAATACAATAATGGGAAAAGATTGTGGCTTGGACTGAAAGATGATGATAAGTATCCT	411
Qy	120	AspMetLeuThrIlysIleHisIleGlySerSerPheGluIlyTyrProLeuTyrValLeu	139
Db	412	GAAATGGTCTCTCGTATTAATAATTGGATCTACTGTITGAAGATAATCCACTATATGTTCG	471
Qy	140	LysValSerGlyIysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis	159
Db	472	AAGATT---GGGGAAAAGAAATGAAGAAGAAAGGCTATTTTATGGATTTGTGGCATTCAC	528
Qy	160	AlaArgGluTrpIleSerProAlaPheCysLeuTprPheIle-----	173
Db	529	GCACGAGAAATGGGTCTCCCGAGCATCTGCCAGTGTGTTGTTCTATCAGCAACCAAAACT	588
Qy	173	-----	173
Db	589	TATGGGAGAAACAAATTTATGACCAAACTCTTGGACCGGAATGAATTTTACATCTTCTCCT	648
Qy	174	-----GlyHis-----AsnArgMetTrpArgLysAsn	182
Db	649	GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAT	708
Qy	183	ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer	202
Db	709	CGTTCAGAACCAAACTCCAAATGCATCGGCACCTGACCTCAACAGGAATTTT---AAT	765
Qy	203	LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu	222
Db	766	GCITTCATGGAATCCATTCTCTAACCAATGACCCCATGTGCAGATAACTATCGGGCTCT	825
Qy	223	TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsn	242
Db	826	GCACCAAGTCCGAGAAAGACAGAAAGCTGTCACTAATTTTCATAGAAGCCACCTGAAT	885
Qy	243	GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer	262
Db	886	GAAATCAAGGTTTACATCACCTTCCATCTCTACTCCAGATGCTATTGTTTCCCTATGGA	945
Qy	263	TyrTrpArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal	282
Db	946	TATACATCAAACTGCCACCTAACCATGAGCACTTGGCCAAAGTTGCCAAGATTGGCACT	1005
Qy	283	ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr	302
Db	1006	GATGTTCTA--TCAACTCGATATGAACCCGCTACATCTATGGCCCAATAGAAATCAACA	1062
Qy	303	LeuTyrLeuAlaProGlyGlyIysAspAspTrpIleTyrAspLeuGlyIleLysTyrSer	322
Db	1063	ATTTACCAGCATATCAGGTCTCTTTTAGACTGGGCTTATGACCTGGGCATCAACACACA	1122
Qy	323	Phe	323
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US-09-675-305-9  
; Sequence 9, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
; FILE REFERENCE: Polynucleotides Encoding the Same  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1311  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-09-675-305-9

Alignment Scores:  
Pred. No.: 1,596-69 Length: 1311  
Score: 619.50 Matches: 136  
Percent Similarity: 51.15% Conservativeness: 64  
Best Local Similarity: 34.78% Indels: 64  
Query Match: 34.45% Gaps: 8  
DB:

US-09-980-881A-3 (1-338) x US-09-675-305-9 (1-1311)

Qy	1	PheGlnSerGlyClnValValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu	20
Db	109	TATGCTGGTGAATAAGTATGATATTTCCCAAAACAGAGAGAGCATATGCACTG	168
Qy	21	GlnAsnLeuThrThrThrGluLeuValLeuThrGlnProValThrAlaAspLeuLe	40
Db	169	AAGAAATATCTTATCAACTTAAGGTGGACCTGTGGCCAGCAGATCTCTCTATGTA	228
Qy	41	ValLys-----LysLysGlnValHisPheValAsnAlaSerAspValAsnVal	58
Db	229	TCAGAGGGAACAGTACTGATGTCATATCCCAAAATGGTTCAGAGCC-----CTG	282
Qy	59	LysAlaHisLeuAsnValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp	78
Db	283	TTAGCCTTCTTACAGAGCAACATCCAGTACAAAGTCTCTCATAGAGATCTTCAGAAA	342
Qy	79	LeuLeuGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSer-----	96
Db	343	ACACTGGAGAGGAGGAGCAGTTCGACACCCAGAGAAACCGAAGATCCCTCTCGATAT	402
Qy	97	TyrTyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGlu	116
Db	403	AATTATGAAGTTATCACTCTCTTAGAGAAATTCAAAATTGGATGCATCTCGAATAA	462
Qy	117	ArgHisProAspMetLeuThrLysIleHisLeuGlySerSerPheGluLysTyrProLeu	136
Db	463	ACTCACTCAGGCTCATTCACATGTTCTTATTTGAAGATCATATGAGGGAAGATCTCT	522
Qy	137	TyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCys	156
Db	523	TTTATTTTAAAGCTG---GGCAGAGCATCAAGACTCAAAAGAGCTGTTTGGATAGCTGT	579
Qy	157	GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle-----	173
Db	580	GGTATTCATGCAAGAGATGGATTGGTCTGCTGCTTTGTCAGTGGTTGTTAAAGAGCT	639
Qy	173	-----	173



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Qy   300 SerGluThrTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyVal 319
Db   1114 TCACAAACGGTTGTATGTAGCTCTGGTAGCTCAATGGATTGGCCCTACAAAATGGATA 1173
Qy   320 LysTyrSerPhe----- 323
Db   1174 CCTATTCGATTTCGTTTCGNACTACCTGCACATGGATATTTTGATTTTTTACTCCAGAG 1233
Qy   324 ----ThrSerAsnProValGlnLysLeu 332
Db   1234 ATGCTCATCAAAACCACCTGTGTACAGAAACTA 1264

RESULT 14
US-09-171-945-124
; Sequence 124, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-124

Alignment Scores:
Pred. No.:          3,74e-69           Length:      2154
Score:             619.50            Matches:     127
Percent Similarity: 54.29%           Conservative: 69
Best Local Similarity: 35.18%        Mismatches:  122
Query Match:       34.45%            Indels:      43
DB:                 3                Gaps:        6

US-09-980-881A-3 (1-338) x US-09-171-945-124 (1-2154)
Qy    1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db   64 TTTGAAGCGAGAAGGTGTTCCGTGTAAACGTTGAAGATGAAATCACAATTAACTAATC 123
Qy   21 GlnAsnLeuThrThrTyrGzGuileValLeuTrpGlnProValThrAlaAspLeulle 40
Db   124 CGCGAGTTGGCCAGCACGCCAGCATTTGACTTCTGGAAGCCAGATTTCTGTCCACAAATC 183
Qy   41 ValLysLysLysGlnValHisPhePheValAsnHisSerAspValAspValAspValLysala 60
Db   184 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAAGATACGTGCTGAGGAAT 243
Qy   61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeulle 80
Db   244 GTTCTTAAGACAGATGAACATAACAATACAGGTACTGTATGAACCACTGAGAAATGTGGTG 303
Qy   81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGln 100
Db   304 GAGGCTCAGTTGTATAGCCGGTT-----CGTGCACAGGACACACAGTTATGAGAAG 354
Qy  101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120

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355	TACACAAGTGGGAAACGATAGAGGCTTGAGACTCAACAAGTCGCCACTGAGAAATCCAGCC	414
121	MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys	140
415	CTCATCTCTCGAGTGTTATCGGAACACACATTTGAGGAGCGGCTATTACCTCTCTGAAG	474
141	ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla	160
475	GTT---GGCAAAAGCTGGACAAAATAAGCTGCCATTTTCATGACTGTGGTTCCTCATGCC	531
161	ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle	173
532	AGAGAGTGGATTTCTCTCTGCAATCTCGCAGTGGTTTGTAAAGAGGCGTGTTCGTACCTAT	591
173	-----	173
592	GGAGTGGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTTATGCTCGCCTGTG	651
174	-----GlyHis-----AsnArgMetTrpArgLysAsnArg	183
652	CTCAATATTGATGGCTACATCTACACTGGACCAAGAGCGGATTTTGGAGAAAGACTCGC	711
184	SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys	203
712	TCCACCATACTGGATCTAGCTGCATTGGCACAGACCCCAACAGAAATTTT---GATGCT	768
204	HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr	223
769	GGTTGGTGTGAAATTTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC	828
224	ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln	243
829	GCAGAGTCTGAAAGGAGACCAAGGCCCTGGCTGATTCATCGCAACAACAACCTCTCTTC	888
244	IleLeuAlaTrpIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr	263
889	ATCAAGGCATATCTGACAATCCACTCGTACTCCCAATGATGATCATACCTTACTCATAT	948
264	ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg	283
949	GCTTACAAACTCGGTGAGAACAAATGCTGAGTTGAAATGCCCTGGCTAAAGCTACTGTGAAA	1008
284	AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu	303
1009	GAACTT---GCCTCATGCGAGGCACCAAGTACACATATGCGCCGGAGCTCAACAACTC	1065
304	TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe	323
1066	TATCCTTCTCTGGACTTCTAAAGACTGGCTTATGACCAAGGAATCAGATATTCCTTC	1125
324	Thr 324	
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**RESULT 15**

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US-08-782-760-5
; Sequence 5, Application US/08782760
; Patent No. 5948668
;
; GENERAL INFORMATION:
;
; APPLICANT: Hartman, Jacob
; APPLICANT: Fulga, Netta
; APPLICANT: Mendelovitch, Simona
; APPLICANT: Gorecki, Marian
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

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Db 418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGC 474  
Qy 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 235  
Db 475 TCTGAACTTACTGTGGACCAAGCCCGAGTCTGAAAAGAGACAAAGGCCCTGGCAGAT 534  
Qy 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255  
Db 535 TTCATCCGCAACAACCTCTCCACCATCAAGGCTACTGACCATCCACTCATACTCACAG 594  
Qy 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275  
Db 595 ATGATGCTCTACCTTACTCTCTATGACTACAACTGCCCTGAGAACTATGAGGAATTGAAT 654  
Qy 276 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295  
Db 655 GCCCTGGTGAAGGTGGCGCAAGGAGCTT---GCCACTCTGCTGATGGCACCAGTACACA 711  
Qy 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyr 315  
Db 712 TATGCCCCAGGAGCTACACATCTATCTGCTGGGGGATCTGACGACTGGTCTTAT 771  
Qy 316 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 335  
Db 772 GATCAGGGAATCAATATTCTTTACCTTTGAACT-CGGGATACAGGCTTCTTTGGCTT 830  
Qy 336 Ser 336  
Db 831 TCT 833

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Job time : 100.797 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 27, 2004, 01:54:23 ; Search time 1619.11 Seconds  
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Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-MAXLEN=2000000000 -USER=US09980881@cgn\_1\_103@runat\_26102004\_084115\_7269  
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-FCAPOP=6 -FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1732	96.3	1728	9	US-09-880-107-2396
4	1708.5	95.0	1344	16	US-10-115-479-69
5	1708.5	95.0	1743	16	US-10-115-479-67
6	1628	90.5	1272	15	US-10-379-836-1
7	1329.5	73.9	1037	16	US-10-115-479-63
8	1290.5	71.8	1132	16	US-10-115-479-65
9	902	50.2	1400	9	US-09-925-302-24
10	902	50.2	1400	10	US-09-925-302-24
11	622	34.6	1254	14	US-10-229-546-3
12	622	34.6	1622	14	US-10-229-546-1
13	622	34.6	1622	15	US-10-429-802-21
14	622	34.6	1622	16	US-10-430-503-12
15	622	34.6	1622	16	US-10-262-511-71
16	622	34.6	1622	16	US-10-641-643-1020
17	622	34.6	1633	15	US-10-341-434-187
18	622	34.6	1740	14	US-10-116-802-95
19	619.5	34.5	1302	17	US-10-477-515-1
20	619.5	34.5	1311	13	US-10-200-344-9
21	619.5	34.5	1993	15	US-10-274-639-33
22	619.5	34.5	1993	16	US-10-333-574-33
23	619.5	34.5	2154	9	US-09-910-059-124
24	618	34.4	1332	9	US-09-954-456-1141
25	617.5	34.3	1907	18	US-10-757-262-127
26	591	32.9	416	9	US-09-960-352-14595
27	571.5	31.8	1218	13	US-10-200-344-13
28	569	31.6	1125	9	US-09-888-615-2
29	569	31.6	1332	15	US-10-176-306-75
30	569	31.6	1603	15	US-10-176-306-73
31	562	31.3	1826	15	US-10-252-157-453
32	554	30.8	1200	14	US-10-200-910-7
33	554	30.8	1200	18	US-10-843-130-7
34	549	30.5	1870	9	US-09-910-059-112
35	549	30.5	1870	17	US-10-608-710-3
36	534.5	29.7	1050	13	US-10-200-344-11
37	533.5	29.7	991	16	US-10-383-201-93
38	527.5	29.3	1260	16	US-10-257-174-16
39	527.5	29.3	1311	14	US-10-200-910-5
40	527.5	29.3	1311	16	US-10-257-174-15
41	527.5	29.3	1311	17	US-10-451-821-1
42	527.5	29.3	1311	18	US-10-843-130-5
43	527.5	29.3	1348	16	US-10-072-012-315
44	527.5	29.3	1641	17	US-10-381-820A-5
45	523.5	29.1	1295	17	US-10-363-829-148

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Pred. No.: 6,31e-206 Length: 1625  
Score: 1749.50 Matches: 336  
Percent Similarity: 94.38% Conservative: 0  
Best Local Similarity: 94.38% Mismatches: 2  
Query Match: 97.30% Indels: 18  
DB: 9 Gaps: 1

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTCCAGAGTGCCCAAGTTCTAGTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 142

Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 143 CAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTGACCTTATT 202

Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspValLysAla 60  
Db 203 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGCAATGTGAAAGCC 262

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGCGGGAATTCATGCAGTGTCTTGTGGCAGATGTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCAAACGACACAGTCCAGCCCGGAGCTCCGCATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCCTCCTCACTAAATGAAATCTATTCTTGGATAGAAATTTATACTGAGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAAATCCCAATTTGGATCTCTCTTTCAGAAAGTACCCACCTCTATGTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTTCTGGAAGAAGAACAGACGACCAAAATGCCATATGGATTGATCTGGGAATCCATGCC 562

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180  
Db 563 AGAAGTGGATCTCTCTGCTTTCTGCTTGGTTTCATAGGCCATATATCGAATGTGAGA 622

Qy 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 623 AAGAACCCTTCTTCTATGCGAACCAATCATTTGCATCGGAACAGACCTGAATAGGAACCTT 682

Qy 201 AlaSerLysHisTrpCysGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 220  
Db 683 GCTTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTATGCTCGGAACCTACTGT 742

Qy 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 240  
Db 743 GGACTTTATCTGAGTCAGAACCGAAGTGAAGCAGTGGCTAGTTCTTCTGGAGAAGAAAT 802

Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 803 ATCAACAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTCTTCCA 862

Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGlu 280  
Db 863 TATTCTCTATACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAGTGAA 922

Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 923 GCAGTTCTGCTATTGAGAAATATGATTAATAATACAGGATATACATGGCCATGGCTCA 982

Qy 301 GluThrLeuTyrLeuAlaProGlyGlyCysAspAspTrpIleTyrAspLeuGlyIleLys 320  
Db 983 GAAACCTTATACCTAGCTCTCTGGAGTGGGACGATGGATCTATGATTTGGGCATCAAA 1042

Qy 321 TyrSerPhe----- 323  
Db 1043 TATTCTGTTTACAATGAATTCGAGATACGGGCACATACGATTTCTTGTGCCGGAGCGT 1102

Qy 324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1103 TACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTTAAAA 1148

RESULT 2  
US-10-212-877-1  
; Sequence 1, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; PRIOR FILING DATE: 2002-08-07  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-877-1

Alignment Scores:  
Pred. No.: 6,31e-206 Length: 1625  
Score: 1749.50 Matches: 336  
Percent Similarity: 94.38% Conservative: 0  
Best Local Similarity: 94.38% Mismatches: 2  
Query Match: 97.30% Indels: 18  
DB: 14 Gaps: 1

US-09-980-881A-3 (1-338) x US-10-212-877-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTCCAGAGTGCCCAAGTTCTAGTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 142

Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 143 CAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTGACCTTATT 202

Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspValLysAla 60  
Db 203 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGCAATGTGAAAGCC 262

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGCGGGAATTCATGCAGTGTCTTGTGGCAGATGTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCAAACGACACAGTCCAGCCCGGAGCTCCGCATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCCTCCTCACTAAATGAAATCTATTCTTGGATAGAAATTTATACTGAGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAAATCCCAATTTGGATCTCTCTTTCAGAAAGTACCCACCTCTATGTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTTCTGGAAGAAGAACAGACGACCAAAATGCCATATGGATTGATCTGGGAATCCATGCC 562

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180

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Db 563 AGAGNATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGCCATATCGAATGTGGAGA 622
Qy 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200
Db 623 AAGAACCGTCTCTTCTATGCGAACAATCATTTGCATCGGAACAGACCTGAATAGGAACCTTT 682
Qy 201 AlaSerLysHisTyrCysGluGluClyAlaSerSerSerCysSerGluThrTyrCys 220
Db 683 GCTTCCAAACACTGTGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGT 742
Qy 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaLaserPheLeuArgAsn 240
Db 743 GGACTTTATCTGAGTCAGACCAAGCAAGTGAAGCGAGTGGCTAGTTCTTGAGAAGAAAT 802
Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260
Db 803 ATCAACCAAGATTAAAGCATACATCAGCATGCATTCATACCTCCAGCATATAGTGTTCCTCA 862
Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280
Db 863 TATTCCTATACACGAAGTAAAGCAAGCAACCAATGAGGAACCTGCTCTAGTAGCCAGTGAA 922
Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300
Db 923 GCAGTTCGTGCTATTGAGAAATATTAGTAAATATACCAAGTATACATGCGCATGGCTCA 982
Qy 301 GluThrLeuTyrLeuAlaProGlyGlyAspAspTyrIleTyrAspLeuGlyIleLys 320
Db 983 GAAACCTTATACCTAGTCTCTGGAGTGGGAGCGATTGGATCTATGATTTGGGCACTCAA 1042
Qy 321 TyrSerPhe----- 323
Db 1043 TATTCGTTTACAACTTCGAGATACGGGCACATACGGATTCTTGCTCCCGGAGCGT 1102
Qy 324 -ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1103 TACATCAAAACCCACCTGTAGAGAGCTTTTGGCGGTGCTCTTAA 1148

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RESULT 3

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US-09-880-107-2396
: Sequence 2396, Application US/09880107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Horne, Darci T.
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Scherf, Uwe
: APPLICANT: Gene Logic, Inc.
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: CURRENT FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2396
: LENGTH: 1728
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396

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Alignment Scores:

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Pred. No.: 1,03e-203 Length: 1728
Score: 1732.00 Matches: 338
Percent Similarity: 86.01% Conservative: 0
Best Local Similarity: 86.01% Mismatches: 0
Query Match: 96.33% Indels: 55
DB: 9 Gaps: 2

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US-09-980-881A-3 (1-338) x US-09-880-107-2396 (1-1728)
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 86 TTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAAACCTCTAGGCAAGTTCAAGTTCTA 145
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 146 CAGAACTCTTACTACAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 205
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db 206 GTGAAGAAAAAACAAAGTCCATTTTTTTTGTAAATGCATCTGATGTGCGAATGTGAAAGCC 265
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 266 CATTTAAATGTGCGGGAATTCATGCAATGCTCTTGTGGCAGAGCTGGAAGATCTTATT 325
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 326 CAACAGCAGATTTCCAAACGACACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 385
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 386 TATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATACTGAGAGCATCCTCGAT 445
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 446 ATGCTTCAAAAATCCCAATTTGGATCTCTATTGAGAAGTACCCACTCTATGTTTAAAG 505
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 506 GTTTCTGGAAGAAACAAACAGCCAAATGCCATATGGAATGACTGTGGAATCCATGCC 565
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175
Db 566 AGAAGATGGAATCTCTCTGCTTCTTCTGCTTGTGTTTCTATAGGCCATATAAATCAATCTAT 625
Qy 175 ----- 175
Db 626 GGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTCTATGTTATGCGCGTG 685
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183
Db 686 GTTAATGTGACGGTTATGACTACTCATGGAAGAAATCGAATGTGAGAAAGAACCGT 745
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 746 TCTTTCTATCGAACAATCAATTCATTCGGAACAGACCTGGAATAGGAACCTTTGCTTCCAAA 805
Qy 204 HisTrpCysGluGluGluValSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 806 CACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGAAACACTCTGTGACATTTAT 865
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243
Db 866 CTTGAGTCAGAACCCAGAGTGAAGCAGTGGCTAGTTCTTCTGAGAAGAAATATCAACCAG 925
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 926 ATTTAAAGCATACATCAGCATGCATTCATACCTCCAGCATATAGTGTGTTCCCATATTCCTAT 985
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 986 ACACGAAGTAAAGCAAGACCATCAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGT 1045
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1046 GCTATTGAGAAACCTAGTAAATATACAGGTATACATGCGCATGCGCTCAGAAACCTTAA 1105
Qy 304 TyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyrSerPhe 323

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Db 1106 TACCTAGCTCCTGGAGTGGGACGATGGATCTATGATTTGGGCATCAATATTCGTTT 1165  
Qy 324 -----ThrSerAs 326  
Db 1166 ACAATTGAACCTTCGAGATACGGCACATACCGGATTTCTTGCTGCGGAGCGTTACATCAAA 1225  
Qy 326 nProProValGluLysLeuProLeuSerLeuLys 338  
Db 1226 CCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1262  
RESULT 4  
US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US2004000205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerkusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 69  
; LENGTH: 1344  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: (31)..(1315)  
US-10-115-479-69  
Alignment Scores: 5.59e-201 Length: 1344  
Pred. No.: 1708.50 Matches: 336  
Score: 1708.50 Conservativeness: 0  
Percent Similarity: 84.42% Mismatches: 2  
Best Local Similarity: 84.42% Indels: 60  
Query Match: 95.02% DB: 3  
Caps: 3  
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Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 97 TTTTCAGAGTGGCCAAAGTTCTAGCTGCTTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 156  
Qy 21 GlnAsnLeuThrThrThrGluLeuValLeuTrpGlnProValThrAlaAspLeuLe 40  
Db 157 CAGAATCTTACTCAACATATGAGATTGTCTCTGGCAGCCGGTAACAGCTGACCTTATT 216  
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 217 GTGAGAGAAAAACAAGTCCATTTTGTAAATGCATCTCATGTCGACATGTGAAGCC 276  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuLe 80  
Db 277 CATTTAAATGTGACGCGGAATTCATGCAATGCTGTCTTGTGGCAGACGTTGAAGATCTTTATT 336  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 337 CAACAGCAGATTTTCCAAACGACACAGTCAGCCCCCGACCTCCGCATCGTACTATGAACAG 396  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 397 TATCACTCACTAAATGAATCTATTCTTGGATAGATTTTATACTGAGAGCATCTTGAT 456  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 457 ATGCTTACAAAAATCCACATTTGGATTCCTCATTTTGAGAAGTACCACACTCTATGTTTAAAG 516  
Qy 141 -----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp 155  
Db 517 GGTTCCTTTGAGCAGGTTTCTGGAAAAAACAAGACGCCAAATAATGCCATATGGATTGAC 576  
Qy 156 CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 577 TGTGGAATCCATGCCAGAGATGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 636  
Qy 175 ----- 175  
Db 637 ATAACCTCAATTCATGGGATAATAGGGCAATATACCAATCTCCTGAGGCTTTGTGGATTTC 696  
Qy 176 -----AsnArgMet 178  
Db 697 TATGTTATGCCGGTGGTTAATGTGGATGGTGTATGACTACTATCGAAAAAAGATCGAATG 756  
Qy 179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198  
Db 757 TGGAGAAAAAGAACCGTTCTTTCTATGCGAACCAATCATTTGCATCGGAACAGACCTGAATAG 816  
Qy 199 AsnPheAlaSerLysHisTrpCysGluGluGluValAserSerSerSerSerGluThr 218  
Db 817 AACTTTGCTTCCAAACACTCGTGTGAGGAAGGTGCATCCAGTTCTCTCATCTCGGAACACC 876  
Qy 219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 238  
Db 877 TACTGTGGACTTTATCTCTGAGTCAGAACCAAGAGTAGGACGAGTGGCTAGTTCTTCGAGA 936  
Qy 239 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258  
Db 937 AGAAATATCAACCCAGATTAAGCATATACATCAGCATGCATTTCATCTCCAGCATATAGTG 996



QY 259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 278  
Db 997 TTTCCATATTCCTATACAGAGTAAAGCAAGCAATGAGAACTGCTCTAGTAGCC 1056  
QY 279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298  
Db 1057 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAATAATACAGGTATACACATGGCCAT 1116  
QY 299 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 318  
Db 1117 GCGTCAGAAACCTTATACCTAGCTCTCGAGGTGGGACGATGGATCTATGATTTGGGC 1176  
QY 319 IleLysTyrSerPhe----- 323  
Db 1177 ATCAAAATATTCGTTTACAAATCGAATTCGAGATCGGGCACATACGGATTCTTGTGCGCG 1236  
QY 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1237 GAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1288

RESULT 5

US-10-115-479-67  
; Sequence 67, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytak, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 67  
; LENGTH: 1743  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (20)..(1304)  
US-10-115-479-67  
Alignment Scores:  
Pred. No.: 8,55e-201 Length: 1743  
Score: 1708.50 Matches: 336  
Percent Similarity: 84.42% Conservative: 0  
Best Local Similarity: 84.42% Mismatches: 2  
Query Match: 95.02% Indels: 60  
DB: 16 Gaps: 3  
US-09-980-881A-3 (1-338) x US-10-115-479-67 (1-1743)  
QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 86 TTTCCAGAGTGCCCAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 145  
QY 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 146 CAGAATCTTACTACAAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTAT 205  
QY 41 VallysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVallyAla 60  
Db 206 GTGAAGAAAAACAAGTCCATTTTTTTGTAATGCAATCTGATGTCGACAACTGTGAAGCC 265  
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 266 CATTTAAATGTGAGCGGAATCCATGCACTGCTGTTGTCGACAGCGTGAAGATCTTAT 325  
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 326 CAACAGCAGATTTCCAAACGACACAGTCAGCCCCCGAGCTCCGCACTGCTATGAACAC 385  
QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 386 TATCACTCACTAAATGAATCTTATTTGGATAGAAATTTTATTAACCTGAGAGGCATCTGAT 445  
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 446 ATGCTTACAAAATCCACATTCGATCTCATTTGAGAGTACCCTCTATGTTTTAAAG 505  
QY 141 -----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp 155  
Db 506 GGTTCCTTTGAGCAGGTTTCTGAAAAAGAAACAAGCAAGCAAAATGCCATATGGATTGAC 565  
QY 156 CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 566 TGTGGAATCCATGCCAGAAATGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 625  
QY 175 ----- 175  
Db 626 ATAACCTCAATTCATGGGATAATAGGGCAATATACCAATCTCTCTGAGGCTTGTGGATTTC 685  
QY 176 -----AsnArgMet 178  
Db 686 TATGTTATGCCAGTGGTTAATGTGGATGTTATGACTACTCTATCGAAAAAGAAATCGAATG 745  
QY 179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198  
Db 746 TGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGATCGGAAACAGACCTGAATAGG 805

199	Qy	AsnPheAlaSerLyHisTrpCysGluGluClyAlaSerSerSerCysSerGluThr	218
806	Db	AACTTTGCTTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGTCGGAAC	865
219	Qy	TyrCysGlyLeuTyrProGluSerGluProGluValysAlaValAlaSerPheLeuArg	238
866	Db	TACTGTGGACTTATCTCTGAGTCAGAACCCAGAGTGAAGGCAGTGGCTAGTTCTTGAGA	925
239	Qy	ArgAsnIleAsnGlnIleLyAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal	258
926	Db	AGAAATATCAACAGATTAAGCATACATCAGCATGCATTCATACTCCAGCATATAGTG	985
259	Qy	PheProTyrSerTyrThrArgSerLySerLyAspHisGluGluLeuSerLeuValAla	278
986	Db	TTTCCATATTCCCTATACACGAAGTAAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCC	1045
279	Qy	SerGluAlaValArgAlaIleGluLyThrSerLyAsnThrArgTyrThrHisGlyHis	298
1046	Db	AGTGAACGAGTTCGTGCTATTGAGAAATTAGTAAATAATACCAAGTATACACATGGCCAT	1105
299	Qy	GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly	318
1106	Db	GGCTCGAACAACCTTATACCTAGTCTCTGAGGTGGGACGATTGGATCTATGATTTGGGC	1165
319	Qy	IleLySyrSerPhe-----	323
1166	Db	ATCAATATTCTGTTTACAAATTGAACCTCGAGATACGGGCACATACGGAATTCCTGCTGCCG	1225
324	Qy	-----ThrSerAsnProProValGluLyLeuLeuProLeuSerLeuLyS	338
1226	Db	GAGCGTTACATCAAAACCCACTGCTAGAGAAGCTTTTGCCTGCTGCTCTAAAA	1277

## RESULT 6

```

US-10-379-836--1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
US-10-379-836-1

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Alignment Scores:		
Pred. No.:	4.86e-191	Length:
Score:	1628.00	Matches:
Percent Similarity:	83.21%	Conservative:
Best Local Similarity:	90.92%	Mismatches:
Query Match:	90.55%	Indels:
DB:	15	Gaps:
		2

US-09-980-881A-3 (1-338) x US-10-379-836-1 (1-1272)

1	PheGlnSerGlyGlnValIleuAlaLeuProArgThrSerArgGlnValGlnValLeu	20
67	TTTCAGAGTGGCCAGGTTCTAGCTGCTTCTCTAGAACCTCTAGGCCAAGTTC	126
21	GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle	40
127	CAGATCTTACTTACAAATATGAGATTGTCTCTGGCAGCCGGTACACAGCGACCTTAT	186

RESULT 7  
US-10-115-479-63  
; Sequence 63, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 63  
; LENGTH: 1037  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (41)..(1007)  
US-10-115-479-63  
Alignment Scores:  
Pred. No.: 3,48e-154  
Score: 1329.50  
Percent Similarity: 76.40%  
Best Local Similarity: 76.40%  
Query Match: 82  
Length: 1037  
Matches: 272  
Conservative: 0  
Mismatch: 2  
Indels: 82

DB: 16 Gaps: 2  
US-09-980-881a-3 (1-338) x US-10-115-479-63 (1-1037)  
QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTT CAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTAGCAAGTTCAAGTTCTA 166  
QY 21 GlnAsnLeuThrThrThrGluLeuValLeuTrpGlnProValThrAlaAspLeuLeu 40  
Db 167 CAGAACTCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226  
QY 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspValAspValLysAla 60  
Db 227 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTGCAACATGTGAAGCC 286  
QY 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80  
Db 287 CATTTAAATGTGAGCGGAATTCATGCAAGTGTCTTCTGGCAGAGCTGGAGAGATCTTATT 346  
QY 81 GlnGlnGlnLeuSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTCCACGACACACAGTCAGCCCCCGAGGCTCCGCATCTGCTACTATGAACAG 406  
QY 101 TyrHisSerLeuAsnGluLeuTyrSerTrpLeuGluPheLeuThrGluArgHisProAsp 120  
Db 407 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAAATCTGAGAGCATCTCGAT 466  
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 467 ATGCTTACAAAAATCCACATCGATCCCTATTGAGAAAGTACCCACTCTATGTTTTTAAG 526  
QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 527 GTTCTCGAAAAGAACACAGACGACCCAAAATGCCATATGATGATGAC----- 571  
QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180  
Db 571 ----- 571  
QY 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 571 ----- 571  
QY 201 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 220  
Db 572 -----TCT 574  
QY 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 240  
Db 575 GGACTTTTATCTGAGTCAGAACAGAGTGAAGGAGTGGCTAGTTCTTTGAGAGAAAT 634  
QY 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 635 ATCAACCCAGATTAAAGCATACATCAGCATGCACTCATCTCCAGCATATAGTGTTCGA 694  
QY 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
Db 695 TATCTCTATACAGAAAGTAAAGCAAGCAAGCCATGAGAACTGTCTCTAGTACCGAGTAA 754  
QY 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 755 GCAGITCGTGCTATTGAGAAAAATTAGTAAAAATACCAGGTATACATACATGCCATGCTCA 814  
QY 301 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 320  
Db 815 GAAACCTTATACCTAGCTCTCTGGAGTGGGAGCATGATGATCTATGATTGGGCATCAAA 874  
QY 321 TyrSerPhe----- 323  
Db 875 TATTCGTTTACAAATTCGAGATACGGGCACATACGGATTCTTGTGCGGAGCGT 934  
QY 324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338

Db 935 TACATCAACCCACCTGTAGAGACCTTTTGGCGCTGTCTCTAAAA 980

RESULT 8

US-10-115-479-65

; Sequence 65, Application US/10115479

; Publication No. US20040006205A1

; GENERAL INFORMATION:

; APPLICANT: Li, Li

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Liu, Xiaohong

; APPLICANT: Miller, Charles E.

; APPLICANT: Spyttek, Kimberly A.

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Zhong, Haihong

; APPLICANT: Smithson, Glendda

; APPLICANT: Casman, Stacie J.

; APPLICANT: Boldog, Ferenc L.;

; APPLICANT: Voss, Edward

; APPLICANT: Vernet, Corine

; APPLICANT: MacDougall, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Anderson, David W.

; APPLICANT: Zhong, Mei

; APPLICANT: Mezes, Peter S.

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Malyanker, Uriel M.

; APPLICANT: Shinkets, Richard A.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-322 B (Cura 622 PT)

; CURRENT APPLICATION NUMBER: US/10/115,479

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 60/281,136

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281,863

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/281,906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282,934

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/283,657

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,678

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,687

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,710

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,234

; PRIOR FILING DATE: 2001-04-17

; PRIOR APPLICATION NUMBER: 60/285,325

; PRIOR FILING DATE: 2001-04-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 198

; SEQ ID NO 65

; LENGTH: 1132

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (41)..(1103)

US-10-115-479-65

Alignment Scores:

Pred. No.: 2,74e-149

Length: 1132

Score: 1290.50

Matches: 263

Percent Similarity:	66.08%	Conservative:	0
Best Local Similarity:	66.08%	Mismatches:	1
Query Match:	71.77%	Indels:	134
DB:	16	Gaps:	4
US-09-980-881A-3 (1-338) x US-10-115-479-65 (1-1132)			
Qy	1	PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu	20
Db	107	TTTCAGAGTGGCCAAAGTTCTAGCTCTCTCCAGAACCTCTAGGCAAGTTCAAGTTCTA	166
Qy	21	GlnAsnLeuThrThrThrGluValLeuTrpGlnProValThrAlaAspLeuIle	40
Db	167	CAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT	226
Qy	41	ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla	60
Db	227	GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAAGCC	286
Qy	61	HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle	80
Db	287	CAITTTAAATGTGAGCGGAATTCATGCAGTGTCTTGTGGCAGACGTGGAGAGATCTTATT	346
Qy	81	GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln	100
Db	347	CAACAGCAGATTTCCACACGACACAGTCAGCCCGAGSCCTCCGCATCTGACTATGAACAG	406
Qy	101	TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp	120
Db	407	TATCACTCACTAAATGAATCTATTCTTGGATGAATTTATACTGAGAGGCATCTCGAT	466
Qy	121	MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys	140
Db	467	ATGCTTACAAAAATCCACATTTGGATTCCTCATTTGAGAAGTACCCTCTATGTTTTAAAG	526
Qy	141	-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp	155
Db	527	GGTTTCTTTGAGCAGGTTTCTGGAAAGAAACAAGCAGCCAAAAATGCCATATGGATTGAC	586
Qy	156	CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis	175
Db	587	TGTGGAATCCATGCCAGAGAATGCGATCTCTCTCTCTTCTGCTTGTGTTTCATAGGCCAT	646
Qy	175	-----	175
Db	647	ATAACTCAATTTCTATGGGATAATAGGCAATATACCAATCTCTCGAGGCTTGTGGATTTC	706
Qy	176	-----AsnArgMet	178
Db	707	TATGTTATGCCGGTGGTTAATGTGGATGTTATGACTACTCATGGAAAAAGATCGAATG	766
Qy	179	TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg	198
Db	767	TGGAGAAAGAACCGTTCTTTCTATGCGAACCAATCATTTGCATCGGAACAGACCTGAAATAGG	826
Qy	199	AsnPheAlaSerLysHisTrpCysGluGluGluValaSerSerSerCysSerGluThr	218
Db	827	AACITTTGCTTCCAAACACTGCTGTGAGAAAGGTGCATCCAGTTCTCTCATGCTCGGAAACC	886
Qy	219	TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg	238
Db	887	TACTGTGGACTTTTATCTCTGAG-----	907
Qy	239	ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal	258
Db	907	-----	907
Qy	259	PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla	278
Db	907	-----	907
Qy	279	SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis	298

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Db 907 ----- 907
Qy 299 GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly 318
Db 908 ---TCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTATGATTTGGGC 964
Qy 319 IleLysTyrSerPhe----- 323
Db 965 ATCAAAATATTCGTTTACAATTGCACTTCGAGATCGGGCACATACGGATTCTTGTGCGC 1024
Qy 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1025 GAGCGTTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGGTCTCTCTAAAA 1076

RESULT 9
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 5,54e-101 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservativeness: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 50.17% Indels: 56
DB: 9 Gaps: 2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGTTGTTTATAGCCCATATA 69
Qy 175 ----- 175
Db 70 ACTCAATTCTATGGGATAATAGGCAATATACCAATCTCTGAGGCTTGTGGATTCTAT 129
Qy 176 -----AsnArgMetTr 179
Db 130 GTTATGCCGGTGTAAATGTTGATGTTATGAACTACTCATGGAAGAAATCGAATGTG 189
Qy 179 pArgLysAsnArgSerPheTyrAlaIleHisCysIleGlyThrAspLeuAsnArgAs 199
Db 190 GAGAAAGAACCGTCTTCTTATCGAACAATCATTCGATCGGAACAGACCTGGAATAGGAA 249
Qy 199 nPheAlaSerLysHisTrpCysGluGluAlaSerSerSerSerSerSerGluThrTy 219
Db 250 CTTTGTCTTCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTTA 309
Qy 219 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
Db 310 CTGTGGACTTTTCTGAGTTCAGAACAGACAGAAAGTGAAGGAGTGGCTAGTTCTTTGAGAAG 369
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Qy 239 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 259
Db 370 AAATATCAACAGATTAAAGCATACATACATCAGCATGCAATTCATCTCCAGCATATAGTGT 429
Qy 259 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 279
Db 430 TCCATATTCCTATACACGAAGTAAAGCAAGACCATGAGAACTGTCTCTAGTAGCCAG 489
Qy 279 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisG 299
Db 490 TGAAGCAGTTCGTCTATTGAGAAACTAGTAAATAATACCAAGTATACACATGCCATGG 549
Qy 299 ySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyI 319
Db 550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGAGCATTTGGATCTATGATTGGGCAT 609
Qy 319 eLysTyrSerPhe----- 323
Db 610 CAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACATACCGATTCTTGTGCGCGA 669
Qy 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 670 CGGTATCATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGGTCTCTCTAAAA 719

RESULT 10
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 5,54e-101 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservativeness: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 50.17% Indels: 56
DB: 10 Gaps: 2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGTTGTTTATAGCCCATATA 69
Qy 175 ----- 175
Db 70 ACTCAATTCTATGGGATAATAGGCAATATACCAATCTCTGAGGCTTGTGGATTCTAT 129
Qy 176 -----AsnArgMetTr 179
Db 130 GTTATGCCGGTGTAAATGTTGATGTTATGAACTACTCATGGAAGAAATCGAATGTG 189
Qy 179 pArgLysAsnArgSerPheTyrAlaIleHisCysIleGlyThrAspLeuAsnArgAs 199
Db 190 GAGAAAGAACCGTCTTCTTATCGAACAATCATTCGATCGGAACAGACCTGGAATAGGAA 249
Qy 199 nPheAlaSerLysHisTrpCysGluGluAlaSerSerSerSerSerSerGluThrTy 219
Db 250 CTTTGTCTTCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTTA 309
Qy 219 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
Db 310 CTGTGGACTTTTCTGAGTTCAGAACAGACAGAAAGTGAAGGAGTGGCTAGTTCTTTGAGAAG 369
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Qy 179 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysileGlyThrAspLeuAsnArgAs 199
Db 190 GAGAAAGAACCGTTCTTTCTATGCAACAATCATTCGTCGAAACAGACCTTGAATAGGAA 249
Qy 199 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 219
Db 250 CTTTGCTTCCAAACACATGCTGTGAGGAAGGTGCATCCAGTTTCTCATGCTCGGAACCTA 309
Qy 219 rCysGluLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
Db 310 CTGTGGACTTTATCTCTGAGTCAGAACCAAGAGTGAAGGCAGTGGCTAGTTTCTTTGAGAA 369
Qy 239 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 259
Db 370 AAATATCAACAGATTAAAGCATCATCATCAGCATGCAITTCATCTCCAGCATATAGTGT 429
Qy 259 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 279
Db 430 TCCATATCTTATACAGAACTAAAGCAAGAACCATGAGGAATGTCTCTAGTAGCCAG 489
Qy 279 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGI 299
Db 490 TGAAGCAGTTCGTGCTATTGAGAAACTAGTAAATAATACCAAGGTATACACATGCGCCATGG 549
Qy 299 ySerGluThrLeuTyrLeuAlaProGlyGlyAlaAspTrpIleTyrAspLeuGlyII 319
Db 550 CTCAGAACCTTTATACCTAGTCTCTGGAGGTGGGAGCATTTGGATCTATGATTTGGGCAT 609
Qy 319 eLysTy-SerPhe----- 323
Db 610 CAATATTCGTTTACAAATTGAACCTTCGAGATACGGGCACATACGGATTCTTGTGCGCGA 669
Qy 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 670 GCGTTATACATAAACCCACCTAGAGAGAGCTTTTGGCGCTGCTCTATAAA 719
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## RESULT 11

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US-10-229-546-3
; Sequence 3, Application US/10229546
; Publication No. US20030082649A1
; GENERAL INFORMATION:
; APPLICANT: Weich, Nadine S.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE
; FILE REFERENCE: MP101-156P1RNM
; CURRENT APPLICATION NUMBER: US/10/229,546
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/316,575
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1254)
US-10-229-546-3
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Alignment Scores:
Pred. No.: 2,35e-66 Length: 1254
Score: 622.00 Matches: 128
Percent Similarity: 55.12% Conservative: 71
Best Local Similarity: 35.46% Mismatches: 118
Query Match: 44
DB: 14 Gaps: 7
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US-09-980-881A-3 (1-338) x US-10-229-546-3 (1-1254)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20

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Db 61 TTTGACAGGAGAGGTGTTCCCGTGAAGCCCGAGATGAAACACAGCAGCATCAT 120
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 121 AAGGACTTGGCCAAACCAATAGCTTCTGGTATCCAGGTGCCACCCACCAAGTA 180
Qy 41 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAsnValLysAla 60
Db 181 GCTGCTAATATGATGGTGGATTTCGAGATTAGTGAAGGAATCCCAAGCCATCCAGTCT 240
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAGAAGAGATT 300
Qy 81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
Db 301 GAGAAACAGTTTGATGTTAAAGAAAGATATCCAGGCGAGGCACAGC-----TACGCA 351
Qy 100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119
Db 352 AAATACATAAATTTGGGAAAAGATTGGCTTGGACTGAAAGAGATGATGGATAAGTATCCT 411
Qy 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
Db 412 GAAATGCTCTCTGATTTAAATTTGATCTACTTGTGGAAGATATCCACATATATGTTCTG 471
Qy 140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159
Db 472 AAGATT---GGGAAAAGAAATGAAAGAAAGAGCTATTTTATGGATTGTGGCATTAC 528
Qy 160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
Db 529 GCACGAGAATGGGTCTCCCGAGCATTTCTGCAGTGGTTGTCTATCATCAGGCAACCAAACT 588
Qy 173 ----- 173
Db 589 TATGGGGAACAAATAATATGACCAAACTCTTGGACCGAATGAATTTTACATTTCTCCT 648
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsn 182
Db 649 GTGTTCAATGTTGATGGATATATTTGGTTCATGACAAAGAACCGCATGTGAGAAAAAAT 708
Qy 183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202
Db 709 CGTTCGAAGAACCAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765
Qy 203 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 222
Db 766 GCTTCATGGAACTCCATTCCTTAACCAACCAATGACCCATGTCAGATTAATCTCGGGGTCT 825
Qy 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242
Db 826 GCACCAAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTTATTAGAAGCCACCTGAAT 885
Qy 243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262
Db 886 GAAATCAAGGTTTATACATCACCTTCCATCTCTACTCCAGATGCTATTTGTTTCCCTATGA 945
Qy 263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
Db 946 TATACATCAAACTGCCACCTAACCATGAGAGCTTGGCCAAAGTTGCAAGATGGCACT 1005
Qy 283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302
Db 1006 GATGTTCTA---TCAACTCGATATGAACCCGCTACATCTATGCCCCCAATAGAATCAACA 1062
Qy 303 LeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322
Db 1063 ATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAACACACA 1122
Qy 323 Phe 323
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US-09-980-881A-3 (1-338) x US-10-429-802-21 (1-1622)





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QY 173 ----- 173
Db 589 TATGGAGAAACAAATATGACCAAACTCTTGGACCGAATGAATTTTACATCTTCT 648
QY 174 ----- 173
Db 649 GTGTTCAATGTTGATGATATATTGGTCTGACGACAAAGACCGCATGTGGAGAAAT 708
QY 183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202
Db 709 CGTTCAGAACCAAACTCCAAATGCTATCGGCACTGACCTCAACAGGAATTTT---AAT 765
QY 203 LysHisTyrCysGluGluGlyAlaSerSerSerSerSerGluThrTyrCysGlyLeu 222
Db 766 GCTTCATGGAATCCATTCCTTAACCAATGACCCATGTCAGATACTATCGGGGCTCT 825
QY 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsn 242
Db 826 GCACAGAGTCGAGAAAGACGAAAGCTGTCACTAATTTTATTAGAACCCACCTGAAT 885
QY 243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262
Db 886 GAAATCAAGGTTTACATCACTTCCATTCCTACTCTCCAGATGCTATTGTTTCCCTATGGA 945
QY 263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
Db 946 TATATCAAACTGCCCTTAACCATGAGGACTTGGCCAAAGTTGCAAGATTCGCCTACT 1005
QY 283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302
Db 1006 GATGTTCTA---TCACTCGATATGAAACCCGCTACATCTATGGCCCAATAGATCAACA 1062
QY 303 LeuTyrLeuAlaProGlyGlyGlyAspAspPheIleTyrAspLeuGlyIleLysTyrSer 322
Db 1063 ATTTACCCGATATCAGGTTCTCTTTAGACTGGGCTTATGACCTGGGCATCAACACACA 1122
QY 323 Phe 323
Db 1123 TTT 1125
RESULT 15
US-10-262-511-71
; Sequence 71, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerkusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
```

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; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 71
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1251)
US-10-262-511-71
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## Alignment Scores:

Pred. No.:	3,598-66	Length:	1622
Score:	622.00	Matches:	128
Percent Similarity:	55.12%	Conservative:	71
Best Local Similarity:	35.46%	Mismatches:	118
Query Match:	34.59%	Indels:	44
DB:	16	Gaps:	7

US-09-980-881A-3 (1-338) x US-10-262-511-71 (1-1622)

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QY 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 61 TTTGACAGGAGAGAGTGTTCGCGGTGAAGCCCGAGGATGAAAAACAAGCAGACATCAT 120
QY 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle 40
Db 121 AAGGACTTGGCCAAACCAATGAGCTTCTGCTATCCAGGTGCCACCCACGATGTA 180
QY 41 VallysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
Db 181 GCTGCTAATATGATGTTGGATTTCGAGTTAGTAGAAGGAATCCCAAGCCATCCAGTCT 240
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGTATTCATGATCTACAGAAGAT 300
QY 81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
Db 301 GAGAAACACAGTTTGTATGTTTAAAGAGATATCCGAGCGAGCAGCAGC-----TACGCA 351
QY 100 GlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHisPro 119
Db 352 AAATACAAATAATGGGAAAGATTTGGCTTGGACTGAAAGATGATGATGATGATGATCT 411
QY 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
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[illegible]

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:31:47 ; Search time 13.2903 Seconds  
(without alignment)  
1227.533 Million cell updates/sec

Title: US-09-980-881A-4  
Perfect score: 246  
Sequence: 1 ASASYEQYHSLNEIYSWIE.....IKSFTSNPPVVEKLLPLSLK 246

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/prodata/1/iaa/PTUS\_COMB.pep: \*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	149	60.6	423	1	US-07-649-591B-3
2	149	60.6	423	1	US-08-277-540-3
3	149	60.6	423	1	US-08-430-787A-3
4	149	60.6	423	2	US-08-869-057-2
5	140	56.9	386	4	US-09-813-133A-2
6	112	45.5	423	4	US-09-813-133A-4
7	15	6.1	417	1	US-07-649-591B-7
8	15	6.1	417	1	US-08-277-540-7
9	15	6.1	417	1	US-08-430-787A-7
10	12	4.9	247	4	US-09-675-305-6
11	12	4.9	247	4	US-10-200-344-6
12	12	4.9	350	4	US-09-675-305-12
13	12	4.9	350	4	US-10-200-344-12
14	12	4.9	437	4	US-09-675-305-10
15	12	4.9	437	4	US-10-200-344-10
16	11	4.5	86	4	US-09-270-767-56648
17	11	4.5	89	4	US-09-513-999C-7648
18	11	4.5	216	4	US-09-270-767-41427
19	11	4.5	307	2	US-08-782-760-6
20	11	4.5	307	5	PCT-US96-00995-6
21	11	4.5	329	4	US-09-011-769A-51
22	11	4.5	349	4	US-09-011-769A-47
23	11	4.5	349	4	US-09-011-769A-60
24	11	4.5	349	4	US-09-011-769A-64
25	11	4.5	396	1	US-07-649-591B-4
26	11	4.5	396	1	US-08-277-540-4
27	11	4.5	396	1	US-08-430-787A-4

28	11	4.5	415	2	US-08-860-882A-57	Sequence 57, Appl
29	11	4.5	415	4	US-09-011-769A-39	Sequence 39, Appl
30	11	4.5	424	4	US-09-011-769A-56	Sequence 56, Appl
31	11	4.5	613	3	US-09-171-945-113	Sequence 113, App
32	11	4.5	716	3	US-09-171-945-125	Sequence 125, App
33	10	4.1	417	1	US-07-649-591B-6	Sequence 6, Appl
34	10	4.1	417	1	US-08-277-540-6	Sequence 6, Appl
35	10	4.1	417	1	US-08-430-787A-6	Sequence 6, Appl
36	10	4.1	417	4	US-09-917-254-66	Sequence 14973, A
37	9	3.7	162	4	US-09-248-796A-14973	Sequence 8, Appl
38	9	3.7	417	1	US-07-649-591B-8	Sequence 8, Appl
39	9	3.7	417	1	US-08-277-540-8	Sequence 8, Appl
40	9	3.7	417	1	US-08-430-787A-8	Sequence 8, Appl
41	7	2.8	130	4	US-09-270-767-57790	Sequence 57790, A
42	7	2.8	171	4	US-09-248-796A-22616	Sequence 22616, A
43	7	2.8	184	4	US-09-513-999C-4204	Sequence 4204, Ap
44	7	2.8	219	2	US-08-925-708-2	Sequence 2, Appl
45	7	2.8	249	4	US-09-252-991A-30320	Sequence 30320, A

ALIGNMENTS

RESULT 1  
US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton Carboxypeptidase  
; TITLE OF INVENTION: No. 5206161 Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear

Query Match 60.6%; Score 149; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 9.8e-142;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 NRMWRKNSFYANNHCIGTDLNRNFASKHWCSESSSCSETYCGLYPESEPEVKAVAS 143  
DB 235 NRMWRKNSFYANNHCIGTDLNRNFASKHWCSESSSCSETYCGLYPESEPEVKAVAS 234



APPLICANT: Morser, Michael J  
APPLICANT: Nagaehima, Mariako  
TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
TITLE OF INVENTION: Risk  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE: Plasma  
TISSUE TYPE: Plasma  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 23..401  
US-08-869-057-2

Query Match 60.6%; Score 149; DB 2; Length 423;  
Best Local Similarity 100.0%; Pred. No. 9.8e-142;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEGASSSSCSETYCGLYPESEPEVKAVAS 143  
Db 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEGASSSSCSETYCGLYPESEPEVKAVAS 294  
QY 144 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203  
Db 295 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354  
QY 204 HGHGSETLYLAPCGDDWIYDLGIKYSFT 232  
Db 355 HGHGSETLYLAPCGDDWIYDLGIKYSFT 383

RESULT 5  
US-09-813-133A-2  
Sequence 2, Application US/09813133A  
Patent No. 6455294  
GENERAL INFORMATION:  
APPLICANT: GAN, Weinui et al  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL001173  
CURRENT APPLICATION NUMBER: US/09/813,133A  
CURRENT FILING DATE: 2001-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO 2  
LENGTH: 386  
TYPE: PRT  
ORGANISM: Human  
US-09-813-133A-2  
Query Match 56.9%; Score 140; DB 4; Length 386;  
Best Local Similarity 100.0%; Pred. No. 1e-132;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 AKNAIWDICGTHAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNRFASKHWC 115  
Db 170 AKNAIWDICGTHAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNRFASKHWC 229  
QY 116 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHIHVPYSTRSK 175  
Db 230 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHIHVPYSTRSK 289  
QY 176 SKDHEELSLVASEAVRAIEK 195  
Db 290 SKDHEELSLVASEAVRAIEK 309  
RESULT 6  
US-09-813-133A-4  
Sequence 4, Application US/09813133A  
Patent No. 6455294  
GENERAL INFORMATION:  
APPLICANT: GAN, Weinui et al  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL001173  
CURRENT APPLICATION NUMBER: US/09/813,133A  
CURRENT FILING DATE: 2001-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Fast-SEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 423  
TYPE: PRT  
ORGANISM: Human  
US-09-813-133A-4

Query Match 45.5%; Score 112; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.8e-104;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEGASSSSCSETYCGLYPESEPEVKAVAS 143  
Db 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEGASSSSCSETYCGLYPESEPEVKAVAS 294  
QY 144 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSKDHEELSLVASEAVRAIEK 195  
Db 295 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSKDHEELSLVASEAVRAIEK 346

RESULT 7  
US-07-649-591B-7  
Sequence 7, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:  
APPLICANT: Dennis Drayna and Daniel Eaton  
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
US-07-649-591B-7

Query Match 6.1%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 63 DCGIHAREWISPAFC 77  
Db 172 DCGIHAREWISPAFC 186

RESULT 8  
US-08-277-540-7  
; Sequence 7, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-277-540-7

Query Match 6.1%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 63 DCGIHAREWISPAFC 77  
Db 172 DCGIHAREWISPAFC 186

RESULT 9  
US-08-430-787A-7  
; Sequence 7, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-430-787A-7

Query Match 6.1%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 63 DCGIHAREWISPAFC 77

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Db      172 DCGIHAREWISPAFC 186
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RESULT 10
US-09-675-305-6
; Sequence 6, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-6

Query Match      4.9%; Score 12; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
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Db      190 WIDCGIHAREWI 201

RESULT 11
US-10-200-344-6
; Sequence 6, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-200-344-6

Query Match      4.9%; Score 12; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
|||||
Db      190 WIDCGIHAREWI 201

RESULT 12
US-09-675-305-12
; Sequence 12, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 350
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-12

Query Match      4.9%; Score 12; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
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Db      190 WIDCGIHAREWI 201

RESULT 13
US-10-200-344-12
; Sequence 12, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 350
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-200-344-12

Query Match      4.9%; Score 12; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
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Db      190 WIDCGIHAREWI 201

RESULT 14
US-09-675-305-10
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; Sequence 10, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-10
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Best Local Similarity 100.0%; Pred.No. 0.00091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 WIDCGIHAREWI 72
Db 190 WIDCGIHAREWI 201
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RESULT 15
US-10-200-344-10
; Sequence 10, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-200-344-10
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Query Match 4.9%; Score 12; DB 4; Length 437;
Best Local Similarity 100.0%; Pred.No. 0.00091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 WIDCGIHAREWI 72
Db 190 WIDCGIHAREWI 201
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:41:12 ; Search time 32.3136 Seconds  
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Perfect score: 246  
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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	149	60.6	211	US-09-925-302-467
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3	149	60.6	423	US-10-379-836-17
4	140	56.9	386	US-09-813-133A-2
5	140	56.9	386	US-10-212-877-2
6	112	45.5	423	US-09-813-133A-4
7	112	45.5	423	US-10-212-877-4
8	112	45.5	428	US-10-115-479-68
9	112	45.5	428	US-10-115-479-70
10	68	27.6	322	US-10-115-479-64
11	52	21.1	354	US-10-115-479-66
12	42	17.1	423	US-10-379-836-2
13	25	10.6	422	US-10-379-836-16

14	10.6	422	14	US-10-379-836-18	Sequence 18, Appl
15	4.9	210	16	US-10-363-829-401	Sequence 401, App
16	12	247	13	US-10-200-344-6	Sequence 6, Appli
17	12	4.9	9	US-09-888-615-60	Sequence 60, Appl
18	12	350	13	US-10-200-344-12	Sequence 12, Appl
19	12	4.9	350	US-10-200-344-12	Sequence 2, Appli
20	12	4.9	434	US-10-200-344-10	Sequence 10, Appl
21	12	4.9	437	US-10-274-639-12	Sequence 12, Appl
22	12	4.9	437	US-10-333-574-12	Sequence 12, Appl
23	12	4.9	437	US-10-757-262-128	Sequence 128, App
24	11	4.5	118	US-10-074-978A-274	Sequence 274, App
25	11	4.5	231	US-10-074-978A-48	Sequence 48, Appl
26	11	4.5	231	US-10-074-978A-50	Sequence 50, Appl
27	11	4.5	231	US-10-074-978A-52	Sequence 52, Appl
28	11	4.5	349	US-10-074-978A-46	Sequence 46, Appl
29	11	4.5	402	US-10-379-836-20	Sequence 20, Appl
30	11	4.5	416	US-10-074-978A-266	Sequence 266, App
31	11	4.5	417	US-10-074-978A-267	Sequence 267, App
32	11	4.5	417	US-10-074-978A-268	Sequence 268, App
33	11	4.5	417	US-10-477-515-3	Sequence 3, Appli
34	11	4.5	613	US-09-910-059-113	Sequence 113, App
35	11	4.5	613	US-10-608-710-4	Sequence 4, Appli
36	11	4.5	716	US-09-910-059-125	Sequence 125, App
37	10	4.1	180	US-10-106-698-6143	Sequence 6143, Ap
38	10	4.1	231	US-10-074-978A-54	Sequence 54, Appl
39	10	4.1	286	US-10-408-765A-1959	Sequence 1959, Ap
40	10	4.1	310	US-10-470-390A-20	Sequence 20, Appl
41	10	4.1	374	US-09-888-615-61	Sequence 61, Appl
42	10	4.1	416	US-10-074-978A-270	Sequence 270, App
43	10	4.1	417	US-10-229-546-2	Sequence 2, Appli
44	10	4.1	417	US-10-229-546-9	Sequence 9, Appli
45	10	4.1	417	US-10-341-434-188	Sequence 188, App

ALIGNMENTS

RESULT 1  
US-09-925-302-467  
; Sequence 467, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 467  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-302-467

Query Match 60.6%; Score 149; DB 9; Length 211;  
Best Local Similarity 100.0%; Pred. NO. 5.8e-135;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	84	NRMWRKNRSFYANNHCIGTDLNPNFASKHWCSESSSSCSTCYGLYPESEPEVKAVAS	143
Db	23	NRMWRKNRSFYANNHCIGTDLNPNFASKHWCSESSSSCSTCYGLYPESEPEVKAVAS	82
QY	144	FLRRNINQIKAYISHMSYSQHVFFPYSTRSKDHEELSLVASEAVRAIEKTSKNTRYT	203
Db	83	FLRRNINQIKAYISHMSYSQHVFFPYSTRSKDHEELSLVASEAVRAIEKTSKNTRYT	142
QY	204	HGHGSETLYIAPGGDDMIYDLGIKYSFT	232

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Db      143 HGHGSETLYLAPGGDDWIYDLGIKYSFT 171
RESULT 2
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCR/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Query Match      60.6%; Score 149; DB 10; Length 211;
Best Local Similarity 100.0%; Pred. No. 5.8e-135;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      84 NRMWRKRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 143
Db      23 NRMWRKRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 82
Qy      144 FLRRNINQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db      83 FLRRNINQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 142
Qy      204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db      143 HGHGSETLYLAPGGDDWIYDLGIKYSFT 171

RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 17
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-836-17

Query Match      60.6%; Score 149; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 1e-134;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      84 NRMWRKRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 143
Db      235 NRMWRKRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 294
Qy      144 FLRRNINQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db      170 AKNAIWDCGIHAREWISPAFCLWFIQHNRMWRKRSFYANNHCIGTDLNRNFASKHWCE 229

Db      295 FLRRNINQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354
Qy      204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db      355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 4
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2

Query Match      56.9%; Score 140; DB 9; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.4e-126;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      56 AKNAIWDCGIHAREWISPAFCLWFIQHNRMWRKRSFYANNHCIGTDLNRNFASKHWCE 115
Db      170 AKNAIWDCGIHAREWISPAFCLWFIQHNRMWRKRSFYANNHCIGTDLNRNFASKHWCE 229
Qy      116 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHVFPYSYTRSK 175
Db      230 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHVFPYSYTRSK 289
Qy      176 SKDHEELSLVASEAVRAIEK 195
Db      290 SKDHEELSLVASEAVRAIEK 309

RESULT 5
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-877-2

Query Match      56.9%; Score 140; DB 14; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.4e-126;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      56 AKNAIWDCGIHAREWISPAFCLWFIQHNRMWRKRSFYANNHCIGTDLNRNFASKHWCE 115
Db      170 AKNAIWDCGIHAREWISPAFCLWFIQHNRMWRKRSFYANNHCIGTDLNRNFASKHWCE 229
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-64

Query Match 27.6%; Score 68; DB 15; Length 322;  
Best Local Similarity 100.0%; Pred. No. 7.3e-57;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 CGLYPESEVKAVASFLRRNINQIKAYISMHSYQHIVFPYSTRSKDHEELSLVAS 187  
DB 178 CGLYPESEVKAVASFLRRNINQIKAYISMHSYQHIVFPYSTRSKDHEELSLVAS 237  
QY 188 EAVRAIEK 195  
DB 238 EAVRAIEK 245

RESULT 11  
US-10-115-479-66  
; Sequence 66, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkete, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 Pt)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 66  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-66

Query Match 21.1%; Score 52; DB 15; Length 354;  
Best Local Similarity 100.0%; Pred. No. 2e-41;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 NRMWRKRSFYANNHCIGTDLNRNPASKHWCEEGASSSSCSETYCGLYPESE 135  
DB 240 NRMWRKRSFYANNHCIGTDLNRNPASKHWCEEGASSSSCSETYCGLYPESE 291

RESULT 12  
US-10-379-836-2  
; Sequence 2, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Papio hamadryas  
US-10-379-836-2

Query Match 17.1%; Score 42; DB 14; Length 423;  
Best Local Similarity 100.0%; Pred. No. 9.6e-32;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 IKAYISMHSYQHIVFPYSTRSKDHEELSLVASEAVRAI 193  
DB 303 IKAYISMHSYQHIVFPYSTRSKDHEELSLVASEAVRAI 344

RESULT 13  
US-10-379-836-16  
; Sequence 16, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-379-836-16

Query Match 10.6%; Score 26; DB 14; Length 422;  
Best Local Similarity 100.0%; Pred. No. 2.4e-16;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 KNAINWIDCGIHAREWISPAFLWFIG 82

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Db      170 KNAIWIDCGIHAREWISPAFLWFIG 195

RESULT 14
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-836-18

Query Match      10.6%; Score 26; DB 14; Length 422;
Best Local Similarity 100.0%; Pred.No. 2.4e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      57 KNAIWIDCGIHAREWISPAFLWFIG 82
Db      170 KNAIWIDCGIHAREWISPAFLWFIG 195

RESULT 15
US-10-363-829-401
; Sequence 401, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 401
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:366783.1.orf1:2000SEP08
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 102
; OTHER INFORMATION: unknown or other
US-10-363-829-401

Query Match      4.9%; Score 12; DB 16; Length 210;
Best Local Similarity 100.0%; Pred.No. 0.0039;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
Db      48 WIDCGIHAREWI 59

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Job time : 32.3136 secs
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GenCore version 5.1.6  
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Perfect score: 246  
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Delop 6.0 , Delext 7.0

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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	60.6	1272	2	US-08-869-057-1 Sequence 1, Appli
2	149	60.6	1749	1	US-07-649-591B-2 Sequence 2, Appli
3	149	60.6	1749	1	US-08-277-540-2 Sequence 2, Appli
4	149	60.6	1749	1	US-08-430-787A-2 Sequence 2, Appli
5	140	56.9	1625	4	US-09-813-133A-1 Sequence 1, Appli
6	68	27.6	55827	4	US-09-813-133A-3 Sequence 3, Appli
7	12	4.9	741	4	US-09-675-305-5 Sequence 5, Appli
8	12	4.9	741	4	US-10-200-344-5 Sequence 5, Appli
9	12	4.9	1050	4	US-09-675-305-11 Sequence 11, Appl
10	12	4.9	1050	4	US-10-200-344-11 Sequence 11, Appl
11	12	4.9	1311	4	US-09-675-305-9 Sequence 9, Appli
12	12	4.9	1311	4	US-10-200-344-9 Sequence 9, Appli

13	12	4.9	2128	4	US-09-675-305-13 Sequence 13, Appl
14	12	4.9	2128	4	US-10-200-344-13 Sequence 13, Appl
15	11	4.5	258	4	US-09-270-767-25119 Sequence 25119, A
16	11	4.5	359	4	US-09-513-999C-3571 Sequence 3571, Ap
17	11	4.5	927	2	US-08-782-760-5 Sequence 5, Appli
18	11	4.5	927	5	PCT-US96-00995-5 Sequence 5, Appli
19	11	4.5	999	2	US-08-860-882A-67 Sequence 67, Appl
20	11	4.5	999	4	US-09-011-769A-50 Sequence 50, Appl
21	11	4.5	1053	2	US-08-860-882A-64 Sequence 64, Appl
22	11	4.5	1053	4	US-09-011-769A-56 Sequence 27, Appl
23	11	4.5	1053	4	US-09-463-451-27 Sequence 28, Appl
c	24	11	1053	4	US-09-463-451-28 Sequence 28, Appl
25	11	4.5	1059	2	US-08-860-882A-74 Sequence 74, Appl
26	11	4.5	1059	2	US-08-860-882A-77 Sequence 77, Appl
27	11	4.5	1059	4	US-09-011-769A-53 Sequence 53, Appl
28	11	4.5	1059	4	US-09-011-769A-63 Sequence 63, Appl
29	11	4.5	1150	4	US-09-270-767-9829 Sequence 9829, Ap
30	11	4.5	1263	2	US-08-860-882A-56 Sequence 56, Appl
31	11	4.5	1263	4	US-09-011-769A-38 Sequence 38, Appl
32	11	4.5	1284	2	US-08-860-882A-71 Sequence 71, Appl
33	11	4.5	1284	4	US-09-011-769A-55 Sequence 55, Appl
34	11	4.5	1870	3	US-09-171-945-112 Sequence 112, App
35	11	4.5	2154	3	US-09-171-945-124 Sequence 124, App
36	10	4.1	1622	4	US-09-023-655-1020 Sequence 1020, App
37	9	3.7	486	4	US-09-248-796A-870 Sequence 870, App
38	8	3.3	873	4	US-09-583-110-2322 Sequence 2322, Ap
39	8	3.3	1535	1	US-08-480-510-1 Sequence 1, Appli
40	8	3.3	1535	5	PCT-US94-01780-1 Sequence 1, Appli
c	41	8	1587	4	US-09-023-655-1192 Sequence 1192, Ap
42	8	3.3	3207	4	US-09-966-997-10 Sequence 10, Appl
c	43	8	5847	4	US-09-962-665-11 Sequence 11, Appl
c	44	8	5847	4	US-09-963-333-11 Sequence 11, Appl
c	45	8	5847	4	US-09-963-677-11 Sequence 11, Appl

ALIGNMENTS

US-08-869-057-1  
Sequence 1, Application US/08869057  
Patent No. 5985562  
GENERAL INFORMATION:  
APPLICANT: Morset, Michael J  
APPLICANT: Nagashima, Mariko  
TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
TITLE OF INVENTION: Risk  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1272 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; PUBLICATION INFORMATION:
; AUTHORS: Eaton, Dan L.
; AUTHORS: Malloy, Beth E.
; AUTHORS: Tsai, Siao P.
; AUTHORS: Henzel, William
; AUTHORS: Drayna, Dennis
; TITLE: Isolation, Molecular Cloning, and Partial
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B
; TITLE: from Human Plasma
; JOURNAL: J. Biol. Chem.
; VOLUME: 266
; ISSUE: 32
; PAGES: 21833-21838
; DATE: No. 5985562 15-1991
;
US-08-869-057-1
Alignment Scores:
Pred. No.: 6,4e-148 Length: 1272
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-4 (1-246) x US-08-869-057-1 (1-1272)
Qy 84 AsnArgMetTrrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 103
Db 703 AATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACATCATGTGTCGGAACAGAC 762
Qy 104 LeuAsnArgAsnPhelAserLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 763 CTGATAGGAACCTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGC 822
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 823 TCGAAACCTACTGTGGAGCTTATCCTCAGTCAGAACAGAGTGAAGCGAGTGGCTAGT 882
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 883 TTCCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGATGCATTCATATCCTCCAG 942
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db 943 CATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGACCATGAGGAAGTGTCT 1002
Qy 184 LeuValAlaSerGluAlaValargAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
Db 1003 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACCTAGTAAATAATACCAGGTATACA 1062
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
Db 1063 CATGCCATGGCTCAGAACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTAT 1122
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232
Db 1123 GATTGGGCATCAATATTCGTTTACA 1149

RESULT 2
US-07-649-591B-2
; Sequence 2, Application US/07649591B
; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd

```

```

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: hybridization probe
; LOCATION: 133 to 178
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
;
; NAME/KEY: potential clip site
; LOCATION: 380 to 382
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
;
; NAME/KEY: signal sequence
; LOCATION: 41 to 106
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
;
US-07-649-591B-2
Alignment Scores:
Pred. No.: 8,76e-148 Length: 1749
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 1 Gaps: 0

US-09-980-881A-4 (1-246) x US-07-649-591B-2 (1-1749)
Qy 84 AsnArgMetTrrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 103
Db 743 AATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACATCATGTGTCGGAACAGAC 802
Qy 104 LeuAsnArgAsnPhelAserLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 803 CTGATAGGAACCTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGC 862
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 863 TCGAAACCTACTGTGGAGCTTATCCTCAGTCAGAACAGAGTGAAGCGAGTGGCTAGT 922
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 923 TTCCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGATGCATTCATCTCCAG 982

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164 HisIleValPheProTyrSerThrArgSerLysSerLysAspHisGluLeuSer 183  
 983 CATATAGTGTTCCTATATCCATATACACGAGTAAAGCAAGACCATGAGCACTGTCT 1042  
 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
 1043 CTAGTAGCCAGTGAAGCAGTCTGCTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 1102  
 204 HisGlyHisGlySerGluThrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
 1103 CATGGCCATGGCTCAGAACCTTATACCTGAGGTCTGGAGGTGGGACGATTGGATCTAT 1162  
 224 AspLeuGlyIleLysTyrSerPheThr 232  
 1163 GATTGGGCATCAATATTCGTTTACA 1189

RESULT 3

US-08-277-540-2  
 ; Sequence 2, Application US/08277540  
 ; Patent No. 5474901  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277,540  
 FILING DATE: 19-JUL-1994  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/167727  
 FILING DATE: 15-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/959944  
 FILING DATE: 14-OCT-1992  
 APPLICATION DATA:  
 APPLICATION NUMBER: 07/649591  
 FILING DATE: 01-FEB-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689D1C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1749 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-08-277-540-2  
 Alignment Scores:  
 Pred. No.: 8,76e-148 Length: 1749  
 Score: 149.00 Matches: 149  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 60.57% Indels: 0  
 DB: 1 Gaps: 0

US-09-980-881A-4 (1-246) x US-08-277-540-2 (1-1749)  
 QY 84 AsnArgMetTyrArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
 Db 743 AATCGAATGTGGAGAAAGAACCGTCTCTTCTATGGAACATCATTCATCGAAGACAGAC 802  
 QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
 Db 803 CTGAATAGGAACTTTGCTTCCAAACACCTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 862  
 QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValValAlaValAlaSer 143  
 Db 863 TCGGAAACCTACTGTGGACTTTATCTCAGTCAGAACCAAGAGTGAAGCACTGCTAGT 922  
 QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaIleSerMetHisSerTyrSerGln 163  
 Db 923 TTCCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTCCCAG 982  
 QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
 Db 983 CATATAGTGTTCCTATATCCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGCACTGTCT 1042  
 QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
 Db 1043 CTAGTAGCCAGTGAAGCAGTCTGCTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 1102  
 QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
 Db 1103 CATGGCCATGGCTCAGAACCTTATACCTGAGGTCTGGAGGTGGGACGATTGGATCTAT 1162  
 QY 224 AspLeuGlyIleLysTyrSerPheThr 232  
 Db 1163 GATTGGGCATCAATATTCGTTTACA 1189

RESULT 4

US-08-430-787A-2  
 ; Sequence 2, Application US/08430787A  
 ; Patent No. 5593674  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/430,787A  
 ; FILING DATE: 27-APR-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/277,540  
 ; FILING DATE: 19-JUL-1994  
 ; APPLICATION NUMBER: 08/167727  
 ; FILING DATE: 15-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/959944  
 ; FILING DATE: 14-OCT-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/649591  
 ; FILING DATE: 01-FEB-91  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hasak, Janet E.  
 ; REGISTRATION NUMBER: 28,616  
 ; REFERENCE/DOCKET NUMBER: 689D1C1D1

## TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-430-787A-2

Alignment Scores:  
Pred. No.: 8.76e-148 Length: 1749  
Score: 149.00 Matches: 149  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.57% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-4 (1-246) x US-08-430-787A-2 (1-1749)

Qy 84 AsnArgMetTTPATGlyAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGGAGAAAGACCGTCTTCTATATGCGAACAATCATTTGCATCGGACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 803 CTGAATAGGAACCTTTGCTTCCAAACACCTGGTGTGAGGAAGGTGCATCCAGTTCTCTATGC 862  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 863 TCGGAACCTACTGTGGACTTTATCTCAGTCAGAACAGAGTGAAGGCGAGTGGCTAGT 922  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTCCTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATATCCAG 982  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 983 CATATAGTGTTCCTATATCTATACAGAACTGAGTAAAGCAACCATGAGGAACCTGTCT 1042  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1043 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACCTAGTAAAAATACCAAGGTATACA 1102  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyr 223  
Db 1103 CATGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGTGGGAGCATTTGATCTAT 1162  
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232  
Db 1163 GATTTGGCATCAAAATATTCGTTTACA 1189

## RESULT 5

US-09-813-133A-1

; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

## Alignment Scores:

Pred. No.: 2.64e-138 Length: 1625  
Score: 140.00 Matches: 230  
Percent Similarity: 98.29% Conservative: 0  
Best Local Similarity: 98.29% Mismatches: 2  
Query Match: 56.91% Indels: 4  
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

Qy 1 AlaserAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 359 GCCTCCGCATCGTACTATGAAACAGTATCACTCAATAAGTAATCTATTCTTGGATAGAA 418  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 419 TTTATACTGAGAGGCATCCTGATATGCTTTACAAAAATCCACATTTGGATCTCTCATTTGAG 478  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThr-AlalysAsnAlaI 60  
Db 479 AAGTACCACCTCTATGTTTAAAGGTTTCTGGAAGAAACAAGC-AGCCAAAAATGCCAT 537  
Qy 60 eTTPilleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTrpPh 80  
Db 538 ATGGATTGACTGTGGAAATCCATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTT 597  
Qy 80 eIleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysI 100  
Db 598 CATAGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACAATCATTTGCAT 657  
Qy 100 eGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSe 120  
Db 658 CGGAACACAGACTGAATAGGAACCTTGTCTTCCAAACACTGGTGTGAGGAAGTGCATCCAG 717  
Qy 120 rSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAl 140  
Db 718 TTCCTCATGTCTGGAACCTACTGTGGACTTATCTCTGAGTCAGAACAGAGTGAAGGC 777  
Qy 140 aValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSe 160  
Db 778 AGTGGCTAGTTTCTTGAGAAAGAAATATCAACAGATTAAGACATACATCAGCATGCATTC 837  
Qy 160 rTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisG 180  
Db 838 ATACTCCAGCATATAGTGTTCATATCTTATACAGAAAGTAAAGCAAGAACCAATGA 897  
Qy 180 uGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnT 200  
Db 898 GGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAAATT-AGTAAAAATA 956  
Qy 200 hrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAsp 220  
Db 957 CCAGGTATACATGCGCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGTGGGACG 1016  
Qy 220 sPTTilleTyrAspLeuGlyIleLysTyrSerPheThr 232  
Db 1017 ATTGGATCTATGATTTGGGCATCAAAATATTCTGTTTACA 1054

## RESULT 6

US-09-813-133A-3

; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; US-09-813-133A-3

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; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3
Alignment Scores:
Pred. No.: 1,05e-60 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.64% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-813-133A-3 (1-55827)
QY 115 GluGluGlyAlaSerSerSerSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db 48643 GAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTCGATCA 48702
QY 135 GluProGluValIysAlaValAlaSerPheLeuArgAtcAsnIleAsnGlnIleLysAla 154
Db 48703 GAACCAAGAGTGAAGCAGTGTCTAGTTCTTGGAGAAGAAATATCAACCAAGATTAAAGCA 48762
QY 155 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 174
Db 48763 TACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATATACAGAGT 48822
QY 175 LysSerLysAspHisGluGluLeu 182
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 7
US-09-675-305-5
; Sequence 5, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 741
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-5
Alignment Scores:
Pred. No.: 0.0022 Length: 741
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-675-305-5 (1-741)
QY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGTATTTCATGCAAGAGATGGATT 603

RESULT 9
US-09-675-305-11
; Sequence 11, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-11
Alignment Scores:
Pred. No.: 0.00311 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0
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US-09-980-881A-4 (1-246) x US-09-675-305-11 (1-1050)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 10
US-10-200-344-11
; Sequence 11, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-11

Alignment Scores:
Pred. No.: 0.00311 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: Gaps: 0

US-09-980-881A-4 (1-246) x US-10-200-344-11 (1-1050)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 11
US-09-675-305-9
; Sequence 9, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-9

Alignment Scores:
Pred. No.: 0.00387 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: Gaps: 0

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Pred. No.: 0.00387 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: Gaps: 0

US-09-980-881A-4 (1-246) x US-09-675-305-9 (1-1311)
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Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 12
US-10-200-344-9
; Sequence 9, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.: 0.00387 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: Gaps: 0

US-09-980-881A-4 (1-246) x US-10-200-344-9 (1-1311)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 13
US-09-675-305-13
; Sequence 13, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-13

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Score:          12.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     4.88%      Indels:      0
DB:              4      Gaps:          0

US-09-980-881A-4 (1-246) x US-09-675-305-13 (1-2128)

Qy      61 TptlleAspCysGlyIleHisAlaArgGluTptlle 72
Db      933 TGGATAGACTGTGGTATTTCATGCAAGAGAGATGGATT 968

RESULT 14
US-10-200-344-13
; Sequence 13, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-13

Alignment Scores:
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Score:          12.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     4.88%      Indels:      0
DB:              4      Gaps:          0

US-09-980-881A-4 (1-246) x US-10-200-344-13 (1-2128)

Qy      61 TptlleAspCysGlyIleHisAlaArgGluTptlle 72
Db      933 TGGATAGACTGTGGTATTTCATGCAAGAGAGATGGATT 968
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RESULT 15
US-09-270-767-25119
; Sequence 25119, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25119
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; LENGTH: 258
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-25119

Alignment Scores:
Pred. No.:      0.00886      Length:      258
Score:          11.00      Matches:      11
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     4.47%      Indels:      0
DB:              4      Gaps:          0

US-09-980-881A-4 (1-246) x US-09-270-767-25119 (1-258)

Qy      65 GlyIleHisAlaArgGluTptlleSerProAla 75
Db      127 GGCATCCACGCCCGGGAATGGATCAGCCCCGCG 159

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Job time : 82.6271 secs
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GenCore version 5.1.6  
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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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Word size: 1

Total number of hits satisfying chosen parameters: 6817637

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Post-processing: Listing first 45 summaries

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- 2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq:
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- 13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq:
- 14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq:
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- 16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:
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- 18: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:
- 19: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq:
- 20: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:
- 21: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	149	60.6	1400	9	US-09-925-302-24 Sequence 24, Appl
2	149	60.6	1400	10	US-09-925-302-24 Sequence 24, Appl
3	149	60.6	1728	9	US-09-880-107-2396 Sequence 2396, Ap
4	140	56.9	1625	9	US-09-813-133A-1 Sequence 1, Appli
5	140	56.9	1625	14	US-10-212-877-1 Sequence 1, Appli
6	112	45.5	1344	16	US-10-115-479-69 Sequence 69, Appl
7	112	45.5	1743	16	US-10-115-479-67 Sequence 67, Appl
8	68	27.6	1037	16	US-10-115-479-63 Sequence 63, Appl
9	68	27.6	55827	9	US-09-813-133A-3 Sequence 3, Appli
10	68	27.6	55827	14	US-10-212-877-3 Sequence 3, Appli
11	52	21.1	1132	16	US-10-115-479-65 Sequence 65, Appl
12	43	17.5	1547	13	US-10-027-632-265133 Sequence 265133,
13	43	17.5	1547	13	US-10-027-632-265134 Sequence 265134,
14	43	17.5	1547	13	US-10-027-632-265135 Sequence 265135,
15	43	17.5	1547	13	US-10-027-632-265136 Sequence 265136,
16	43	17.5	1547	15	US-10-027-632-265133 Sequence 265133,
17	43	17.5	1547	15	US-10-027-632-265134 Sequence 265134,
18	43	17.5	1547	15	US-10-027-632-265135 Sequence 265135,
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21	17	6.9	416	9	US-09-960-332-14595 Sequence 14595, A
22	16	6.5	65	10	US-09-908-975-26009 Sequence 26009, A
23	14	5.7	431	9	US-09-917-800A-468 Sequence 468, App
24	13	5.3	65	10	US-09-908-975-25938 Sequence 25938, A
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26	12	4.9	948	9	US-09-888-615-1 Sequence 1, Appli
27	12	4.9	1050	13	US-10-200-344-11 Sequence 11, Appl
28	12	4.9	1187	14	US-10-198-846-13457 Sequence 13457, A
29	12	4.9	1295	17	US-10-363-829-148 Sequence 148, App
30	12	4.9	1302	17	US-10-477-515-1 Sequence 1, Appli
31	12	4.9	1311	13	US-10-200-344-9 Sequence 9, Appli
32	12	4.9	1907	18	US-10-757-262-127 Sequence 127, App
33	12	4.9	1993	15	US-10-274-639-33 Sequence 33, Appl
34	12	4.9	1993	16	US-10-333-574-33 Sequence 33, Appl
35	12	4.9	2128	13	US-10-200-344-13 Sequence 13, Appl
36	11	4.5	230	14	US-10-060-036-3042 Sequence 3042, Ap
37	11	4.5	230	14	US-10-060-036-3068 Sequence 3068, Ap
38	11	4.5	230	14	US-10-060-036-3096 Sequence 3096, Ap
39	11	4.5	230	14	US-10-060-036-3131 Sequence 3131, Ap
40	11	4.5	230	14	US-10-060-036-3150 Sequence 3150, Ap
41	11	4.5	230	14	US-10-060-036-3153 Sequence 3153, Ap
42	11	4.5	230	14	US-10-060-036-3168 Sequence 3168, Ap
43	11	4.5	230	14	US-10-060-036-3175 Sequence 3175, Ap
44	11	4.5	230	14	US-10-060-036-3175 Sequence 3175, Ap
45	11	4.5	230	14	US-10-060-036-3181 Sequence 3181, Ap

ALIGNMENTS

RESULT 1  
US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 2,22e-146 Length: 1400
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 179 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACATCATTCGTCGGAACAGAC 238
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 239 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 298
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 299 TCGGAACCTTACTGTGGACTTTATCTGAGTCAGAACAGAGTGAAGCGAGTGGCTAGT 358
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 359 TTCTTGAGAAGAAATATCAACAGATTAAAGCAGATACATCAGCATGCATTCATCTCCAG 418
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 419 CATATAGTGTTCCTATATTCATACAGAAAGTAAAGCAAGCAACCATGAGGAACCTGTCT 478
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 479 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 538
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyr 223
DB 539 CATGCCATGGCTCAGAAACCTTATACCTAGCTCTGGAGGTGGGAGCATTTGGATCTAT 598
QY 224 AspLeuGlyIleLysTyrSerPheThr 232
DB 599 GATTGGGCATCAAAATATTCGTTTACA 625

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RESULT 2
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

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Alignment Scores:
Pred. No.: 2,22e-146 Length: 1400
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 10 Gaps: 0

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QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 179 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACATCATTCGTCGGAACAGAC 238
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 239 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 298
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 299 TCGGAACCTTACTGTGGACTTTATCTGAGTCAGAACAGAGTGAAGCGAGTGGCTAGT 358
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 359 TTCTTGAGAAGAAATATCAACAGATTAAAGCAGATACATCAGCATGCATTCATCTCCAG 418
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 419 CATATAGTGTTCCTATATTCATACAGAAAGTAAAGCAAGCAACCATGAGGAACCTGTCT 478
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 479 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 538
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyr 223
DB 539 CATGCCATGGCTCAGAAACCTTATACCTAGCTCTGGAGGTGGGAGCATTTGGATCTAT 598
QY 224 AspLeuGlyIleLysTyrSerPheThr 232
DB 599 GATTGGGCATCAAAATATTCGTTTACA 625

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RESULT 3
US-09-880-107-2396
; Sequence 2396, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Logic, Inc.
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2396
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396

Alignment Scores:
Pred. No.: 2,71e-146 Length: 1728
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00%				Mismatches: 0
Query Match: 60.57%				Indels: 0
DB:				Gaps: 0
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QY	104	LeuAsnArgAspPheAlaSerLysHisTTPCysGluGluGlyAlaSerSerSerCys	123	
DB	782	CTGAATAGGAACCTTTCCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCATGC	841	
QY	124	SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer	143	
DB	842	TCGGAACCTTACTGTGGACTTATCTCTGAGTCAGAACCAAGTGAAGCAGTGGCTAGT	901	
QY	144	PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln	163	
DB	902	TTCCTTGAGAAAGAAATATCAACAGATTAAAGCATACATCAGCATGCAATTCATACCCCAG	961	
QY	164	HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluIleuSer	183	
DB	962	CATATAGTGTTCCTATATTCCTATACACGAAGTAAAGCAAGACCATGAGGAACGTGCT	1021	
QY	184	LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr	203	
DB	1022	CTAGTAGCCAGTGAACGAGTTCGTGTATTTGAGAAACCTAGTAAATAATACCGGTATACA	1081	
QY	204	HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTTPileTyr	223	
DB	1082	CATGGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGTGGGACGATTGGATCAT	1141	
QY	224	AppLeuGlyIleLysTyrSerPheThr	232	
DB	1142	GATTTGGGCATCAATATTCGTTTACA	1168	
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US-09-813-133A-1				
; Sequence 1, Application US/09813133A				
; Publication No. US20020137179A1				
; GENERAL INFORMATION:				
; APPLICANT: GAN, Weiniu et al				
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.				
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND				
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND				
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND				
; FILE REFERENCE: CL001173				
; CURRENT APPLICATION NUMBER: US/09/813,133A				
; CURRENT FILING DATE: 2001-06-06				
; NUMBER OF SEQ ID NOS: 4				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 1				
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; TYPE: DNA				
; ORGANISM: Human				
US-09-813-133A-1				
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Pred. No.:	7,24e-137	Length:	1625	
Score:	140.00	Matches:	230	
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Query Match:	56.91%	Indels:	4	
DB:	9	Gaps:	0	
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QY	1	AlaSerAlaSerTyrTyrGluThrHisSerLeuAsnGluIleTyrSerTTPileGlu	20	
DB	359	GCCTCCGCATCGTACTACTGAACAGTATCACTCAATAATGAAATCTATTCCTGGATAGAA	418	
QY	21	PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu	40	

DB	419	TTTATAACTGAGAGGCATCCTGATATCTTCAAAAAATCCCATTTGGATCCTCATTTGAG	478	
QY	41	LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThr-AlaLysAsnAlaIle	60	
DB	479	AAGTACCACCTCTATGTTTTTAAGGTTCTCGAAAAAGAACAGC-AGCCAAAATGCCAT	537	
QY	60	eTTPileAspCysGlyIleHisAlaArgGluTTPileSerProAlaPheCysLeuTTPPh	80	
DB	538	ATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCTGCTTTCTGCTTGGTT	597	
QY	80	eIleGlyHisAsnArgMetTTPArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle	100	
DB	598	CATAGGCCATTAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAAATCATTTGCAT	657	
QY	100	eGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTTPCysGluGluGlyAlaSerSe	120	
DB	658	CGGAACACACCTGAATAGAACTTTTGTCTTCANACACTGGTGTGAGGAAGGTGCATCCAG	717	
QY	120	rSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAl	140	
DB	718	TTCTCTCATGCTCGGAACCTACTGTGGACTTTATCTGAGTCAGAACCCAGAAAGTGAAGGC	777	
QY	140	aValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSe	160	
DB	778	AGTGCTAGTTTCTTGAGAGAAATATCAACACAGATTAAAGCATACATCAGCATGCATTC	837	
QY	160	rTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisG1	180	
DB	838	ATATCTCCAGCATATAGTGTTCCTATATTCCTATACAGAGTAAGCAAGACCATGCA	897	
QY	180	uGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnT	200	
DB	898	GGAACTGCTCTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAAATT-AGTAAAAATA	956	
QY	200	hrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspA	220	
DB	957	CCAGGTATACACATGCGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGTGGGACG	1016	
QY	220	spTTPileTyrAspLeuGlyIleLysTyrSerPheThr	232	
DB	1017	ATTGGATCTATGATTGGGCATCAAAATATTCGTTTACA	1054	
RESULT 5				
US-10-212-877-1				
; Sequence 1, Application US/10212877				
; Publication No. US20030017574A1				
; GENERAL INFORMATION:				
; APPLICANT: GAN, Weiniu et al				
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,				
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND				
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,				
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND				
; FILE REFERENCE: CL001173DIV				
; CURRENT APPLICATION NUMBER: US/10/212,877				
; CURRENT FILING DATE: 2002-08-07				
; PRIOR APPLICATION NUMBER: 09/813,133				
; PRIOR FILING DATE: 2001-03-21				
; NUMBER OF SEQ ID NOS: 4				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 1				
; LENGTH: 1625				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-212-877-1				
Alignment Scores:				
Pred. No.:	7,24e-137	Length:	1625	
Score:	140.00	Matches:	230	
Percent Similarity:	98.29%	Conservative:	0	
Best Local Similarity:	98.29%	Mismatches:	2	
Query Match:	56.91%	Indels:	4	
DB:	14	Gaps:	0	

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US-09-980-881A-4 (1-246) x US-10-212-877-1 (1-1625)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 359 GCCTCCGCATCGTACTATGAACAGATACCTCACTCACTAAATGAATCTATTCTTGGATAGAA 418
Qy 21 PhelleThrGluArgHisProAspMetLeuThrIleHisIleGlySerSerPheGlu 40
Db 419 TTTATAACTGAGAGGCATCCTGATATGCTTCAAAAAATCCCATTTGGATCCTCATTTGAG 478
Qy 41 LysTyrProLeuTyrValLeuIleValSerGlyIleValSerGluGlnThrAlaLysAsnAlaIle 60
Db 479 AAGTACCACCTCTATGTTTAAAGGTTTCTGAAAAGAACCAAGC-AGCCAAAAATGCCAT 537
Qy 60 eTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPh 80
Db 538 ATGGATTGACGTGGAATCCATGCCAGAGATGGATCTCTCTGCTTCTGCTGTGTGTT 597
Qy 80 eIleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
Db 598 CATAGGCCATAATCGAATGTGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCAT 657
Qy 100 eGlyThrAspLeuAsnArgAsnPheAlaSerIleHisTrpCysGluGluGlyAlaSerSe 120
Db 658 CGGAACAGACCTGAAATAGAACTTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAG 717
Qy 120 rSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAl 140
Db 718 TTCCTCATGCTCGGAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGC 777
Qy 140 aValAlaSerPheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSe 160
Db 778 AGTGCTAGTTTCTTGAAGAAGAAATATCAACCAGATTAAAGCATATACATCAGCATGCATTC 837
Qy 160 rTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGl 180
Db 838 ATACTCCAGCATATAGTGTGTTTCCATATTCCATACAGCAAGTAAAGCAAGACCATGA 897
Qy 180 uGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnT 200
Db 898 GGAAGTGTCTAGTAGCAGTGAAGCAGTTCGTCTATTGAGAAAT-AGTAAATAATA 956
Qy 200 hArgTyrThrHisGlyHisGlySerGluThrLeuTyrIleAlaProGlyGlyAspA 220
Db 957 CCAGGTATACACATGCCATGGCTCAGAAACCTTATACCTAGTCTCTCGAGGTGGGACG 1016
Qy 220 spTrpIleTyrAspLeuGlyIleLysTyrSerPheThr 232
Db 1017 ATTGGATCATGATTTGGGCATCAAAATATTCGTTTACA 1054

RESULT 6
US-10-115-479-69
; Sequence 69, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei

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; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.: 1.54e-107 Length: 1344
Score: 112.00 Matches: 148
Percent Similarity: 98.67% Conservative: 0
Best Local Similarity: 98.67% Mismatches: 1
Query Match: 45.53% Indels: 2
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-69 (1-1344)

Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 748 AATCGAATGTGGAGAAAGAACCCGTTCTTCTATCGGAACAATCATTCATCGGAACAGAC 807
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 808 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCATGC 867
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 868 TCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACAGAGTGAAGGCAGTGGCTAGT 927
Qy 144 PheLeuArgArgAsnIleAsnGlnIleAlaTyrIleSerMetHisSerTyrSerGln 163
Db 928 TTCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATTCATCTATCTCCAG 987
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 988 CATATAGTGTTCCTATATTCCTATACAGGAAGTAAAGCAAGACCATGAGGAAGTGTCT 1047

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QY 184 LeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrTh 203
Db 1048 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAT-AGTAAATATACCGGTATAC 1106
QY 203 rHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrPileTy 223
Db 1107 ACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATTGGATCTA 1166
QY 223 rAspLeuGlyIleLysTyrSerPheThr 232
Db 1167 TGATTGGGCATCAAAATATTGGTTACA 1194

RESULT 7
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication NO. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Fatturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
US-10-115-479-67
Alignment Scores:
Pred. No.: 1,97e-107 Length: 1743
Score: 112.00 Matches: 148
Percent Similarity: 98.67% Conservative: 0
Best local Similarity: 98.67% Mismatches: 1
Query Match: 45.53% Indels: 2
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-67 (1-1743)
QY 84 AsnArgMetTyrArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 737 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCATCGGAACAGAC 796
QY 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123
Db 797 CTGAATAGGAACCTTTGCTTCCAAACACCTGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 856
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 857 TCGGAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGT 916
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 917 TTTCTGAGAAGAAATATCAACCCAGATTAAAGCATACATCAGCATCATCTATCTATCTCCAG 976
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db 977 CATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGCAACCATGAGGAAGTGTCT 1036
QY 184 LeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrTh 203
Db 1037 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAT-AGTAAATATACCGGTATAC 1095
QY 203 rHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrPileTy 223
Db 1096 ACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATTGGATCTA 1155

RESULT 8
US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication NO. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
```

```
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine B.
/ APPLICANT: Malyanker, Uriel M.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Mazur, Ann
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-322 B (Cura 622 PT)
/ CURRENT APPLICATION NUMBER: US/10/115,479
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,657
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,678
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,687
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 198
/ SEQ ID NO 63
/ LENGTH: 1037.
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (41)...(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.: 1,96e-61 Length: 1037
Score: 68.00 Matches: 104
Percent Similarity: 98.11% Conservative: 0
Best Local Similarity: 98.11% Mismatches: 1
Query Match: 27.64% Indels: 2
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-63 (1-1037)

Qy 128 CysGlyLeuTyrProGluSerGluProGluVallylsAlaValAlaSerPheLeuArg 147
Db 572 TGTGACCTTTATCTCTGAGTCAGAACAGACAGAGTGAAGCGAGTGGCTAGTTCTTGAGAAGA 631
Qy 148 AsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhe 167
Db 632 AATATCAACCAAGATTAAAGCATATCATGATGCATCTACTCCAGCATATAGTGT 691
Qy 168 ProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSer 187
Db 692 CCATATTCTTATACACGAAGTAAAGCAAGACCATGAGGAACGTCTCTAGTAGCCAGT 751
Qy 188 GluAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrThrHisGlyHisG1 207
Db 752 GAAGCAGTTCGTGCTATTGAGAAAAATT-AGTAAAAAATACCAGGTATACACATGGCCATGG 810
Qy 207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyValGlyAspAspTrpIleTyrAspLeuGlyI1 227
Db 811 CTCGAAACCTTATACCTAGTCTCTGGAGGTGGGACCATGGATCTATGATTGGGCAT 870
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Qy 227 eLysTyrSerPheThr 232
Db 871 CAAATATTCGTTTACA 886

RESULT 9
US-09-813-133A-3
/ Sequence 3, Application US/09813133A
/ Publication No. US20020137179A1
/ GENERAL INFORMATION:
/ APPLICANT: GAN, Weiniu et al
/ TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: CL001173
/ CURRENT APPLICATION NUMBER: US/09/813,133A
/ CURRENT FILING DATE: 2001-06-06
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 55827
/ TYPE: DNA
/ ORGANISM: Human
US-09-813-133A-3

Alignment Scores:
Pred. No.: 8.46e-60 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.64% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-813-133A-3 (1-55827)

Qy 115 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db 48643 GAGGAAGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTTATCTCGAGTCA 48702
Qy 135 GluProGluVallylsAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 154
Db 48703 GAACCAAGTGAAGGCAGTGGCTAGTTCTTGAGAGAAATATCAACACGATTTAAAGCA 48762
Qy 155 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 174
Db 48763 TACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATCTCTATACACGAAGT 48822
Qy 175 LysSerLysAspHisGluGluLeu 182
Db 48823 AAAAGCAAGACCATGAGGAACGTG 48846

RESULT 10
US-10-212-877-3
/ Sequence 3, Application US/10212877
/ Publication No. US20030017574A1
/ GENERAL INFORMATION:
/ APPLICANT: GAN, Weiniu et al
/ TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: CL001173DIV
/ CURRENT APPLICATION NUMBER: US/10/212,877
/ CURRENT FILING DATE: 2002-08-07
/ PRIOR APPLICATION NUMBER: 09/813,133
/ PRIOR FILING DATE: 2001-03-21
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 55827
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-212-877-3

Alignment Scores:
```

```

Pred. No.: 8,46e-60 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.64% Indels: 0
DB: 14 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-212-877-3 (1-55827)

QY 115 GluGluGlyAlaSerSerSerSerGluThrTyrcysGlyLeuTyProGluSer 134
Db 48643 GAGGAAGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTTATCTCGAGTCA 48702

QY 135 GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 154
Db 48703 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 48762

QY 155 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrcysGlyLeuTyProGluSer 174
Db 48763 TACATCAGATGCATTCATACCTCCAGCATATAGTGTTCATATTCCTATACCAAGT 48822

QY 175 LysSerLysAspHisGluGluLeu 182
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 11
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Hailong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1103)
US-10-115-479-65

Alignment Scores:
Pred. No.: 1,35e-44 Length: 1132
Score: 52.00 Matches: 52
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.14% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-65 (1-1132)

QY 84 AsnArgMetTyrArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 758 AATCGAATGTGGAGAAAGACCGTTCTTTCTATGCGAAACAATCATTCATCGGAACAGAC 817

QY 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123
Db 818 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 877

QY 124 SerGluThrTyrCysGlyLeuTyProGluSerGlu 135
Db 878 TCGGAACCTACTGTGGACTTTATCTCGATCAGAA 913

RESULT 12
US-10-027-632-265133
; Sequence 265133, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265133
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265133

Alignment Scores:
Pred. No.:      5,14e-35      Length:      1547
Score:          43.00        Matches:      43
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     17.48%      Indels: 0
DB:              13         Gaps: 0

US-09-980-881A-4 (1-246) x US-10-027-632-265133 (1-1547)

Qy 115 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db 1417 GAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 1476

Qy 135 GluProGluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 154
Db 1477 GAACCAAGTGAAGGAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536

Qy 155 TyrIleSer 157
Db 1537 TACATCAGC 1545

RESULT 14
US-10-027-632-265135
; Sequence 265135, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265135
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265135

Alignment Scores:
Pred. No.:      5,14e-35      Length:      1547
Score:          43.00        Matches:      43
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     17.48%      Indels: 0
DB:              13         Gaps: 0

US-09-980-881A-4 (1-246) x US-10-027-632-265135 (1-1547)

Qy 115 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db 1417 GAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 1476

Qy 135 GluProGluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 154
Db 1477 GAACCAAGTGAAGGAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536

Qy 155 TyrIleSer 157
Db 1537 TACATCAGC 1545

RESULT 15
US-10-027-632-265134
; Sequence 265134, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265134
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265134

Alignment Scores:
Pred. No.:      5,14e-35      Length:      1547
Score:          43.00        Matches:      43
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     17.48%      Indels: 0
DB:              13         Gaps: 0

US-09-980-881A-4 (1-246) x US-10-027-632-265134 (1-1547)
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Thu Oct 28 07:16:16 2004

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US-10-027-632-265136
; Sequence 265136, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265136
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1547)
; OTHER INFORMATION: n = A, T, C or G
US-10-027-632-265136

Alignment Scores:
Pred. No.:      5,14e-35      Length:      1547
Score:          43.00      Matches:      43
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      17.48%      Indels:    0
DB:              13      Gaps:      0

US-09-980-881A-4 (1-246) x US-10-027-632-265136 (1-1547)

QY      115  GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db      1417  GAGGAAGGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGACTTTTATCCTGAGTCA 1476

QY      135  GluProGluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 154
Db      1477  GAACCAAGAGTGAAGGCGAGTGGCTAGTTCTTGAGAAGAAATATCAACCAGATTAAAGCA 1536

QY      155  TyrIleSer 157
Db      1537  TACATCAGC 1545
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Search completed: October 27, 2004, 09:21:50  
Job time : 367.475 secs





Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	57	4.3	19	3	US-09-309-317-5	Sequence 5, Appli
2	42.5	3.2	16	4	US-09-541-345-44	Sequence 44, Appl
3	40	3.0	18	4	US-09-693-822B-19	Sequence 19, Appl
4	40	3.0	19	4	US-09-693-822B-8	Sequence 8, Appli
5	40	3.0	19	4	US-09-693-822B-23	Sequence 23, Appl
6	40	3.0	19	4	US-09-693-822B-24	Sequence 24, Appl
7	39.5	3.0	13	4	US-09-402-641-1	Sequence 1, Appli
8	39.5	3.0	15	3	US-08-142-590B-5	Sequence 5, Appli
9	39.5	3.0	18	2	US-08-747-915-4	Sequence 4, Appli
10	39.5	3.0	18	3	US-08-467-023-211	Sequence 211, App
11	39.5	3.0	18	3	US-08-142-590B-4	Sequence 4, Appli
12	39.5	3.0	18	3	US-08-142-590B-24	Sequence 24, Appl
13	39.5	3.0	18	4	US-09-285-783-4	Sequence 4, Appli
14	39	2.9	19	4	US-09-693-822B-25	Sequence 25, Appl
15	38.5	2.9	17	4	US-09-822-624-20	Sequence 20, Appl
16	38	2.8	14	2	US-08-685-589A-198	Sequence 198, App
17	38	2.8	16	4	US-09-340-620A-47	Sequence 47, Appl
18	38	2.8	17	2	US-08-685-589A-140	Sequence 140, App
19	38	2.8	19	1	US-08-382-013A-59	Sequence 59, Appl
20	38	2.8	19	1	US-08-382-013A-71	Sequence 71, Appl
21	38	2.8	19	4	US-08-617-832B-25	Sequence 25, Appl
22	37.5	2.8	17	4	US-09-440-781-66	Sequence 66, Appl
23	37	2.8	9	2	US-08-637-759B-330	Sequence 330, App
24	37	2.8	9	3	US-08-871-355A-330	Sequence 330, App
25	37	2.8	9	3	US-09-201-945-330	Sequence 330, App
26	37	2.8	12	3	US-08-293-728-9	Sequence 9, Appli
27	37	2.8	12	3	US-09-421-868-9	Sequence 9, Appli

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CEA binding
; OTHER INFORMATION: polypeptide
US-09-541-345-44

Query Match          3.2%; Score 42.5; DB 4; Length 16;
Best Local Similarity 43.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 60 IWIDCGIHAREWISPA 75
    ||| : . : |||
Db 1 IW-DCNLFKNQWFCPA 15

RESULT 3
US-09-693-822B-19
; Sequence 19, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-19

Query Match          3.0%; Score 40; DB 4; Length 18;
Best Local Similarity 38.1%; Pred. No. 9.4e+02;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 97 NHCIGTDLNRNFASKHWCEEG 117
    :||| ||| ||| |||
Db 2 HHC-----YKRKFHEKHCHRG 18

RESULT 4
US-09-693-822B-8
; Sequence 8, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-8

Query Match          3.0%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 97 NHCIGTDLNRNFASKHWCEEG 117
```

```
; ||| ||| ||| |||
Db 2 HHC-----YKRKFHEKHCHRG 18

RESULT 5
US-09-693-822B-23
; Sequence 23, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-23

Query Match          3.0%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 97 NHCIGTDLNRNFASKHWCEEG 117
    :||| ||| ||| |||
Db 2 HHC-----YKRKFHEKHCHRG 18

RESULT 6
US-09-693-822B-24
; Sequence 24, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-24

Query Match          3.0%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 97 NHCIGTDLNRNFASKHWCEEG 117
    :||| ||| ||| |||
Db 2 HHC-----YKRKFHEKHCHRG 18

RESULT 7
US-09-402-641-1
; Sequence 1, Application US/09402641
; Patent No. 6528619
; GENERAL INFORMATION:
; APPLICANT: BUERGLE, Markus
; APPLICANT: GRAEFF, Heinrich
```

APPLICANT: KESSLER, Horst  
APPLICANT: MAGDOLEN, Viktor Robert  
APPLICANT: KOENIG, Bernhard  
APPLICANT: KOPPIZ, Marcus  
APPLICANT: RIEMER, Christoph  
APPLICANT: SCHMITT, Manfred  
APPLICANT: WEIDLE, Ulrich  
APPLICANT: WILHELM, Olaf  
TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR  
FILE REFERENCE: Case 20367US  
CURRENT APPLICATION NUMBER: US/09/402,641  
CURRENT FILING DATE: 2000-01-10  
PRIOR APPLICATION NUMBER: EP97106024.9  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: PCT/EP98/02178  
PRIOR FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide "cyclo  
US-09-402-641-1

Query Match 3.0%; Score 39.5; DB 4; Length 13;  
Best Local Similarity 37.5%; Pred. No. 6.5e+02;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
Db 1 CVS---NKYFSNIHWC 13

RESULT 8  
US-08-142-5908-5  
Sequence 5, Application US/08142590B  
Patent No. 6120765  
GENERAL INFORMATION:  
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and  
TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,590B  
FILING DATE: 25-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,318  
FILING DATE: 02-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REFERENCE/DOCKET NUMBER: 35,965  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

GOETINCK,

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-142-5908-5

Query Match 3.0%; Score 39.5; DB 3; Length 15;  
Best Local Similarity 37.5%; Pred. No. 8.1e+02;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
Db 2 CVS---NKYFSNIHWC 14

RESULT 9  
US-08-747-915-4  
Sequence 4, Application US/08747915  
Patent No. 5942492  
GENERAL INFORMATION:  
APPLICANT: Jones, Terence R.  
APPLICANT: Haney, David N.  
APPLICANT: Varga, Janos  
TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,915  
FILING DATE: 12-NOV-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 32904-200001.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-747-915-4

Query Match 3.0%; Score 39.5; DB 2; Length 18;  
Best Local Similarity 37.5%; Pred. No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
Db 3 CVS---NKYFSNIHWC 15

RESULT 10  
US-08-467-023-211  
Sequence 211, Application US/08467023  
Patent No. 6090386  
GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
APPLICANT: Pollock, Joanne;

```

; APPLICANT: Bond, Julian F.;
; APPLICANT: Garman, Richard D;
; APPLICANT: Kuo, Mei-Chang;
; APPLICANT: Yeung, Siu-mei H.;
; APPLICANT: Brauer, Andrew;
; APPLICANT: Exley, Mark A.;
; APPLICANT: Powers, Steven P.
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; TITLE OF INVENTION: Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.
; STREET: 610 Lincoln St
; CITY: Waltham
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,023
; FILING DATE: June 6, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,225
; FILING DATE: December 6, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: 025.6 US2 (IMI-028CPD2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-467-023-211

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Query Match 3.0%; Score 39.5; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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Qy 52 KEQTAKNAIWD 63
Db 2 KERTATN-IWID 12

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RESULT 11
US-08-142-590B-4
; Sequence 4, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-142-590B-4

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Query Match 3.0%; Score 39.5; DB 3; Length 18;
Best Local Similarity 37.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

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Qy 99 CIGTDLNRNFASKHWC 114
Db 5 CVS--NKYFSNIHWC 17

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RESULT 12
US-08-142-590B-24
; Sequence 24, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-142-590B-24

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Query Match 3.0%; Score 39.5; DB 3; Length 18;  
Best Local Similarity 37.5%; Pred No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
| : : : : :  
Db 4 CVS---NKYFSNIHWC 16

RESULT 13  
US-09-285-783-4  
; Sequence 4, Application US/09285783  
; Patent No. 6514710  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Terence R.  
; Haney, David N.  
; Varga, Janos  
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RADER, FISHMAN & GRAUER  
; STREET: 1233 20TH STREET NW, SUITE 501  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285,783  
; FILING DATE: 05-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LIVNAT, SEMUEL  
; REGISTRATION NUMBER: 33,949  
; REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 955-8787  
; TELEFAX: (202) 955-3751  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-285-783-4

Query Match 3.0%; Score 39.5; DB 4; Length 18;  
Best Local Similarity 37.5%; Pred No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
| : : : : :  
Db 3 CVS---NKYFSNIHWC 15

RESULT 14  
US-09-693-822B-25  
; Sequence 25, Application US/09693822B  
; Patent No. 6555650  
; GENERAL INFORMATION:  
; APPLICANT: Lajoie, Gilles A.  
; TITLE OF INVENTION: Cyclic Analogs of Histatins  
; FILE REFERENCE: 36555-0002  
; CURRENT APPLICATION NUMBER: US/09/693,822B  
; CURRENT FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: CA 2,285,673

; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cyclic analogues of histatin  
US-09-693-822B-25

Query Match 2.9%; Score 39; DB 4; Length 19;  
Best Local Similarity 38.1%; Pred No. 1.3e+03;  
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

QY 97 NHCIGTDLNRNFASKHWCCEG 117  
: : : : :  
Db 2 HHC-----WKRKFHEKHCHRG 18

RESULT 15  
US-09-822-624-20  
; Sequence 20, Application US/09822624  
; Patent No. 6440714  
; GENERAL INFORMATION:  
; APPLICANT: Abell, Creed W.  
; APPLICANT: Kwan, Sua-Wah  
; APPLICANT: Zhou, Binhua  
; APPLICANT: Wo, Bo  
; TITLE OF INVENTION: Tyr393 and Tyr398 Mutants of Monoamine Oxidase B  
; FILE REFERENCE: D6237PCT  
; CURRENT APPLICATION NUMBER: US/09/822,624  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 2000-03-30  
; PRIOR FILING DATE: US 60/193,178  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 20  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence flanking the covalent FAD  
; OTHER INFORMATION: binding residue of human monooxidase B (MAO B)  
US-09-822-624-20

Query Match 2.9%; Score 38.5; DB 4; Length 17;  
Best Local Similarity 53.3%; Pred No. 1.3e+03;  
Matches 8; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 113 WCEEGASSSSCSEY 127  
| : : : : :  
Db 1 WCEE-QYSGGCYTY 14

Search completed: October 27, 2004, 01:31:43  
Job time : 12.7691 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:13:21 ; Search time 31.0106 Seconds  
(without alignments)  
2568.304 Million cell updates/sec

Title: US-09-980-881A-4  
Perfect score: 1338  
Sequence: 1 ASASYVEQVHSLNEIYSWIE.....IKYSFTSPNPVKKLPLSLK 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 260209

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	4.3	19	9 US-09-799-760-5	Sequence 5, Appli
2	48	3.6	11	16 US-10-343-509-10	Sequence 10, Appl
3	46	3.4	11	15 US-10-410-764-87	Sequence 87, Appl
4	42.5	3.2	16	10 US-09-825-517A-44	Sequence 44, Appl
5	41	3.1	18	16 US-10-742-379-90	Sequence 90, Appl
6	39.5	3.0	13	16 US-10-756-289-2	Sequence 3, Appli
7	39.5	3.0	15	16 US-10-756-289-2	Sequence 2, Appli
8	39.5	3.0	18	14 US-10-349-543-4	Sequence 4, Appli
9	39.5	3.0	19	10 US-09-791-524-1	Sequence 1, Appli
10	39	2.9	19	10 US-09-791-524-2	Sequence 2, Appli
11	38.5	2.9	17	9 US-09-822-624-20	Sequence 20, Appl
12	38	2.8	16	9 US-09-728-721-47	Sequence 47, Appl
13	38	2.8	16	14 US-10-295-981-47	Sequence 47, Appl

Sequence 23, Appl  
Sequence 247, Appl  
Sequence 54, Appl  
Sequence 25, Appl  
Sequence 25, Appl  
Sequence 32, Appl  
Sequence 66, Appl  
Sequence 22, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 30, Appl  
Sequence 74, Appl  
Sequence 1864, Ap  
Sequence 15, Appl  
Sequence 75, Appl  
Sequence 75, Appl  
Sequence 75, Appl  
Sequence 75, Appl  
Sequence 75, Appl  
Sequence 75, Appl  
Sequence 194, App  
Sequence 181, App  
Sequence 41546, A  
Sequence 49, Appl  
Sequence 14, Appl  
Sequence 16, Appl  
Sequence 49, Appl  
Sequence 96, Appl  
Sequence 1133, Ap  
Sequence 15, Appl  
Sequence 1148, Ap

ALIGNMENTS

RESULT 1  
US-09-799-760-5  
; Sequence 5, Application US/09799760  
; Patent No. US20010001771A1  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley  
; APPLICANT: Tremblay, Patrick  
; APPLICANT: Moore, Richard  
; APPLICANT: Westaway, David  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Lee, Inyoul  
; TITLE OF INVENTION: PrP-like Gene  
; FILE REFERENCE: 6510-130CON  
; CURRENT APPLICATION NUMBER: US/09/799,760  
; CURRENT FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 09/309,317  
; PRIOR FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized peptide  
US-09-799-760-5

Query Match 4.3%; Score 57; DB 9; Length 19;  
Best Local Similarity 44.4%; Pred. No. 91;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 97 NHCIGTDLNRNFASKHWC 114

Db 1 NHCFGAENRYAANYIC 18

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RESULT 2
US-10-343-509-10
; Sequence 10, Application US/10343509
; Publication No. US20040101865A1
; GENERAL INFORMATION:
; APPLICANT: BASF
; TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
; FILE REFERENCE: 0050/51654
; CURRENT APPLICATION NUMBER: US/10/343.509
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Euglena gracilis
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = (Phe/Tyr)
US-10-343-509-10

Query Match      3.6%; Score 48; DB 16; Length 11;
Best Local Similarity 70.0%; Pred No. 3.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      217 GGDHWYDLG 226
Db      1 GGDGWAYDIG 10

RESULT 3
US-10-410-764-87
; Sequence 87, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; FILE REFERENCE: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520MNM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Zinc carboxypeptidase zinc-binding region 2
US-10-410-764-87

Query Match      3.4%; Score 46; DB 15; Length 11;
Best Local Similarity 63.6%; Pred No. 5.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      159 HSYSQHIVFPY 169
Db      1 HSYQMLMPY 11

RESULT 4
US-09-825-517A-44
; Sequence 44, Application US/09825517A
; Publication No. US20030203415A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
; FILE REFERENCE: DYX-016.1 (3421.1005-001)
; CURRENT APPLICATION NUMBER: US/09/825,517A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/541,345
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEA binding polypeptide
US-09-825-517A-44

Query Match      3.2%; Score 42.5; DB 10; Length 16;
Best Local Similarity 43.8%; Pred No. 2.3e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy      60 IWDCGIHAREWISPA 75
Db      1 IW-DCNLFKNQWFCPA 15

RESULT 5
US-10-742-379-90
; Sequence 90, Application US/10742379
; Publication No. US20040181033A1
; GENERAL INFORMATION:
; APPLICANT: Han, HQ
; APPLICANT: Min, Hosung
; APPLICANT: Boone, Thomas Charles
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN
; FILE REFERENCE: A-828 (US)
; CURRENT APPLICATION NUMBER: US/10/742,379
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/435,923
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 634
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:  
OTHER INFORMATION: Myostatin Binding Peptide  
US-10-742-379-90

Query Match 3.1%; Score 41; DB 16; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.8e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 112 HWCQG 117  
DB 2 HWCQG 7

RESULT 6  
US-10-756-289-3  
Sequence 3, Application US/10756289  
Publication No. US20040138110A1  
GENERAL INFORMATION:  
APPLICANT: Kessler, Horst  
APPLICANT: Graeff, Heinrich  
APPLICANT: Schmitt, Manfred  
APPLICANT: Magdolen, Viktor  
APPLICANT: Wilhelm, Olaf G.  
APPLICANT: Riemer, Christoph  
APPLICANT: Buegle, Markus  
TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
FILE REFERENCE: 100564-09040  
CURRENT APPLICATION NUMBER: US/10/756,289  
CURRENT FILING DATE: 2004-01-14  
PRIOR APPLICATION NUMBER: US/09/402,464  
PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: EP 97 106 024.9  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1...12  
OTHER INFORMATION: D-amino acids may be substituted for corresponding L-  
OTHER INFORMATION: amino acids at  
OTHER INFORMATION: positions 1,2,3,9, 11, and 12.  
US-10-756-289-3

Query Match 3.0%; Score 39.5; DB 16; Length 13;  
Best Local Similarity 37.5%; Pred. No. 3.5e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
DB 1 CVS---NKYFSNIHWC 13

RESULT 7  
US-10-756-289-2  
Sequence 2, Application US/10756289  
Publication No. US20040138110A1  
GENERAL INFORMATION:  
APPLICANT: Kessler, Horst  
APPLICANT: Graeff, Heinrich  
APPLICANT: Schmitt, Manfred  
APPLICANT: Magdolen, Viktor  
APPLICANT: Wilhelm, Olaf G.  
APPLICANT: Riemer, Christoph  
APPLICANT: Buegle, Markus  
TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
FILE REFERENCE: 100564-09040  
CURRENT APPLICATION NUMBER: US/10/756,289  
CURRENT FILING DATE: 2004-01-14  
PRIOR APPLICATION NUMBER: US/09/402,464

PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: EP 97 106 024.9  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-756-289-2

Query Match 3.0%; Score 39.5; DB 16; Length 15;  
Best Local Similarity 37.5%; Pred. No. 4.2e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
DB 2 CVS---NKYFSNIHWC 14

RESULT 8  
US-10-349-543-4  
Sequence 4, Application US/10349543  
Publication No. US20030166514A1  
GENERAL INFORMATION:  
APPLICANT: Jones, Terence R.  
Haney, David N.  
Varga, Janos  
TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
CYCLINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RADER, FISHMAN & GRAUER  
STREET: 1233 20TH STREET NW, SUITE 501  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/349,543  
FILING DATE: 22-Jan-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/285,783  
FILING DATE: 05-Apr-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: LIVNAT, SHMUEL  
REGISTRATION NUMBER: 33,949  
REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 955-8787  
TELEFAX: (202) 955-3751  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-349-543-4

Query Match 3.0%; Score 39.5; DB 14; Length 18;  
Best Local Similarity 37.5%; Pred. No. 5.4e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 99 CIGTDLNRNFASKHWC 114  
DB 3 CVS---NKYFSNIHWC 15

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RESULT 9
US-09-791-524-1
; Sequence 1, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-1

Query Match          3.0%; Score 39.5; DB 10; Length 19;
Best Local Similarity 37.5%; Pred. No. 5.8e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 99 CIGTDLNRFASKHWC 114
| : | : | : |
Db 6 CVS---NKYFSNIHWC 18

RESULT 10
US-09-791-524-2
; Sequence 2, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-2

Query Match          2.9%; Score 39; DB 10; Length 19;
Best Local Similarity 50.0%; Pred. No. 6.6e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 105 NNFASKHWC 114
| : | : |
Db 9 NKYFSNIHWC 18

RESULT 11
US-09-822-624-20
; Sequence 20, Application US/09822624
; Publication No. US2002004233A1
; GENERAL INFORMATION:
; APPLICANT: Abell, Creed W.
; APPLICANT: Kwan, Sua-Wah
; APPLICANT: Zhou, Binhua
; APPLICANT: Wo, Bo
; TITLE OF INVENTION: Tyr393 and Tyr398 Mutants of Monoamine Oxidase B
; FILE REFERENCE: D6237PCT
; CURRENT APPLICATION NUMBER: US/09/822,624
; CURRENT FILING DATE: 2001-03-30
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; PRIOR APPLICATION NUMBER: 2000-03-30
; PRIOR FILING DATE: US 60/193,178
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 20
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence flanking the covalent PAD
; OTHER INFORMATION: binding residue of human monooxidase B (MAO B)
US-09-822-624-20

Query Match          2.9%; Score 38.5; DB 9; Length 17;
Best Local Similarity 53.3%; Pred. No. 6.4e+03;
Matches 8; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 113 WCEBASSSCSETY 127
| | | | |
Db 1 WCEB-QYSGGYTTY 14

RESULT 12
US-09-728-721-47
; Sequence 47, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-47

Query Match          2.8%; Score 38; DB 9; Length 16;
Best Local Similarity 52.6%; Pred. No. 6.6e+03;
Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;

Qy 127 YCGLYPESEPEVKAVASFL 145
| | | | |
Db 1 YC--YPERDPE--EVFAFL 15

RESULT 13
US-10-295-981-47
; Sequence 47, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
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GenCore version 5.1.6  
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Run on: October 27, 2004, 01:43:22 ; Search time 64.6271 Seconds  
(without alignments)  
2705.583 Million cell updates/sec

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Perfect score: 1338  
Sequence: 1 ASASYEQHSINETYWIE.....IKYFSTSPPPVEKLLPLSLK 246

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO spooll\_p/US0980881/runat 26102004 084114 7227/app query.fasta\_1.1429  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=std.rn1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US0980881 @CGN 1 1 177 @runat 26102004 084114 7227 -NCPU=6 -ICPU=3  
-NM MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1289.5	96.4	1625	US-09-813-133A-1	Sequence 1, Appli
2	1272	95.1	1272	US-08-869-057-1	Sequence 1, Appli
3	1272	95.1	1749	US-07-649-591B-2	Sequence 2, Appli
4	1272	95.1	1749	US-08-277-540-2	Sequence 2, Appli
5	1272	95.1	1749	US-08-430-787A-2	Sequence 2, Appli
6	610	45.6	927	US-08-782-760-5	Sequence 5, Appli
7	610	45.6	927	PCT-US96-00995-5	Sequence 5, Appli
8	582	43.5	921	US-08-696-139-3	Sequence 3, Appli
9	582	43.5	1215	US-08-696-139-1	Sequence 1, Appli
10	567	42.4	999	US-08-860-882A-67	Sequence 67, Appli
11	567	42.4	999	US-09-011-769A-50	Sequence 50, Appli
12	567	42.4	1053	US-08-860-882A-64	Sequence 64, Appli

13	567	42.4	1053	4	US-09-011-769A-46	Sequence 46, Appli
14	567	42.4	1263	2	US-08-860-882A-56	Sequence 56, Appli
15	567	42.4	1263	4	US-09-011-769A-38	Sequence 38, Appli
16	567	42.4	1284	2	US-08-860-882A-71	Sequence 71, Appli
17	567	42.4	1284	4	US-09-011-769A-55	Sequence 55, Appli
18	560	41.9	1053	4	US-09-463-451-27	Sequence 27, Appli
19	560	41.9	1053	4	US-09-463-451-28	Sequence 28, Appli
20	560	41.9	1059	2	US-08-860-882A-74	Sequence 74, Appli
21	560	41.9	1059	2	US-09-011-769A-59	Sequence 59, Appli
22	559	41.8	1059	2	US-08-860-882A-77	Sequence 77, Appli
23	559	41.8	1059	4	US-09-011-769A-63	Sequence 63, Appli
24	556.5	41.6	1311	4	US-09-675-305-9	Sequence 9, Appli
25	556.5	41.6	1311	4	US-10-200-344-9	Sequence 9, Appli
26	552	41.3	1622	4	US-09-023-655-1020	Sequence 1020, Ap
27	549	41.0	1870	3	US-09-171-945-112	Sequence 112, App
28	549	41.0	2154	3	US-09-171-945-124	Sequence 124, App
29	525.5	39.3	2128	4	US-09-675-305-13	Sequence 13, Appli
30	525.5	39.3	2128	4	US-10-200-344-13	Sequence 13, Appli
31	492	36.8	1200	4	US-09-710-099-7	Sequence 7, Appli
32	492	36.8	1200	4	US-10-200-910-7	Sequence 7, Appli
33	471.5	35.2	1050	4	US-09-675-305-11	Sequence 11, Appli
34	471.5	35.2	1050	4	US-10-200-344-11	Sequence 11, Appli
35	465.5	34.8	1257	3	US-08-640-906-1	Sequence 1, Appli
36	465.5	34.8	1257	3	US-09-395-936-1	Sequence 5, Appli
37	465.5	34.8	1311	4	US-09-710-099-5	Sequence 5, Appli
38	465.5	34.8	1311	4	US-10-200-910-5	Sequence 3, Appli
39	459	34.3	1251	3	US-08-640-906-3	Sequence 3, Appli
40	459	34.3	1251	3	US-09-395-936-3	Sequence 3, Appli
41	405.5	30.3	945	4	US-09-710-099-3	Sequence 11, Appli
42	405.5	30.3	945	4	US-09-710-099-11	Sequence 3, Appli
43	405.5	30.3	945	4	US-10-200-910-3	Sequence 11, Appli
44	405.5	30.3	945	4	US-10-200-910-11	Sequence 11, Appli
45	403.5	30.2	2247	4	US-09-710-099-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 3.46e-156 Length: 1625  
Score: 1289.50 Matches: 244  
Percent Similarity: 92.42% Conservative: 0  
Best Local Similarity: 92.42% Mismatches: 2  
Query Match: 96.38% Indels: 18  
DB: 4 Gaps: 1

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

Qy	1	AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu	20
Db	359	GCTCCGCATCGTACTATGAAACAGATATCACTACTAAATGAAATCTATTCTTGGATAGAA	418
Qy	21	PheIleThrGluArgHisProAspMetLeuThrLysIleHisGlySerSerPheGlu	40

Db	419	TTTATAACTGAGAGGCATCTCGATATATGCTTACAAAAATCCACATPGGATCCTCATTTTGAG	478
Qy	41	LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle	60
Db	479	ARGTACCACCTCTATGTTTTTAAGGTTTCTGGAAGAACAAGCAGGCCAAAATGCCATA	538
Qy	61	TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe	80
Db	539	TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCGCTTTCTGCTGTGTGGTTC	598
Qy	81	IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle	100
Db	599	ATAGGCCATAATTCGAATGTGGAGAAAGACCGTTCTTTCTATGCGAACAACTCATTTGCATC	658
Qy	101	GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer	120
Db	659	GGAACAGACCTGAATAGAACTTTTGCTTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGT	718
Qy	121	SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla	140
Db	719	TCCTCATGTCGGAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGCA	778
Qy	141	ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer	160
Db	779	GTGGCTAGTTTCTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATTC	838
Qy	161	TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu	180
Db	839	TACTCCAGCATATAGTGTGTTTCCATATTCCTATACAGAAAGTAAAGCAAGACCATGAG	898
Qy	181	GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr	200
Db	899	GAACGTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAAATTAGTAAAAATACC	958
Qy	201	ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspAsp	220
Db	959	AGGTATACATATGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGGTGGGGACGAT	1018
Qy	221	TrpIleTyrAspLeuGlyIleLysTyrSerPhe-----	231
Db	1019	TGGATCTATGATTTGGGCATCAAAATATTCGTTTACAATGAACTTCGAGATACGGGCACA	1078
Qy	232	-----ThrSerAsnProProValGluLysLeuLeuProLe	243
Db	1079	TACGGATTCTTGTCGCCGAGCGTTATACAAACCCACCTGTAGAGAAGCTTTTGCCGCT	1138
Qy	243	uSerLeuLys 246	
Db	1139	GTCTCTAAAA 1148	

## RESULT 2

```

US-08-869-057-1
; Sequence 1, Application US/08869057
; Patent No. 5985562
; GENERAL INFORMATION:
; APPLICANT: Morser, Michael J
; APPLICANT: Nagashima, Mariko
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease
; TITLE OF INVENTION: Risk
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Berlex Biosciences Legal Department
; STREET: 15049 San Pablo Avenue
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804-0099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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Db 763 CTGAATAGCAACTTTGCTTCCAAACACTGGTGTGAGGAAGTGCATCCCATCTCTCATGC 822  
Qy 124 SerGluThrTyCysGlyLeuTyrProGluSerGluProGluValIleValAlaSer 143  
Db 823 TCGGAACCTACTGTGGACTTTTATCTGTAGTCAGAACCAAGTGAAGCAGTGGCTAGT 882  
Qy 144 PheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 883 TTCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTCCAG 942  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
Db 943 CATATAGTGTTCATATCTCTATACAGCAAGTAAAGCAAGACCATCAGGAACTGTCT 1002  
Qy 184 LeuValAlaSerGluValAlaGlnIleGluLysThrSerIleAsnThrArgTyrThr 203  
Db 1003 CTAGTAGCCAGTGAACGACTGTGTCTATTGAGAAACATAGTAAATAATACAGGTATACA 1062  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
Db 1063 CATGGCAGTGGCTCAGAACCTTATACCTAGCTCTCTGGAGTGGGGACGATTGGATCTAT 1122  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1123 GATTTGGGCATCAATATTTCGTTTACAATTGAACCTTCGAGATACGGGCACATACGGATTTC 1182  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeu 246  
Db 1183 TTGCTGCGGAGCGTTTACATCAACCCACCTGTGAGAGAGCTTTTCCCGCTGTCTCTAAA 1242  
Qy 246 s 246  
Db 1243 A 1243

RESULT 3

US-07-649-591B-2  
: Sequence 2, Application US/07649591B  
: Patent No. 5206161  
: GENERAL INFORMATION:  
: APPLICANT: Dennis Drayna and Daniel Eaton  
: TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 460 Point San Bruno Blvd  
: CITY: South San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94080  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: patin (Genentech)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/649,591B  
: FILING DATE: 19910201  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Hasak, Janet E.  
: REGISTRATION NUMBER: 28,616  
: REFERENCE/DOCKET NUMBER: 689  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 415/266-1896  
: TELEFAX: 415/952-9861  
: TELEX: 910/371-7168  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1749 bases  
: TYPE: NUCLEIC ACID

STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: hybridization probe  
LOCATION: 133 to 178  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: potential clip site  
LOCATION: 380 to 382  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: 41 to 106  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-649-591B-2  
Alignment Scores:  
Pred. No.: 7,12e-154 Length: 1749  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-4 (1-246) x US-07-649-591B-2 (1-1749)  
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Db 383 GCCTCCGCATCGTACTATGAACAGATCACTCACTAAATGAATCTATTCTTGGATAGAA 442  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAATCCCATTTGGATCCTCAITTTGAG 502  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 503 AAGTACCCACTCTATGTTTAAAGGTCTTCGAAAAGAACAAACAGCCAAAATGCATA 562  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 563 TGGATTGACTGTGAATCCATGCCAGAGAAATGGATCTCTCTGCTTTCTGCTTTGTGGTTC 622  
Qy 81 IleGlyHis----- 83  
Db 623 ATAGGCCATATAACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTT 682  
Qy 83 ----- 83  
Db 683 GTGGATTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAG 742  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGAGAAAGAACCGTTCTTTCTATGCGAACCAATCATTCGATCGGAACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyValaSerSerSerCys 123  
Db 803 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 862  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValIleValAlaLaser 143  
Db 863 TCGAAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGT 922  
Qy 144 PheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCTATTCATCTCCAG 982  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
Db 983 CATATAGTGTTCCTATATTCCTATATACGAAGTAAAGCAAGACCATGAGGAACCTGTCT 1042

QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
 Db 1043 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACTAGTAAATAATACCAGGTATACA 1102  
 QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyValAspAspTrpIleTyr 223  
 Db 1103 CATGCCATGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 1162  
 QY 224 AspLeuGlyIleLysTyrSerPhe----- 231  
 Db 1163 GATTGGGCATCAATAATTCTGTTTCACTTGAACCTTGCAGATACGGGACATACGGATTC 1222  
 QY 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
 Db 1223 TTGCTGCCGAGCGGTATCATCAACCCACCTGTAGAGAAGCTTTGGCGCTGTCTCTAAA 1282  
 QY 246 s 246  
 Db 1283 A 1283

RESULT 4

US-08-277-540-2  
 ; Sequence 2, Application US/08277540  
 ; Patent No. 5474901  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277,540  
 FILING DATE: 19-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/167727  
 FILING DATE: 15-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/959944  
 FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/649591  
 FILING DATE: 01-FEB-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689D1C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1749 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-277-540-2

Alignment Scores:  
 Pred. No.: 7,12e-154 Length: 1749  
 Score: 1272.00 Matches: 246  
 Percent Similarity: 81.73% Conservative: 0

Best Local Similarity: 81.73% Mismatches: 0  
 Query Match: 95.07% Indels: 55  
 DB: 1 Gaps: 2  
 US-09-980-881A-4 (1-246) x US-08-277-540-2 (1-1749)  
 QY 1 AlaserAlaserTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
 Db 383 GCCTCCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATCTTTGGATGAA 442  
 QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
 Db 443 TTATAACTGAGAGCATCCTGATATGCTTACAAAATCCACATTTGGATCTCTCATTTGAG 502  
 QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
 Db 503 AAGTACCACCTCTATGTTTAAAGGTTTCTGGAAAAGAACAAACAGCAAAATGCCATA 562  
 QY 61 TrpIleAspCysGlyIleHisAlaAtqGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
 Db 563 TGGATTGACTGTGAATCCATGCGAGAGATGGATCTCTCTGCTTTCTGCTTGTGGTTC 622  
 QY 81 IleGlyHis----- 83  
 Db 623 ATAGCCCATATACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCTCTGAGGTT 682  
 QY 83 ----- 83  
 Db 683 GTGGATTCTTATGTTATGCGCGTGTAAATGTGGACGGTTATGACTACTCATGGAATAAG 742  
 QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
 Db 743 AATCGAATGTGGAAAAGAACCGGTTCTTCTATCGGAACAATCAATTCATCGGAACAGAC 802  
 QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaLaserSerSerCys 123  
 Db 803 CTGNAATAGGAACITTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCATGC 862  
 QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
 Db 863 TCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACAGAGTGAAGGAGTGGCTAGT 922  
 QY 144 PheLeuArgArgAsnIleAsnGlnIleValAlaTyrIleSerMetHisSerTyrSerGln 163  
 Db 923 TTCTTGAGAGAAATATCAACAGATTAAGACATACATCAGCATGCAATTCATCTCCAG 982  
 QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
 Db 983 CATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAAAGACCATGAGAACTGTCT 1042  
 QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
 Db 1043 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAACTAGTAAAAAATACCAGGTATACA 1102  
 QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyValAspAspTrpIleTyr 223  
 Db 1103 CATGCCATGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 1162  
 QY 224 AspLeuGlyIleLysTyrSerPhe----- 231  
 Db 1163 GATTGGGCATCAATAATTCTGTTTCACTTGCAGATACGGGACATACGGATTC 1222  
 QY 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
 Db 1223 TTGCTGCCGAGCGGTATCATCAACCCACCTGTAGAGAAGCTTTGGCGCTGTCTCTAAA 1282  
 QY 246 s 246  
 Db 1283 A 1283  
 RESULT 5  
 US-08-430-787A-2  
 ; Sequence 2, Application US/08430787A



Patent No. 5593674  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA: 07/959944  
APPLICATION NUMBER: 14-OCT-1992  
FILING DATE: 01-FEB-91  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-430-787A-2

Alignment Scores:  
Pred. No.: 7,12e-154 Length: 1749  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-4 (1-246) x US-08-430-787A-2 (1-1749)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 383 GCCTCCGATCGTACTATGACAGTATCACTCACTAAATGAATCTATTCTGGATAGAA 442  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrIleHisIleGlySerSerPheGlu 40  
Db 443 TTTATTAACAGAGGCACTCTGATATGCTTACAAAAATCCACATTCCTCATTGAG 502  
Qy 41 LysTyrProLeuTyrValLeuValSerGlyIleValSerGlyIleGlnThrAlaLysAsnAlaIle 60  
Db 503 AAGTACCCTCTATGTTTAAAGGTTCTGGAAGAACAAACAGCCAAAATGCCATA 562  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 563 TGGATTGACTGTGGAATCCATGCGAGAGATGGATCTCTCTCTTCTCTGTGTGTTTC 622

Qy 81 IleGlyHis----- 83  
Db 623 ATAGCCATATAACTCAATTCATGGGATAATAGGCAATATACCAATCTCTCTGAGGCTT 682  
Qy 83 ----- 83  
Db 683 GTGGATTTCTATGTTATCCCGGTGGTTAATGTGGACGGTTATGACTACTCATCGSAAAAAG 742  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATGTGATCGGAACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123  
Db 803 CTGAATAGGAACCTTTGCTTCCAAACACATGGTGTGAGGAAGGTGCATCCAGTTCTCATGC 862  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValaLys 143  
Db 863 TCGGAACCTTACTGTGGACTTTTATCCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGT 922  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTCITGAGAAGAAATATCAACCAAGATTAAAGCATACATCAGCATTCATCTCTCCAG 982  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 983 CATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGACCATGAGGAACCTGTCT 1042  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1043 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAACCTAGTAAAAATACACAGGTATACA 1102  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspAspTrpIleTyr 223  
Db 1103 CATGCCATGGCTCAGAAACCTTATACCTAGTCTCTCGAGGTGGGACGATTGGATCTAT 1162  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1163 GATTTGGGCATCAATATTCGTTTACAAATTCGAGATACGGGCACATACGGATTTC 1222  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1223 TTGCTGCCGAGCGTTTACATCAACCCACCTGTAGAGAAGCTTTTGGCCGCTGTCTCTAAA 1282  
Qy 246 s 246  
Db 1283 A 1283  
RESULT 6  
US-08-782-760-5  
Sequence 5, Application US/08782760  
Patent No. 5948668  
GENERAL INFORMATION:  
APPLICANT: Hartman, Jacob  
APPLICANT: Fulga, Netta  
APPLICANT: Mendelovitch, Simona  
APPLICANT: Gorecki, Marian  
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
TITLE OF INVENTION: CARBOXYPEPTIDASE B  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,760
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,233
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
; US-08-782-760-5

Alignment Scores:
Pred. No.:      8,48e-69      Length:      927
Score:          610.00      Matches:     126
Percent Similarity: 60.50%      Conservative: 44
Best Local Similarity: 44.84%      Mismatches: 71
Query Match:      45.59%      Indels:     41
DB:                2          Gaps:        5

US-09-980-881a-4 (1-246) x US-08-782-760-5 (1-927)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
   |||||
Db 1 GCAGTGGACACAGCTACACCAAGTACCAACATCGGGAACGATTGAGCGCTGGATTCAA 60

Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
   |||||
Db 61 CAAGTGGCCACTGATATCCAGACCTTGCTACTCAGAGCGTCATTGGAAACCAATTGAA 120

Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
   |||||
Db 121 GGACGTAACATGATGCTCTCAAGATT--GGTAAACTAGACCCGAATAAGCCTGCCATC 177

Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
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Db 178 TTCATCGATTGGTGGTTTCCATGCAAGAGAGTGGATTCTCTCGCATTCGTGACGTGGTTT 237

Qy 81 Ile----- 81
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Db 238 GTGAGAGAGGCTGTCGGTACCTATTAATCAAGAGATCCACATGAACACGTTCTTAGATGAA 297

Qy 82 -----GlyHis----- 83
   :
Db 298 CTGGATTCTATGTTCTGCTGTGTCACACATTGATGCTATGCTACACCTGGACTAAG 357

Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
   |||||
Db 358 GACAGAAATGTGGAGAAAACCGCTCTACTATGCTGGAAGTTCCTGCTGGGTGTAGAC 417

Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
   |||||
Db 418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGC 474

Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
   |||||
Db 475 TCTGAACTTACTGTGGACACCGCCCGAGTCTGAAAAGAGACAAAGGCCCTTGGCAGAT 534
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;
;
; 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
; |||||
; 535 TTCATCGCAACACCTCTCCACCATCAGGCTTACCTGACCATCCACTCATACTACAG 594
;
; 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
; |||||
; 595 ATGATGCTCTACCTTACTCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654
;
; 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
; |||||
; 655 GCCTGTGTGAAGGTGGCGCAAGAGAGCTT---GCCACTCTGCATGCGCACCAAGTACACA 711
;
; 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
; |||||
; 712 TATGGCCAGGAGCTACAACTATCTCTGCTGCTGGGGATCTGACGACTGCTGCTTAT 771
;
; 224 AspLeuGlyIleLysTyrSerPheThrSerAsnProValGluLysLeuLeuProLeu 243
; |||||
; 772 GATCAGGAATCAAAATATCTCTTACCTTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830
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; 244 Ser 244
; |||
; 831 TCT 833

RESULT 7
PCT-US96-00995-5
; Sequence 5, Application PC/TUS9600995
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00995
; FILING DATE: 25-JAN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
; PCT-US96-00995-5

Alignment Scores:
Pred. No.:      8,48e-69      Length:      927
Score:          610.00      Matches:     126
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Percent Similarity: 60.50% Conservative: 44  
Best Local Similarity: 44.84% Mismatches: 71  
Query Match: 45.59% Indels: 41  
DB: 5 Gaps: 5

US-09-980-881A-4 (1-246) x PCT-US96-00995-5 (1-927)

QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGlu 20  
DB 1 GCAAGTGGACACAGCTACACCAAGTACACCAACTCGGAAACGATTGAGCGGTGGATTCAA 60  
QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
DB 61 CRAAGTGGCACTGATAATCCAGACCTTGCTCACTCAGAGCGTCAATGGAAACACCAITTTGAA 120  
QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
DB 121 GGAGCTAATCATGTCTCAAGATT---GGTAAAACTAGACCGAATAAGCGCTCCCATC 177  
QY 61 TrpIleAspCysGlyIleHisAlaArgGluTyrPheSerProAlaPheCysLeuTrpPhe 80  
DB 178 TTCTCATGATTGGTTTCCATCAAGAGAGTGGATTTCCTCGCATTCGTCAGTGGTTT 237  
QY 81 Ile----- 81  
DB 238 GTGAGAGGCTGTCGTACCTATATCAAGAGATCCATGAACAGCTTCTAGATGAA 297  
QY 82 -----GlyHis----- 83  
DB 298 CTGATTTCATGTTCTGCTGTGGTCAACATTGATGCTTGTCTACACCTGGACTAAG 357  
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
DB 358 GACAGATGTGAGAAAAACCGCTCTACTATGCTGGAGTTCCTGCTGGGTGTAGAC 417  
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
DB 418 CCCAACAGGAATTT---AATGCTGGCTGTGTGAAGTGGAGCTTCTCGAGTCCCTGC 474  
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValaSer 143  
DB 475 TCTGAACTTACTGTGGACCGCCAGAGTCTGAAAAGAGACAAAGCCCTGGCAGAT 534  
QY 144 PheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
DB 535 TTATCCGCAACAACCTCTCCACCATCAAGGCTCTGACCATCCACTCATACTACAG 594  
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
DB 595 ATGATGCTCTACCTTACTCTCTATGACTACAACTGCCTGAGAACTATAGGAATTGAT 654  
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
DB 655 GCCCTGGTGAAGGTGCGGCAAGGAGCTT---GCCACTCTGCTGTCGCAACCAAGTACACA 711  
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyr 223  
DB 712 TATGGCCCGAGGACTACAAATCTATCTGCTGCTGGGGGATCTGACGACTGGTCTTAT 771  
QY 224 AspLeuGlyIleLysTyrSerPheThrSerAsnProValGluLysLeuProLeu 243  
DB 772 GATCAGGGAATCAATATTCCTTTACCTTTGAACT---CCGGGATACAGGCTTCTTTGGCTT 830  
QY 244 Ser 244  
DB 831 TCT 833

RESULT 8

US-08-696-139-3  
; Sequence 3, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.

APPLICANT: Greenen, David P.  
APPLICANT: Hersberger, Charles L.  
APPLICANT: Larson, Jeffrey L.  
APPLICANT: Sterner, Jane L.  
APPLICANT: Zhang, Haichao  
TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/696.139  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,258  
FILING DATE: 16-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-8681  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..921  
US-08-696-139-3

Alignment Scores:  
Pred. No.: 3,48e-65 Length: 921  
Score: 582.00 Matches: 117  
Percent Similarity: 59.47% Conservative: 40  
Best Local Similarity: 44.32% Mismatches: 67  
Query Match: 43.50% Indels: 40  
DB: 1 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-696-139-3 (1-921)

QY 6 TyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArg 25  
DB 16 TATGAAAGTACAACTGGGAAACGATCGAGGCTTGACACTAGCAAGTCCACAGTAA 75  
QY 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45  
DB 76 AATCCAGACCTCATCTCGCACGCCATCGGAACATACATTTTAGGAAACAATATATAC 135  
QY 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65  
DB 136 CTCCTCAAGTT---GGCAAACTGGACCAATAAGCTGCCATTTTCATGAGCTGGT 192  
QY 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81  
DB 193 TTCCATGCCAGAAATGGATTTCCCATTCATTTGCCAGTGGTTTGTGTGAGAGGCTGTT 252  
QY 81 ----- 81

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Db 253 CTCACCTATGATGATGAGAGTCACATGACAGAAATTCCTCAACAAGCTAGACTTTTATGTC 312
Qy 82 -----GlyHis-----AsnArgMetTrpArg 88
Db 313 TTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGACCGAATGTGGAGA 372
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 373 AAGACCCGCTCTACCAATGCTGGAACTACCTGCGATTGGCACAGACCCCAACAGAAATTTT 432
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTrpCys 128
Db 433 ---GATGCTGGTGGTGACAACTGGAGCCCTCTACAGACCCCTGGATGAGACTTACTGT 489
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 490 GGATCTGCTGCAGAGTCTGAAAGAGAGACCAAGCCCTGGCTGATTTTATACGCAACAA 549
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 550 CTCCTCTCCATCAAGCATCTACGATCCACTCATACTACAGATGATACTCTACCCCT 609
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 610 TATTCCTATGATTACAACTCCCGAGAACAAATGCTGAGTTGAATACTGGCTAAGGCT 669
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 670 GCGGTGAAGAACTT---GCTACACTGTATGGCACCAAGTACATACATACGGGCCAGGAGCT 726
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyClyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 727 ACAACAAATCTATCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAA 786
Qy 229 TyrSerPheThr 232
Db 787 TATTCCTTCACC 798

RESULT 9
US-08-696-139-1
; Sequence 1, Application US/08696139
; Patent No. 5672496
; GENERAL INFORMATION:
; APPLICANT: Fayerman, Jeffrey T.
; APPLICANT: Greenen, David P.
; APPLICANT: Hershenberger, Charles L.
; APPLICANT: Larson, Jeffrey L.
; APPLICANT: Sterner, Jane L.
; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696.139
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,258
; FILING DATE: 16-NOV-1993
; ATTORNEY/AGENT INFORMATION:
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; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1215
US-08-696-139-1

Alignment Scores:
Pred. No.: 5,49e-65 Length: 1215
Score: 582.00 Matches: 117
Percent Similarity: 59.47% Conservative: 40
Best Local Similarity: 44.32% Mismatches: 67
Query Match: 43.50% Indels: 40
DB: 1 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-696-139-1 (1-1215)
Qy 6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
Db 310 TATGAGAAGTACAACAACACTGGGAAACGATCGAGCTTGGACTAAGCAAGTCACCAGTGAA 369
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 370 AATCCAGACCTCATCTCTCGCACAGCCATCGGAACACTACATTTTATAGAAAATATATATAC 429
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
Db 430 CTCCTCAAGTT---GCAAAACCTGGACCAATAAGCTGCCATTTTCATGGACTGTGGT 486
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
Db 487 TTCCATGCCAGAGAATGGATTTCCTCATGCTTTTCCATGCTTTTGCAGTGGTTTGTGAGAGAGGCTGT 546
Qy 81 ----- 81
Db 547 CTCACCTATGATATGAGAGTCATGACAGAAATTCCTCAACAAGCTAGACTTTTATGTC 606
Qy 82 -----GlyHis-----AsnArgMetTrpArg 88
Db 607 TTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGA 666
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 667 AAGACCCGCTCTACCAATGCTGGAACTACCTGCTGATTCGCACAGACCCCAACAGAAATTTT 726
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 128
Db 727 ---GATGCTGGTGGTGACAACTGGAGCCCTCTACAGACCCCTGCGATGAGACTTACTGT 783
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 784 GGATCTGCTGCAGAGTCTGAAAGAGACCAAGCCCTGGCTGATTTTATACGCAACAA 843
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 844 CTCCTCTCCATCAAGACATACCTGACGATCCACTCATCTACTACAGATGATACTCTACCCCT 903
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 904 TATTCCTATGATTACAAACTCCCGAGAACATGCTGAGTTGAATAACCTGGCTAAGGCT 963
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
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Db 964 GCGTGAAGAACTT---GCTACACTGTATGGCACCACAGTACACATACGGCCCGAGGCT 1020  
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspAspTrrPileTyrAspLeuGlyIleLys 228  
Db 1021 ACAACAATCTATCTCTCTCTGGGGCTCTGATGACTTGGGCTTATGACCAAGGAATCAAA 1080  
Qy 229 TyrSerPheThr 232  
Db 1081 TATTCCTTCACC 1092

RESULT 10

US-08-860-882A-67  
; Sequence 67, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HUW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 999 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-860-882A-67  
Alignment Scores:  
Pred. No.: 3 45e-63 Length: 999  
Score: 567.00 Matches: 111  
Percent Similarity: 58.36% Conservative: 46  
Best Local Similarity: 41.26% Mismatches: 72  
Query Match: 42.38% Indels: 40  
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-860-882A-67 (1-999)  
Qy 1 AlaSerAlaSerTyrTyrGluInTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 67 GCAACTGGTCACTCTTACGAGAGTACAAACAGTGGGAAACGATAGAGGCTTGGACTCAA 126

Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 127 CAAGTCGCCACTGAGAAATCCAGCCCTCATCTCTCGCATGTTATCGGAACACCAATTTGAG 186  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluInThrAlaLysAsnAlaIle 60  
Db 187 GGACGCGCTATTATCTCTCTGAAGGTT---GCAAAAGCTGGACAAATAAGCCTCCCAATT 243  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 244 TTCATGGAGCTGTGGTTTCCATGCCAGAGTGGATTCTCTCTGCAATTTCCAGTGGTTT 303  
Qy 81 Ile-----GlyHis----- 83  
Db 304 GTAAGAGAGGCTGTTCGTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 363  
Qy 82 -----GlyHis----- 83  
Db 364 TTAGACTTTTATGCTCGCTGTCTCAATATTTGATGGCTACATCTACACCTGGACCAAG 423  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 424 AGCCGATTTTGGAGAAAGACTCGCTCCACCACCTAGTCTAGCTGATTTGGCACAGAC 483  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 484 CCCAACAGAAATTTT---GATGCTGTGGTGTGAAATTTGGAGCCTCTCGAAACCCCTGT 540  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 541 GATGAAACTTACTGTGGACCTCGCCGACAGAGTCTGAAAAGAGAGACCAAGCCCTGGCTGT 600  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 601 TTCATCCCGCAACAAACTCTCTTCCATCAAGGCATATCTGACAACTCCATCTGTTCTCCAA 660  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
Db 661 ATGATGATCTACCTTACTCATATCTTACAACTCGGTGAGACAAATGCTGAGTTGAAT 720  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 721 GGCCTGGCTAAAGCTACTGTGAAAGAACTT---GCCTCACTGCACGCGCACCAAGTACACA 777  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspAspTrpIleTyr 223  
Db 778 TATGCGCCGGAGCTACAACTATCTCTGCTGTGGGGCTCTGACAGCTGGGCTTAT 837  
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232  
Db 838 GACCAAGGATCAGATATTCCTTCACC 864

RESULT 11

US-09-011-769A-50  
; Sequence 50, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.  
BLAKEY, David C.  
DAVIES, David H.  
HENNAM, John F.  
HENNEQUIN, Laurent F.A.  
MARSHAM, Peter R.  
DOWELL, Robert I.  
DOWELL, Robert I.  
TITLE OF INVENTION: Chemical Compounds  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pillsbury Madison & Sutro, LLP  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.

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; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
;
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
;
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..987
;
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..987
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-011-769A-50

Alignment Scores:
Pred. No.: 3,456-63 Length: 999
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 4 Gaps: 5

US-09-980-881A-4 (1-246) x US-09-011-769A-50 (1-999)
Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGlu 20
Db 67 GCNACTGCTACTCTTAGCAGAGTACACCAAGTGGGNAAGCATAGAGGCTTGACTCAA 126
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 127 CAAGTCGCCAGTGAAGTCCAGCCCTCATCTCTCGCAGTGTATCGGAACACACATTTGAG 186
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 187 GGACGCGGTATTACCTCCTCAAGGTT---GGCAAAAGCTGACAAAATAAGCCGTCATT 243
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPhe 80
Db 244 TTCATGACTGTGTTTCCATGCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 303
Qy 81 Ile-----GlyHis----- 81
Db 304 GTAAGAGAGGCTGTTTCGTACCTATGAGCGTGAGATCCAAAGTACAGAGCTTCTCGACAAG 363
Qy 82 -----GlyHis----- 83
Db 364 TTAGACTTTTATGCTGCTGCTGCTCAATATTGATGGCTACATCTACACCTGACCAAG 423
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 424 AGCCGATTTTGGAGAAGACTCGCTCCACCCATAGCTAGCTAGCTGATCTGATGGACAGAC 483
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;
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; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
;
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
;
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..987
;
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..987
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-011-769A-50

Alignment Scores:
Pred. No.: 3,456-63 Length: 999
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 4 Gaps: 5

US-09-980-881A-4 (1-246) x US-09-011-769A-50 (1-999)
Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGlu 20
Db 67 GCNACTGCTACTCTTAGCAGAGTACACCAAGTGGGNAAGCATAGAGGCTTGACTCAA 126
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 127 CAAGTCGCCAGTGAAGTCCAGCCCTCATCTCTCGCAGTGTATCGGAACACACATTTGAG 186
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 187 GGACGCGGTATTACCTCCTCAAGGTT---GGCAAAAGCTGACAAAATAAGCCGTCATT 243
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPhe 80
Db 244 TTCATGACTGTGTTTCCATGCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 303
Qy 81 Ile-----GlyHis----- 81
Db 304 GTAAGAGAGGCTGTTTCGTACCTATGAGCGTGAGATCCAAAGTACAGAGCTTCTCGACAAG 363
Qy 82 -----GlyHis----- 83
Db 364 TTAGACTTTTATGCTGCTGCTGCTCAATATTGATGGCTACATCTACACCTGACCAAG 423
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 424 AGCCGATTTTGGAGAAGACTCGCTCCACCCATAGCTAGCTAGCTGATCTGATGGACAGAC 483
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Qy 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123
Db 484 CCACACAGAAATTTT---GATGCTGTGGTGTGAAATTTGGAGCCTCTCGAAACCCCTGT 540
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 541 GATGAAACTTACTGTGGAGCTGGCGAGACTCTGAAAGAGGAGACCAAGGCCCTGGCTGAT 600
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 601 TTCATCGCAACAACTCTCTTCCATCAAGGCATATCTGACAACTCCACTCGTACTCCCAA 660
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 661 ATGATGATCTACCTTACTCATATGCTTACAAACTCGTGAACAACATGCTGAGTTGAT 720
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
Db 721 GCCCTGGCTAAAGCTACTGTGAAGAACTT---GCCCTACTGCACGGCACCAGTACACA 777
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrIleTyr 223
Db 778 TATGCCCGGAGGCTACACAACTATCTCTGCTGCTGGGGGCTCTGACGACTGGGCTTAT 837
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232
Db 838 GACCAGGAATCAGATATCTCTTCAACC 864

RESULT 12
US-08-860-882A-64
; Sequence 64, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOI, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM, JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1053 bases
; TYPE: nucleic acid
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Thu Oct 28 07:16:17 2004

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-860-882A-64

Alignment Scores:
Pred. No.: 3,76e-63 Length: 1053
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-860-882A-64 (1-1053)
QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
DB 67 GCAACTGGTCACTCTTACGAGAGTACAAACAGTGGGAACGATAGAGCTTGGACTCAA 126
QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
DB 127 CAAAGTCCCACTGAGAAATCCAGCCCTCATCTCGCAGTGTATCGGAACCAATTTGAG 186
QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 187 GGACGGCTATTACCTCTGAAGGTT--GGCAAGCTGGACAAAATAGCGCTGCCATT 243
QY 61 TrpIleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTrpPhe 80
DB 244 TTCATGCACTGTGGTTTTCATGTCAGAGAGTGATTTCTCTGTCATTCTGCCAGTGGTTT 303
QY 81 Ile----- 81
DB 304 GTAAGAGAGCTGTTCTGATCTATGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG 363
QY 82 -----GlyHis----- 83
DB 364 TTAGACTTTTATGCTGCTGCTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 423
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 424 AGCCGATTTTGGAGAAAGACTCGCTCCACCATACTGGATCTAGCTGGCATTTGCCACAGAC 483
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGluAlaSerSerSerCys 123
DB 484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATGGAGCCCTCTCGAAACCCCTGT 540
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 541 GATGAAACTTACTGTGGACCTGCCGAGAGTCTGMAAAGGAGACCAAGGCCCTGGCTGAT 600
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 601 TTCATCGCAACAAACTCTCTTCATCAAGGCATATCTGACAAATCCACTCGTACTCCCAA 660
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 661 ATGATGATCTACCCCTTACTCATATGCTTCAAACTCGGTGAGAACAAATGCTGAGTTGAAI 720
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 721 GCCCTGGCTAAAGCTACTGTGAAGAACTT---GCCTCACTGCGACGCAACCAAGTACACA 777
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspTrpIleTyr 223
DB 778 TATGCCCCGGGAGCTACAAACATCTATCTGCTGCTGGGGCTCTGACGACTGGCTTAT 837
QY 224 AspLeuGlyIleLysTyrSerPheThr 232
DB 838 GACCAAGGAATTCAGATATTCCTTACC 864

RESULT 13
US-09-011-769A-46
; Sequence 46, Application US/09011769A
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; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1053 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1047
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..1047
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-011-769A-46

Alignment Scores:
Pred. No.: 3,76e-63 Length: 1053
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-09-011-769A-46 (1-1053)
QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
DB 67 GCAACTGGTCACTCTTACGAGAGTACAAACAGTGGGAACGATAGAGCTTGGACTCAA 126
QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
DB 127 CAAAGTCCCACTGAGAAATCCAGCCCTCATCTCGCAGTGTATCGGAACCAATTTGAG 186
QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 187 GGACGGCTATTACCTCTGAAGGTT--GGCAAGCTGGACAAAATAGCGCTGCCATT 243
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Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 244 TTCATGGAGCTGTGGTTTCCAGCCAGAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 303
Qy 81 Ile----- 81
Db 304 GTAAGAGAGGCTGTTTCGTACCTATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAA 363
Qy 82 -----GlyHis----- 83
Db 364 TTAGACTTTTATGCTCCTGCTGCTCAATATGATGCTACATCTACACCTGGACCAAG 423
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 424 AGCCGATTTTGGAGAAAGACTCGCTCCACCATATCTGGATCTAGCTGCAATGGCACAGAC 483
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAATTTGGAGCTCTCGAAACCCCTGT 540
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 541 GATGAACCTTACTGTGGACCTGCCGACAGTCTGAAAGAGAGACCAAGGCCCTGGCTGAT 600
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 601 TTCATCCGCAACAACCTCTCTCCATCAAGGCATATCTGACAATCCACTCGTACTCTCCAA 660
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 661 ATGATGATCTACCTTCTATCTATGCTTACAACTCGGTGAGACAATGCTGAGTTGAT 720
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
Db 721 GCCCTGGCTAAAGCTACTGTGAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 777
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
Db 778 TATGCCCGGAGCTACACAACATCTATCTCTGCTGGGGGCTCTGACGACTGGGCTTAT 837
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232
Db 838 GACCAGGAATCAGATATCTCTTACC 864
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## RESULT 14

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US-08-860-882A-56
; Sequence 56, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAW, JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESS: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/860,882A
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; FILING DATE: JUNE 23, 1997
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; CLASSIFICATION: 424
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; ATTORNEY/AGENT INFORMATION:
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; NAME: DONALD J. BIRD
```

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; REGISTRATION NUMBER: 25,323
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; REFERENCE/DOCKET NUMBER: 9901/238653
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; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (202) 861-3027
```

```
; TELEFAX: (202) 822-0944
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; TELEX: 6174627 CUSH
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; INFORMATION FOR SEQ ID NO: 56:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1263 bases
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; TYPE: nucleic acid
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; STRANDEDNESS: single
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; TOPOLOGY: linear
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US-08-860-882A-56
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## Alignment Scores:

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Pred. No.: 5.08e-63 Length: 1263
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5
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US-09-980-881A-4 (1-246) x US-08-860-882A-56 (1-1263)
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Qy 1 AlaSerIleSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 325 GCAACAGACACAGATTATGAGAAAGTACACAAAGTGGGAAACGATAGAGGCTTGACCTCAA 384
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 385 CAAGTCCCACTGAGAAATCCAGCCCTCATCTCTCGCAGTGTATCGGAACACCATTTGAG 444
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 445 GGACGCGCTATTACCTCTCTGAAGTT---GGCAAGCTGGACAAATAAGCCTGCCAAT 501
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 502 TTCATGGAGCTGTGGTTTCCATGCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 561
Qy 81 Ile----- 81
Db 562 GTAAGAGAGGCTGTTTCGTACCTATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAA 621
Qy 82 -----GlyHis----- 83
Db 622 TTAGACTTTTATGCTGCTGCTGCTCAATATGATGGCTACATCTACACCTGACCAAG 681
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 682 AGCCGATTTTGGAGAAAGACTCGCTCCACCATATCTGGATCTAGCTGCAATGGCACAGAC 741
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 742 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAATTTGGAGCTCTCGAAACCCCTGT 798
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 799 GATGAACCTTACTGTGGACCTGCCGACAGTCTGAAAGAGAGACCAAGGCCCTGGCTGAT 858
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 859 TTCATCCGCAACAACCTCTCTCCATCAAGGCATATCTGACAATCCACTCGTACTCTCCAA 918
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 919 ----- 942
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919	ATGATGATCTACCCTTACTCATATGTCTTCAAACTCGGTGAGAACAAATGCTGAGTTGAAT	978
D <sub>B</sub>		
184	LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr	203
Q <sub>y</sub>	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::	
D <sub>B</sub>		
979	GCCCTGGCTTAACCTACTGTGAAGAAGACTT---GCCTCAC TG CAGCGCACCAAGTACACA	1035
D <sub>B</sub>		
204	HISGLYHISGLYSERGLUTHRYLEUTYRLEUAlAProGLYGlyGLYAspAspTrpIleTyr	223
Q <sub>y</sub>	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::	
D <sub>B</sub>		
1036	TATGGCCCCGGAGCTACACAATCTATCTGCTGTGGGGGCTCTGACGACTGGGCTTAT	1095
D <sub>B</sub>		
224	ASPLeUGLYILELysTYRSerPheThr	232
Q <sub>y</sub>	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::	
D <sub>B</sub>		
1096	GACC AAGGAATCAGATATTCC TT CACC	1122
D <sub>B</sub>		

## RESULT 15

RECORDED 15  
 US-09-011-769A-38  
 Sequence 38, Application US/09011769A  
 Patent No. 6436691  
 GENERAL INFORMATION:  
 APPLICANT: SLATER, Anthony M.  
 BLAKEY, David C.  
 DAVIES, David H.  
 HENNAW, John F.  
 HENNEQUIN, Laurent F.A.  
 MARSHAM, Peter R.  
 DOWELL, Robert I.  
 TITLE OF INVENTION: Chemical Compounds  
 NUMBER OF SEQUENCES: 87  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pillsbury Madison & Sutro, LLP  
 STREET: 1100 New York Ave., N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.

MIF 000000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS word  
  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA: PCT/GB96/01975  
APPLICATION NUMBER: 13-AUG-1996  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 16-AUG-1995  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ. ID NO. 38.

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, INFORMATION FOR SEQ ID NO: 38:
,   SEQUENCE CHARACTERISTICS:
,     LENGTH: 1263 base pairs
,     TYPE: nucleic acid
,     STRANDEDNESS: single
,     TOPOLOGY: linear
,   MOLECULE TYPE: other nucleic acid
,   SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-011-769A-38

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Alignment Scores:	
Pred. NO.:	5.08e-63
Score:	567.00
Percent Similarity:	58.3%
Best Local Similarity:	41.2%
Query Match:	42.3%
DB:	4
	Gaps: 5
	Indels: 40
	Mismatches: 72
	Conservative: 46
	Matches: 111
	Length: 1263

US-09-980-881A-4 (1-246) x US-09-011-769A-38 (1-1263)

Qy	1	AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAenGluIleTyrSerTrrpIleGlu	20
Db	325	GCACAGGACACAGTTATGAGAGGTACACAAGTGGGAAACGATAGAGGCTTGGACTCA	384
Qy	21	PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu	40
Db	385	CAAGTCGCCACTGAGAACTCCAGCCCTCATCTCGCAGTGTATTATCGGAACCAATTTGAG	444
Qy	41	LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIle	60
Db	445	GGACGGCGCTATTACCTCTCTGAAGGTT--GGCAAGCTGGGACAAAATAAGCTCGCAT	501
Qy	61	TrpIleAspCysGlyIleHisAlaArgGluTrrpIleSerProAlaPheCysLeuTrrpPhe	80
Db	502	TTCTAGCATGTGGTTCATGCCAGAGAGTGGATTCTCTCGCATCTGCCAGTGGTTT	561
Qy	81	Ile-----	81
Db	562	GTAAGAGAGGCTGTTCTGTACTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAG	621
Qy	82	-----GlyHis-----	83
Db	622	TTAGACTTTTATGTCCTGGCTGTGCTCAATATATGATGGCTACATCTACCTGGACCAAG	681
Qy	84	AsnArgMetTrpArgLysAenArgSerPheTyrAlaAsnAenHisCysIleGlyThrAsp	103
Db	682	AGCGATTTTGGAGAAGAAGACTCGCTCCACCCATACCTGGATCTAGCTGTCATTGGCAGAC	741
Qy	104	LeuAsnArgAenPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys	123
Db	742	CCCAACAGAAATTTT--GATGTGGTGTGTGTGAATTTGGAGCCCTCTCGAAACCCCTGT	798
Qy	124	SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer	143
Db	799	GATCAAACTTACTGTGGACCTGCGCGAGAGTCTGAAAAGGAACCAAGGCCCTTGGCTGAT	858
Qy	144	PheLeuArgArgAenIleAenGlnIleLysAlaTyrIleSerMethHisSerTyrSerGln	163
Db	859	TTATCGCGCAACAACTCTCTTCCATCAAGGCATATCTGCAATCCACTCGTACTCCCAA	918
Qy	164	HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer	183
Db	919	ATGATGATCTACCCCTTACTCATATGCTTACAAACTCGGTGAGAACCAATGCTGAGTTGAAT	978
Qy	184	LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAenThrArgTyrThr	203
Db	979	GCCTGTGCTAAAGCTACTGTGAAGAAGACTT--GCCTACTGCGCGGCACCAAGTACACA	1035
Qy	204	HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr	223
Db	1036	TATGCCCGGGAGACTACAAACAATCTATCTCTGTCTGCTGGGGGCTCTGACGACTGGCTTAT	1095
Qy	224	AspLeuGlyIleLysTyrSerPheThr	232
Db	1096	GACCAAGGAATCAGATATTCCTTCACC	1122

Search completed: October 27, 2004, 02:01:25  
Job time : 71.6271 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 27, 2004, 01:54:23 ; Search time 1178.4 Seconds  
(without alignments)  
1070.424 Million cell updates/sec

Title: US-09-980-881A-4  
Perfect score: 1338  
Sequence: 1 ASASYEQYHSLNEIYSWIE.....IKSYFTSPNPVKKLPLSLK 246

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US0980881@cgn\_1\_1034\_@runat\_26102004\_084115\_7269  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FCAPOP=6 -FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Alignment Scores:

Result No.	Score	Query Match	Length	DB ID	Description
1	1289.5	96.4	1625	9	US-09-813-133A-1
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3	1272	95.1	1728	9	US-09-880-107-2396
4	1248.5	93.3	1344	16	US-10-115-479-69
5	1248.5	93.3	1743	16	US-10-115-479-67
6	1177	88.0	1272	15	US-10-379-836-1
7	902	67.4	1400	9	US-09-925-302-24
8	902	67.4	1400	10	US-09-925-302-24
9	869.5	65.0	1037	16	US-10-115-479-63
10	830.5	62.1	1132	16	US-10-115-479-65
11	556.5	41.6	1302	17	US-10-477-515-1
12	556.5	41.6	1311	13	US-10-200-344-9
13	556.5	41.6	1993	15	US-10-274-639-33
14	556.5	41.6	1993	16	US-10-333-574-33
15	554.5	41.4	1907	18	US-10-757-262-127
16	552	41.3	1254	14	US-10-229-546-3
17	552	41.3	1622	14	US-10-229-546-1
18	552	41.3	1622	15	US-10-429-802-21
19	552	41.3	1622	16	US-10-430-503-12
20	552	41.3	1622	16	US-10-262-511-71
21	552	41.3	1622	16	US-10-641-643-1020
22	552	41.3	1633	15	US-10-341-434-187
23	552	41.3	1740	14	US-10-116-802-95
24	550.5	41.1	1125	9	US-09-888-615-2
25	550.5	41.1	1332	15	US-10-176-306-75
26	550.5	41.1	1603	15	US-10-176-306-73
27	549	41.0	1870	9	US-09-910-059-112
28	549	41.0	2154	9	US-10-608-710-3
29	549	41.0	2154	9	US-09-910-059-124
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31	543.5	40.6	1826	15	US-10-252-157-453
32	533.5	39.9	991	16	US-10-383-201-93
33	525.5	39.3	2128	13	US-10-200-344-13
34	523.5	39.1	1295	17	US-10-363-829-148
35	492	36.8	1200	14	US-10-200-910-7
36	492	36.8	1200	18	US-10-843-130-7
37	471.5	35.2	1050	13	US-10-200-344-11
38	465.5	34.8	1254	9	US-09-925-297-58
39	465.5	34.8	1260	15	US-10-345-680-66
40	465.5	34.8	1260	16	US-10-236-174-16
41	465.5	34.8	1279	16	US-10-236-417-217
42	465.5	34.8	1290	16	US-10-236-417-219
43	465.5	34.8	1311	14	US-10-200-910-5
44	465.5	34.8	1311	16	US-10-257-174-15
45	465.5	34.8	1311	17	US-10-451-821-1

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

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Pred. No.:      1.39e-159      Length:      1625
Score:          1289.50      Matches:      244
Percent Similarity: 92.42%      Conservative: 0
Best Local Similarity: 92.42%      Mismatches: 2
Query Match:      96.38%      Indels:      18
DB:              9          Gaps:      1

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 359 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAATCTATCTTGGATAGAA 418
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 419 TTTATAACTGAGAGGCATCTGATATGCTTCAAAAATCCCAATGGCATCTCATTTGAG 478
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 479 AAGTACCCCACTCTATGTTTAAAGGTTTCTGAAAAGAACAGCAGCCAAAATGGCCATA 538
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 539 TGGATTGACTGTGGAATCCATGCCAGAGATGGAATCTCTCTGCTTCTGTTGGTTTC 598
Qy 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
Db 599 ATAGGCCATAATCGAATGTGGAGAACACCGTCTTCTATGCGAACCAATCATTTGCATC 658
Qy 101 GlyThrAspLeuAsnArgMetTrpArgLysAsnArgSerPheTyrAlaLysAsnThr 120
Db 659 GGAACAGACCTGAAATGAGAACGAAACCGTCTTCTATGCGAACCAATCATTTGCATC 718
Qy 121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
Db 719 TCCTCATGCTCGAAACCTACTGTGGACTTTATCTGAGTCAGAACCAAGAGTGAAGCA 778
Qy 141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
Db 779 GTGGTAGTTTCTTGAGAGAAATATCAACAGATTAAAGCAAGACCATTCATTC 838
Qy 161 TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
Db 839 TACTCCAGCATATAGTGTTCATATTCCTATACAGAAATTAAGCAAGACCATTCATTC 898
Qy 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
Db 899 GAACTGTCTCTAGTAGCCAGTGAAGCAGTTCTGCTGCTATTTAGAAAAATAGTAAAAATACC 958
Qy 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAsp 220
Db 959 AGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCAT 1018
Qy 221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe 231
Db 1019 TGGATCTATGATTTGGGCATCAAAATATTCGTTTTACAATTTGAACCTTCGAGATACGGGCACA 1078
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLe 243
Db 1079 TAGCGATTCTTGCTCGCGAGCGTTACATCAACCCACCTGTAGAGAAGCTTTTGGCGCT 1138
Qy 243 uSerLeuLys 246
Db 1139 GTCTCTAAA 1148

```

## RESULT 2

```

US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

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; TITLE OF INVENTION: USBS THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-212-877-1

```

```

Alignment Scores:      1.39e-159      Length:      1625
Pred. No.:            1289.50      Matches:      244
Score:                92.42%      Conservative: 0
Percent Similarity: 92.42%      Mismatches: 2
Best Local Similarity: 96.38%      Indels:      18
Query Match:          14          Gaps:      1
DB:

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```
US-09-980-881A-4 (1-246) x US-10-212-877-1 (1-1625)
```

```

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 359 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAATCTATCTTGGATAGAA 418
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 419 TTTATAACTGAGAGGCATCTGATATGCTTCAAAAATCCCAATGGCATCTCATTTGAG 478
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 479 AAGTACCCCACTCTATGTTTAAAGGTTTCTGAAAAGAACAGCAGCCAAAATGGCCATA 538
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 539 TGGATTGACTGTGGAATCCATGCCAGAGATGGAATCTCTCTGCTTCTGTTGGTTTC 598
Qy 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
Db 599 ATAGGCCATAATCGAATGTGGAGAACACCGTCTTCTATGCGAACCAATCATTTGCATC 658
Qy 101 GlyThrAspLeuAsnArgMetTrpArgLysAsnArgSerPheTyrAlaLysAsnThr 120
Db 659 GGAACAGACCTGAAATGAGAACGAAACCGTCTTCTATGCGAACCAATCATTTGCATC 718
Qy 121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
Db 719 TCCTCATGCTCGAAACCTACTGTGGACTTTATCTGAGTCAGAACCAAGAGTGAAGCA 778
Qy 141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
Db 779 GTGGTAGTTTCTTGAGAGAAATATCAACAGATTAAAGCAAGACCATTCATTC 838
Qy 161 TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
Db 839 TACTCCAGCATATAGTGTTCATATTCCTATACAGAAATTAAGCAAGACCATTCATTC 898
Qy 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
Db 899 GAACTGTCTCTAGTAGCCAGTGAAGCAGTTCTGCTGCTATTTAGAAAAATAGTAAAAATACC 958
Qy 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAsp 220
Db 959 AGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCAT 1018
Qy 221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe 231
Db 1019 TGGATCTATGATTTGGGCATCAAAATATTCGTTTTACAATTTGAACCTTCGAGATACGGGCACA 1078
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLe 243
Db 1079 TAGCGATTCTTGCTCGCGAGCGTTACATCAACCCACCTGTAGAGAAGCTTTTGGCGCT 1138
Qy 243 uSerLeuLys 246
Db 1139 GTCTCTAAA 1148

```

Db 1079 TACGATTTCTGCTCCGGAGCGTTACATCAACCCACCTGTAGAGAAGCTTTTGGCGCT 1138  
Qy 243 uSerLeuLys 246  
Db 1139 GTCTCTAAAA 1148

RESULT 3

US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

Alignment Scores:

Pred. No.: 3,17e-157 Length: 1728  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 9 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-880-107-2396 (1-1728)

Qy 1 AlaSerAlaSerTyrTrpGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGlu 20  
Db 362 GCCTCGCATCGTACTATGAACAGTATCACTCAATAATGAAATCTATTCTTGGATAGAA 421  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 422 TTTTAACTGAGAGGCATCTGTATGCTTTACAAAATCAACATTTGGATCCTCATTTGAG 481  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 482 AAGTACCCACTCTATGTTTAAAGGTTCTCGAAAAGAACAAACAGCCAAAATGCCATA 541  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 542 TGGATTGACTGTGGAATCCATGTCAGAGAATGGATCTCTCTGCTTTCTGCTTGTGGTTC 601  
Qy 81 IleGlyHis----- 83  
Db 602 ATAGGCCATATACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTT 561  
Qy 83 ----- 83  
Db 662 GTGATTTCTATGTATGCGGTGGTTAATGTGACGGTTATGACTACTCATCGAAAAAG 721  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 722 AATCGAATGTGGAGAAGAACCGTTCTTTCTATGCGAACCAATCATTTGCATCGGAACAGAC 781  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123

Db 782 CTGAATAGGAACCTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCATGC 841  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 842 TCGAAAACCTTACTGTGGACTTTATCCCTAGTCAGAACCCAGAGTGAGGCACTGGCTAGT 901  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 902 TTCTTGAGAGAATATCAACCAGATTAAAGCATACATCAGCATGCATTATCATCTCCAG 961  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 962 CATATAGTGTTCATATTTCTATACAGAAAGTAAAGCAAGCAAGCAAGCAAGCAAGCAAG 1021  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1022 CTAGTAGCCAGTGAAGCAGTTCTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 1081  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyr 223  
Db 1082 CATGCCATGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCATTTGGATCTAT 1141  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1142 GATTTGGGCATCAAAATATTCTGTTTACAATTTGAACCTTCGAGATACGGGCACATACGATTC 1201  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1202 TTGTCGCGGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAA 1261  
Qy 246 s 246  
Db 1262 A 1262

RESULT 4

US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shalomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03

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; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.:      2,71e-154      Length:      1344
Score:          1248.50      Matches:      244
Percent Similarity: 79.74%      Conservative: 0
Best Local Similarity: 79.74%      Mismatches: 2
Query Match:     93.31%      Indels:      60
DB:              16      Gaps:      3

US-09-980-881A-4 (1-246) x US-10-115-479-69 (1-1344)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 373 GCCTCCGCATCGTACTATGAACAGATATCACTCACTAAATGAATCAATCTCTTGATAGAA 432
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 433 TTTATACTGAGGCGCATCTCGATATGCTTACAAAAATCCACATTTGGATCTCTCATTTGAG 492
Qy 41 LysTyrProLeuTyrValLeuLys-----ValSerGlyLysGluGlnThr 55
Db 493 AAGTACCACCTCTATGTTTTAAAGGGTTCTTTGAGCGGGTTTCTGGAAAGAAACAAGCA 552
Qy 56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla 75
Db 553 GCCAAAATGCCATATGGAATGACTGTGGAATCCATGCCAGAGATGGATCTCTCTGCT 612
Qy 76 PheCysLeuTrpPheIleGlyHis----- 83
Db 613 TTCTGCTTGTGGTTCATAGGCGCATATACTCAATTTCTATGGGATAATAGGCAATATACC 672
Qy 83 ----- 83
Db 673 AATCTCTGAGGCTTGTGGATTTCTATGTTATGGGTGGTTAATGTGGATGGTTATGAC 732
Qy 84 -----AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98
Db 733 TACTCATGAAAAAGAAATCGAATGTGGAGAGAAACCGTTCTTCTTCTATGCGAACAATCAT 792
Qy 99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisIleTrpCysGluGluGlyAla 118
Db 793 TGCATCGGAACAGACCTGAATAGGAACCTTCTTCCAAACACTGGTGTGAGGAAGGTGCA 852
Qy 119 SerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
Db -----

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Db 853 TCAGTTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCAAGAGTG 912
Qy 139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaIleSerMet 158
Db 913 AAGGCAGTGGCTAGTTTCTTTGAGAAGAAATATCAACCCAGATTAAAGCATACATCAGCATG 972
Qy 159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178
Db 973 CATTCATACTCCCGAGCATATAGTGTTCCTATATTCCTATACAGAGTAAAGCAAGAC 1032
Qy 179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198
Db 1033 CATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAATTAGTAAA 1092
Qy 199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly 218
Db 1093 AATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTCGGAGGTGGG 1152
Qy 219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 1153 GACGATTGGATCTATGATTGGGCGATCAAAATATTCGTTTACAATTGAACCTTCGAGATACG 1212
Qy 232 -----ThrSerAsnProProValGluLysLeuLe 241
Db 1213 GGACATACCGATTCTTGTGCTCGCGGCGGTATACATCAAAACCCACCTGTAGAGAAGCTTTT 1272
Qy 241 uProLeuSerLeuLys 246
Db 1273 GCGGCTGCTCTAAAA 1288

RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Caeman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; FILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934

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;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,657  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,678  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,687  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; PRIOR APPLICATION NUMBER: 60/285,325  
;; PRIOR FILING DATE: 2001-04-19  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 198  
;; SEQ ID NO 67  
;; LENGTH: 1743  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (20)..(1304)  
US-10-115-479-67

Alignment Scores:  
Pred. No.: 4,12e-154 Length: 1743  
Score: 1248.50 Matches: 244  
Percent Similarity: 79.74% Conservative: 0  
Best Local Similarity: 79.74% Mismatches: 2  
Query Match: 93.31% Indels: 60  
DB: 16 Gaps: 3

US-09-980-881A-4 (1-246) x US-10-115-479-67 (1-1743)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 362 GCCTCGCATCTGCTACTATGACAGATATCACTCACTAAATGAATCTATTCTTGGATAGAA 421  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 422 TTATTAACCTGAGAGGCATCTGATATGCTTACAAAATCCACATTTGGATCCTCATTTGAG 481  
Qy 41 LysTyrProLeuTyrValLeuLys-----ValSerGlyLysGluGlnThr 55  
Db 482 AAGTACCCACTCTATGTTTAAAGGGTTCTTTGACGAGCTTCTGGAAGAAACAAGCA 541  
Qy 56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla 75  
Db 542 GCCAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGATGGATCTCTCTGCT 601  
Qy 76 PheCysLeuTrpPheIleGlyHis----- 83  
Db 602 TTCTGCTTGTGTTTCATAGGCCATATAAATCACTTCTATGGGATAATAGGGCAATATACC 661  
Qy 83 ----- 83  
Db 662 AATCTCTGAGGCTTGTGGATTTCTATGTTATGCCAGTGTGTAATGGATGTTATGAC 721  
Qy 84 -----AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98  
Db 722 TACTCATGNAAGAAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGGAACAATCAT 781  
Qy 99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla 118  
Db 782 TGCATCGGAACACACCTGAATAGAACTTTGCTTCCAAACACTGGTGTGAGGAAGTGCA 841  
Qy 119 SerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138  
Db 842 TCCAGTTCTTCATGCTCGGAACCTACTGTGGACTTTATCTGAGTCAGAACACAGAGTG 901  
Qy 139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158  
Db 902 AAGCAGTGGCTAGTTCTTGGAGAGAAATATCAACAGATTAAGCATACATCAGCATG 961

Qy 159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178  
Db 962 CATTCACTACCCAGCATATAGTGTTCCTCATATTCATACAGAGTAAAGCAAGAC 1021  
Qy 179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198  
Db 1022 CATGAGGAACCTGCTCTAGTAGCCAGTGAACAGTTCGTGCTATTTGAGAAATTTAGTAA 1081  
Qy 199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly 218  
Db 1082 AATACCAAGGTATACACATGGCCATGGCTCAGAACTTTATACCTAGCTCTGGAGTGG 1141  
Qy 219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231  
Db 1142 GACGATTGGATCTATGATTGGGCATCAAAATATTTCGTTTACAAATTGAACATTCGAGATACG 1201  
Qy 232 -----ThrSerAsnProProValGluLysLeuLe 241  
Db 1202 GGCACATACGGATTCTTGTCTCCGAGCGTTTACATCAAAACCCACCTGTAGAGAAAGCTTTT 1261  
Qy 241 uProLeuSerLeuLys 246  
Db 1262 GCCGCTGTCTCTAATA 1277

# RESULT 6

US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: TAFI  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1272  
; TYPE: DNA  
; ORGANISM: Papio hamadryas  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1269)  
US-10-379-836-1

Alignment Scores:  
Pred. No.: 7,14e-145 Length: 1272  
Score: 1177.00 Matches: 228  
Percent Similarity: 78.41% Conservative: 8  
Best Local Similarity: 75.75% Mismatches: 10  
Query Match: 87.97% Indels: 55  
DB: 15 Gaps: 2

US-09-980-881A-4 (1-246) x US-10-379-836-1 (1-1272)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 343 GCCTCGCATCTGCTACTATGACAGATATCACTCACTAAATGAATCTATTCTTGGATAGAA 402  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 403 CTATAACTGAGAAGTATCTCTGATATGCTTACAAAATCCACATTTGGATCCTCTATGAG 462  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 463 AAGCAGTGGCTAGTTCTTAAAGGTTTCTGGAAGAAACAACAGCCAAATGCAATG 522  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80

```

Db 523 TGGATTGACTGTGGAATCCAGCCAGAGATGGATCTCCCTGCTTCTTGCTTGTGGTTC 582
Qy 81 IleGlyHis----- 83
Db 583 ATAGGCCATATACTGAATACTACGGGATAATAGGGAATATACCAATCTTCTGAGGCAT 642
Qy 83 ----- 83
Db 643 GTGGAATTTCTATGTTATGTCAGTGGTTAATGTGAGTGGTTATGACTACTCATNGGAAAAAG 702
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 703 AATCGAATGTGGAGAGAACCGTCTTCTTATCGGACCAATCGTTGCATCGGACAGAC 762
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 763 CTGAACAGGAACCTTGGCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTTCTCATGC 822
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 823 TCGGAACCTTACTGTGGACTTTATCTCGAGTCAGAACCAAGCGGCGGTGCTAAT 882
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 883 TTCTTGAGAGAAATATCAACCAATTAAGCATACATCAGCATGCATTCTATCTCCAG 942
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db 943 CATATCGTGTTCCTATATTCCTATCTCGAAGCAAAAGCAAGACACGAGGAATTGTCT 1002
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
Db 1003 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTTCAGAAAAACCAAGTAAATAATATCAGTATACA 1062
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
Db 1063 CATGGCCGTGGCTCAGAAACCTTATACCTAGCTCTCGAGGTGCGGAGTTGATCTAT 1122
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231
Db 1123 GATTGGGCATCAATATTCGTTTACAATTCGAGATACGGGCAAAATACGGATTC 1182
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246
Db 1183 TTGCTGCTGAGCTTACATCAAAACCCACTTGTAAAGACGCTTTTGGCGTGTCTCTAAA 1242
Qy 246 s 246
Db 1243 A 1243

```

## RESULT 7

```

US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)

```

```

; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

```

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Alignment Scores:
Pred. No.: 1.99e-108 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservative: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 67.41% Indels: 56
DB: 9 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)
Qy 65 GlyLeuHisAlaArgGluTyrIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 83
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTCTCTGCTTGTGGTTTCATAGGCCATATA 69
Qy 83 ----- 83
Db 70 ACTCAATCTTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTAT 129
Qy 84 -----AsnArgMetTr 87
Db 130 GTTATGCGCGTGGTTAATGTGGATGGTTATGAACCTACTCATCGAAAAAGAAATCGAATGTG 189
Qy 87 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 107
Db 190 GAGAAAGAACCGTCTTCTTCTATCGAACCAATCATTCATCGAACACAGACCTGAATAGGAA 249
Qy 107 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 127
Db 250 CTTTGTCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309
Qy 127 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 147
Db 310 CTGTGAGCTTTATCTCTGAGTCAGAACCAAGTGAAGCAGTGGTAGTTCTTGTGGAAG 369
Qy 147 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 167
Db 370 AAATATCAACCAAGTAAAGCATACATCAGCATGCATTCATCTACTCCAGCATATAGTGT 429
Qy 167 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 187
Db 430 TCCATATTCCTATACAGAAAGTAAAGCAAGCAACATGAGAAACTGTCTCTAGTAGCCAG 489
Qy 187 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisG1 207
Db 490 TGAAGCAGTTTCGTGCTATTGAGAAAACTAGTAAAAAATACCAGGTATACATGSCCATGG 549
Qy 207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyI1 227
Db 550 CTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTGGATCTATGATTTGGGCAT 609
Qy 227 eLysTyrSerPhe----- 231
Db 610 CAAATATTCGTTTACAACTTGAATTCGAGATACGGGCACATACGGATTTCTGTGCGGGA 669
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246
Db 670 GCGTTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGTGTCTCTATAAA 719

```

## RESULT 8

```

US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08

```



;; PRIOR APPLICATION NUMBER: 60/124,270  
;; PRIOR FILING DATE: 1999-03-12  
;; NUMBER OF SEQ ID NOS: 896  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 24  
;; LENGTH: 1400  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (25)  
;; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

Alignment Scores:  
Pred. No.: 1,99e-108 Length: 1400  
Score: 902.00 Matches: 181  
Percent Similarity: 76.05% Conservative: 0  
Best Local Similarity: 76.05% Mismatches: 1  
Query Match: 67.41% Indels: 56  
DB: 10 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)

Qy 65 GlylleHieAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheilleGlyHis--- 83  
Db 10 GGATCCATGCCAGANATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGCCCATATA 69  
Qy 83 ----- 83  
Db 70 ACTCAATTCATGGGATAATAGGCAATATACCAATCTCTCGAGGCTGTGATTTCTAT 129  
Qy 84 -----AsnArgMetTr 87  
Db 130 GTTATGCCGGTGTTTAATCTGGATGTTATGAACACTACTCATCGAAAAAGATCGAATGG 189  
Qy 87 pArglyAsnArgSerPheTyrAlaAsnAenHisCysilleGlyThrAspLeuAsnArgAs 107  
Db 190 GAGAAGAACCGTTCTTTCTATGCGAACATCATTCGATCGGACAGACCTGAATAGGAA 249  
Qy 107 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 127  
Db 250 CTTTGCTTCCAAACACTGGTGAGGAGGTGCTCAGTCCAGTCTCATGTCGGAACCTTA 309  
Qy 127 rCysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 147  
Db 310 CTGTGGACTTTATCTCTGAGTCAGAACCAAGTGAAGGAGGCTGTGTCTTCTTGAGAAG 369  
Qy 147 gAenlleAsnGlnlleLysAlaTyriLeSerMetHisSerTyrSerGlnHisIleValPh 167  
Db 370 AATATCAACAGATTAAAGCATACATCAGCATGCAATTCATATCCAGCATATAGTGT 429  
Qy 167 eProTySerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 187  
Db 430 TCCATATTCCTATACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAG 489  
Qy 187 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyThrHisGlyHisGl 207  
Db 490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCGGTATACACATGGCCCGG 549  
Qy 207 ySerGluThrLeuTyLeuAlaProGlyGlyGlyAspAspTrpIleTyAspLeuGlyI 227  
Db 550 CTCAGAACCTTATACCTAGCTCTCGAGGTGGGACGATTGGATCTATGATTTGGGCAT 609  
Qy 227 eLysTySerPhe----- 231  
Db 610 CAATATTCGTTTACAATTTGAGATACGGGCACATACCGATTCTTGCTGCCGGA 669  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 670 GCGTTACATCAAAACCCACCTGTGAGAAGCTTTTGGCGCTGTCTCTTAAAAA 719

RESULT 9

US-10-115-479-63  
;; Sequence 63, Application US/10115479  
;; Publication No. US20040006205A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Li, Li  
;; APPLICANT: Gerlach, Valerie L.  
;; APPLICANT: Liu, Xiaohong  
;; APPLICANT: Miller, Charles E.  
;; APPLICANT: Spytek, Kimberly A.  
;; APPLICANT: Zerhusen, Bryan D.  
;; APPLICANT: Pena, Carol E.A.  
;; APPLICANT: Shenoy, Suresh G.  
;; APPLICANT: Zhong, Haihong  
;; APPLICANT: Smithson, Glendda  
;; APPLICANT: Casman, Stacie J.  
;; APPLICANT: Boldog, Perenc L.;  
;; APPLICANT: Voss, Edward  
;; APPLICANT: Vernet, Corine  
;; APPLICANT: MacDougall, John A.  
;; APPLICANT: Rastelli, Luca  
;; APPLICANT: Anderson, David W.  
;; APPLICANT: Zhong, Mei  
;; APPLICANT: Mezes, Peter S.  
;; APPLICANT: Furtak, Katarzyna  
;; APPLICANT: Patturajan, Meera  
;; APPLICANT: Burgess, Catherine E.  
;; APPLICANT: Malyanker, Uriel M.  
;; APPLICANT: Shimkets, Richard A.  
;; APPLICANT: Taupier, Raymond J.  
;; APPLICANT: Edinger, Shlomit R.  
;; APPLICANT: Mazur, Ann  
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
;; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
;; CURRENT APPLICATION NUMBER: US/10/115,479  
;; CURRENT FILING DATE: 2002-11-18  
;; PRIOR APPLICATION NUMBER: 60/281,136  
;; PRIOR FILING DATE: 2001-04-03  
;; PRIOR APPLICATION NUMBER: 60/281,863  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/281,906  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/282,934  
;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,657  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,678  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,687  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; PRIOR APPLICATION NUMBER: 60/285,325  
;; PRIOR FILING DATE: 2001-04-19  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 198  
;; SEQ ID NO 63  
;; LENGTH: 1037  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (41)..(1007)  
US-10-115-479-63  
Alignment Scores:  
Pred. No.: 2,45e-104 Length: 1037  
Score: 869.50 Matches: 180  
Percent Similarity: 68.18% Conservative: 0  
Best Local Similarity: 68.18% Mismatches: 2  
Query Match: 64.99% Indels: 82  
DB: 16 Gaps: 2



503	Db	AAGTACCCACTCTATGTTTTAAAGGGTTTTCTTTGAGCAGCGTTTTCTGTGAAAGAACACGA	562
56	Qy	AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla	75
563	Db	GCCAAAATGCCATATGGATTGACTGTGGAAATCCATGCCAGAGATGGATCTCTCTGCT	622
76	Qy	PheCysLeuTrpPheIleGlyHis	83
623	Db	TTCTGCTTGTGGTTTCATAGGCCATATAACTCAATTTCTATGGGATAATAGGGCAATATACC	682
83	Qy	-----	83
683	Db	AATCTCTGAGGCTTGTGGATTTCTATGTTATGCCGTGTTAATGTGGATGGTTATGAC	742
84	Qy	-----AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis	98
743	Db	TACTCATGGAAAAAGAAATCGAAATGTGGAGAAAGAACCGTTCTTCTATGGCAACAATCAT	802
99	Qy	CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla	118
803	Db	TGCATCGGAACAGACCTGAATAGAACTTTGGCTTCCAAACACTGGTGTGAGGAAGTGCA	862
119	Qy	SerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal	138
863	Db	TCCAGTTCTCATGCTCGGAAACCTACTGTGGACTTTATCCTCAG	907
139	Qy	LysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMet	158
907	Db	-----	907
159	Qy	HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp	178
907	Db	-----	907
179	Qy	HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys	198
907	Db	-----	907
199	Qy	AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly	218
908	Db	-----TCAGAAACCTTTATACCTAGCTCTCTGGAGGTGG	940
219	Qy	AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe	231
941	Db	GACGATGGATCTATGATTTGGGCATCAATATTTTCGTTACAAATTGAATTCGAGATACG	1000
232	Qy	-----ThrSerAsnProProValGluLysLeuLe	241
1001	Db	GGCACATACGGATTTCTGTGCCGGAGCGTTTACATCAAAACCCACTCTGTAGAGAGCTTTT	1060
241	Qy	uProLeuSerLeuLys	246
1061	Db	GCCGCTGTCTCTAAAA	1076

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RESULT 11
US-10-477-515-1
; Sequence 1, Application US/10477515
; Publication No. US20040136976A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN ZINC CARBOXYPEPTIDASE B-LIKE PROTEIN
; FILE REFERENCE: LIO355 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/477,515
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/292,329
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-515-1

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Alignment Scores:			
Pred. No.:	8,98e-63	Length:	1302
Score:	556.50	Matches:	113
Percent Similarity:	53.45%	Conservative:	42
Best Local Similarity:	38.97%	Mismatches:	77
Query Match:	41.59%	Indels:	58
DB:	17	Gaps:	5
US-09-980-881A-4 (1-246) x US-10-477-515-1 (1-1302)			
Qy	6	TyrGluGlnTyrHisSerLeuAanGluIleTyrSerTrpIleGluPheIleThrGluArg	25
Db	406	TATGAAGTTTATCACCTCTTAGAAGAAATTCAAAATTGGATGCATCATCTGTAATAAAACT	465
Qy	26	HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr	45
Db	466	CACTCAGGCCTCATTCACATGTTCTCTATTGGAGATCATATGAGGGAAGATCTCTTTTT	535
Qy	46	ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly	65
Db	526	ATTTTAAAGCTG--GGCAGCAGATCAGACTCAAAGAGCTGTTTGGATAGACTGTGGT	582
Qy	66	IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle	81
Db	583	ATTTCATCGAAGATGATTGTTCTGCTGCTCTTTGTGTCAGTGGTTGTAAAAAGAGCTCTT	642
Qy	81	-----	81
Db	643	CTAAATATTAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTCTATATC	702
Qy	82	-----GlyHisAsnArgMetTrpArg	88
Db	703	ATGCCTGTGTTAAAGCTCGATGATACCATTTTAGTTGGACCAATGATCAATTTGGAGA	762
Qy	89	LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsn	108
Db	763	AAACAAGGTCACAGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGG	822
Qy	109	AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys	128
Db	823	AAAGTGAG--TGGTGTGATGAAGGAGCTTCTATGCACCCCTGTGTGATGACACATCTGT	879
Qy	129	GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn	148
Db	880	GGCCCTTTTCAGAAATCTGAGCCGGAAGTGAAGCTGTAGTAACTTCTTCGAAACAC	939
Qy	149	IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro	168
Db	940	AGAAAGCACATTTAGGGCTTATCTCTCTCTTCATGCATATGCTCAGATGTTTACTGTATCCC	999
Qy	169	TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu	188
Db	1000	TATTTCTTACAAATATGCAACAATTCCCAATTTTAGATGTGTGAATCTGCAGCTTATAAA	1059
Qy	189	AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer	208
Db	1060	GCTGTGAATGCCTTCTAGTCAGTA--TACGGGTACGATACAGATATGGACGACCTCC	1116
Qy	209	GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys	228
Db	1117	ACAAGTTGTATGTAGCTCTGTTAGCTCAATGGATTGGGCTACAAAAATGGAATACCT	1176
Qy	229	TyrSerPhe-----	231
Db	1177	TATGCATTTGCTTTTCGAACACTAGTGACATGGATATTTTGGATTTTACTCCCGAGATG	1236
Qy	232	-ThrSerAsnProValGluLysLeu	240
Db	1237	CTCATCAACCCACTGTACAGAACTA	1264

RESULT 12  
US-10-200-344-9

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; Sequence 9, Application US/10200344
; Publication No. US20020173641A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020173641A1el Human Carboxypeptidases and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.: 9,08e-63 Length: 1311
Score: 556.50 Matches: 113
Percent Similarity: 53.45% Conservative: 42
Best Local Similarity: 38.97% Mismatches: 77
Query Match: 41.59% Indels: 58
DB: 13 Gaps: 5

US-09-980-881A-4 (1-246) x US-10-200-344-9 (1-1311)

Qy 6 TyrGluGlnTyrHisSerLeuAsnGluileTyrSerTrpIleGluPheIleThrGluArg 25
Db 406 TATGAAGTTTATCATCTCTTGAAGAAATTCAAATTCGATCATCTCGAATAAACT 465
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 466 CACTCAGCGCTCAITTCATCATGTTCTTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT 525
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
Db 526 ATTTTAAAGCTG---GGCAGAGATCAGCATCAAGAGCTGTTGGATAGACTGTGGT 582
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
Db 593 ATTCATGCAAGAATGATGTTGGTCTGCTCTTTTGTCTAGTGGTTTGTAAAGAAGCTCTT 642
Qy 81 ----- 81
Db 643 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 702
Qy 82 -----GlyHisAsnArgMetTrpArg 88
Db 703 ATGCTGTGTTAACTCGATGGATACCATTTTAGTTGGACCAATGATCGATTTGGAGA 762
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 763 AAAACAAGGTCAAGGAATCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGG 822
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerGluThrTyrCys 128
Db 823 AAAGTGAAG---TGGTGTGATGAAGAGCTTCTATGCACCCCTTGTGATGCACATACCTGT 879
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
Db 880 GGCCCTTTTCAGAAATCTGACCGGAGTGAAGGCTGTAGCTAATCTTCCTCGAAACAC 939
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 940 AGAAAGCACATTAGGGCTTATCTCTCTCTTTTCATGTCATATGTCATGTCAGATGTTACTGCC 999
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Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGlu 188
Db 1000 TATTTTACAAATATGACCAATTTCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1059
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1060 GCTGTGAATCAGCTTCAGTCAGTA---TAGGGGTAGCATACAGATATGACCAAGCTCC 1116
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 1117 ACAACGTTGTATGTAGCTCTGTAGTCAATGATGGCTGCTACAAAAATGGAATACCT 1176
Qy 229 TyrSerPhe----- 231
Db 1177 TATGCAATTTGCTTCGAACTACGTGACACTGGATATTTTGGATTTTACTCCCCAGAGATG 1236
Qy 232 -ThrSerAsnProValGluLysLeu 240
Db 1237 CTATCAACACCCTGTACAGAACTA 1264

RESULT 13
US-10-274-639-33
; Sequence 33, Application US/10274639
; Publication No. US20030232349A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGEANE, Angelo M.; GANDHI, Ameena R.
; APPLICANT: HAFALIA, April J.A.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra; TRIBOULEY, Catherine M.
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.
; APPLICANT: NGUYEN, Darniel B.; LEE, Ernestine A.
; APPLICANT: KHAN, Farrah A.; YUE, Henry
; APPLICANT: AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.
; APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Juming; THANGAVELU, Kavitha
; APPLICANT: DING, Li; KEARNEY, Liam
; APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.
; APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.
; APPLICANT: BURFORD, Neil; WALIA, Narinder K.
; APPLICANT: LAL, Preeti G.; LEE, Sally
; APPLICANT: TODD, Stephen; LO, Terence P.
; APPLICANT: TANG, Y. Tom; ELLIOTT, Vicki S.
; APPLICANT: AZIMZAI, Valda; LU, Yan
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0167 USA
; CURRENT APPLICATION NUMBER: US/10/274,639
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/22397
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/220,063
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,680
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,544
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,717
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/225,988
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/227,568
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 1993
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030232349A1 4948403CB1
US-10-274-639-33
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Alignment Scores:		1.78e-62	Length:	1993
Pred. No.:	Score:	556.50	Matches:	113
Percent Similarity:		53.45%	Conservative:	42
Best Local Similarity:		38.97%	Mismatches:	77
Query Match:		41.59%	Indels:	58
DB:		15	Gaps:	5
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Qy	26	HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTrpProLeuTyr	45	
Db	803	CACTCAGGCCTCATTCACATGTTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT	862	
Qy	46	ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly	65	
Db	863	ATTTTAAAGCTG---GGCAGACGATCACCAGCTCAAAGAGCTGTTGGATAGACTGTGT	919	
Qy	66	IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle	81	
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Qy	81	-----	81	
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Qy	189	AlaValArgAlaIleGluLysThrSerLysAsnThrArgTrpThrHisGlyHisGlySer	208	
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Qy	209	GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys	228	
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RESULT 14				
US-10-333-574-33				
; Sequence 33, Application US/10333574				
Publication No. US200400091962A1				
GENERAL INFORMATION:				
APPLICANT: INCYTE GENOMICS, INC.				
APPLICANT: DELEGANE, Angelo M.; GANDHI, Ameena R.				
APPLICANT: HAFALIA, April J.A.; LU, Dyrung Aina M.				
APPLICANT: ARVIZO, Chandra S.; TRIBOULEY, Catherine M.				
APPLICANT: DAS, Debopriya; KALLICK, Deborah A.				
APPLICANT: NGUYEN, Damiel B.; LEE, Ernestine A.				
APPLICANT: KHAN, Farrah A.; YUE, Henry				
APPLICANT: AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.				
APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi				
APPLICANT: YANG, Junning; THANGAVELU, Kavitha				
APPLICANT: DING, Li; KEARNEY, Liam				
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.				
APPLICANT: BAUGHN, Mariah R.; BOROMSKY, Mark L.				
APPLICANT: BURFORD, Neil; CHAWLA, Narinder K.				
APPLICANT: LAL, Preeti G.; LEE, Sally				
APPLICANT: TODD, Stephen; LO, Terence P.				
APPLICANT: TANG, Y. Tom; ELLIOTT, Vicki S.				
APPLICANT: AZIMZAI, Yalda; LU, Yan				
TITLE OF INVENTION: PROTEASES				
FILE REFERENCE: PI-0167 USN				
CURRENT APPLICATION NUMBER: US/10/333,574				
CURRENT FILING DATE: 2003-01-21				
PRIOR APPLICATION NUMBER: US 01/22397				
PRIOR FILING DATE: 2001-07-17				
PRIOR APPLICATION NUMBER: US 60/220,063				
PRIOR FILING DATE: 2000-07-21				
PRIOR APPLICATION NUMBER: US 60/221,680				
PRIOR FILING DATE: 2000-07-28				
PRIOR APPLICATION NUMBER: US 60/223,544				
PRIOR FILING DATE: 2000-08-04				
PRIOR APPLICATION NUMBER: US 60/224,717				
PRIOR FILING DATE: 2000-08-11				
PRIOR APPLICATION NUMBER: US 60/225,988				
PRIOR FILING DATE: 2000-08-16				
PRIOR APPLICATION NUMBER: US 60/227,568				
PRIOR FILING DATE: 2000-08-23				
NUMBER OF SEQ ID NOS: 42				
SOFTWARE: PERL Program				
SEQ ID NO 33				
LENGTH: 1993				
TYPE: DNA				
ORGANISM: Homo sapiens				
FEATURE:				
NAME/KEY: misc_feature				
OTHER INFORMATION: Incyte ID No: 4948403CB1				
US-10-333-574-33				
Alignment Scores:		1.78e-62	Length:	1993
Pred. No.:	Score:	556.50	Matches:	113
Percent Similarity:		53.45%	Conservative:	42
Best Local Similarity:		38.97%	Mismatches:	77
Query Match:		41.59%	Indels:	58
DB:		16	Gaps:	5
US-09-980-881A-4 (1-246) x US-10-333-574-33 (1-1993)				
Qy	6	TyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArg	25	
Db	743	TATGAAGTTTATCACTCTTACAGAAATTCAAAATTTGGATGCATCATCTGAATAAACT	802	
Qy	26	HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTrpProLeuTyr	45	
Db	803	CACTCAGGCCTCATTCACATGTTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT	862	
Qy	46	ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly	65	
Db	863	ATTTTAAAGCTG---GGCAGACGATCACCAGCTCAAAGAGCTGTTGGATAGACTGTGT	919	
Qy	66	IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle	81	
US-10-333-574-33				
; Sequence 33, Application US/10333574				



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Qy 229 TyrSerPhe----- 231
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Qy 232 -ThrSerAsnProValGluLysLeu 240
Db 1453 CTCATCAAAACCCACCTGTACAGAACTA 1480

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